

# WEBS ON THE WEB (WOW): 3D VISUALIZATION OF ECOLOGICAL NETWORKS ON THE WWW FOR COLLABORATIVE RESEARCH AND EDUCATION

Ilmi Yoon<sup>1</sup>, Rich Williams<sup>2</sup>, Eli Levine<sup>1</sup>, Sanghyuk Yoon<sup>1</sup>, Jennifer Dunne<sup>3</sup>, Neo Martinez<sup>4</sup>

<sup>1</sup>San Francisco State University

<sup>2</sup>National Center for Ecological Analysis and Synthesis

<sup>3</sup>Santa Fe Institute

<sup>4</sup>Cornell University

*This paper describes information technology being developed to improve the quality, sophistication, accessibility, and pedagogical simplicity of ecological network data, analysis, and visualization. We present designs for a WWW demonstration/prototype web site that provides database, analysis, and visualization tools for research and education related to food web research. Our early experience with a prototype 3D ecological network visualization guides our design of a more flexible architecture design. 3D visualization algorithms include variable node and link sizes, placements according to node connectivity and trophic levels, and visualization of other node and link properties in food web data. The flexible architecture includes an XML application design, FoodWebML, and pipelining of computational components. Based on users' choices of data and visualization options, the WWW prototype site will connect to an XML database (Xindice) and return the visualization in VRML format for browsing and further interactions.*

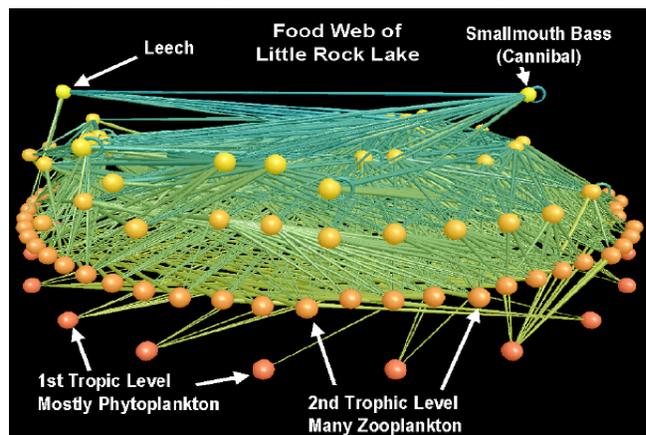
## 1. INTRODUCTION

The study of complex networks pervades social and natural sciences and is central to researchers' efforts to understand large systems of dynamically interacting components [Crosby97][Freeman00][Strogatz01]. In ecology, such network analysis is most developed in food-web research [Pimm91][Polis96][Williams00]. Food webs describe who eats whom among species within a habitat, and food webs have long been a central paradigm for studying biocomplexity in many arenas beyond ecology [Wilbur97][Strogatz01]. Ecologists have found that complexity of food-web networks is central to their stability, functioning, and dynamics [Pimm91][Polis96][Williams00].

To date, food-web data sets contain tens to hundreds of functionally distinct nodes and hundreds to thousands of links between them. Rarely if ever is a single researcher an expert in all the organisms in a large ecological network. Instead, constructing a single food web usually requires synthesizing the contributions of many different researchers familiar with different parts of the ecosystem. Due to the difficulty of synthesizing complex networks, collection of such networks through a standardized collaborative system that supports the analysis and visualization of the data will greatly contribute to ecological research.

This research requires the synthesis of structural and functional information about one or many networks. Structure relates to which organisms occur in the network and whom the organisms interact with. Function relates to the details of the dynamics of

network interactions such as the size of trophic flows that travel along network links and the functional responses of consumers to the density of their resources. Structural issues around ecological and other networks have been largely pursued separate from functional issues [Strogatz01]. Our Internet-accessible database, analysis and visualization tools are designed to integrate structural and functional network research while facilitating scientific collaboration, data mining, and theory development by a wider array of ecologists and other network researchers. An accessible repository of information on a species' biology and interspecies interactions would also help researchers of particular subsystems to explore the broader ecological context



**Fig. 1** – FoodWeb3D Visualization of Little Rock Lake, Wisconsin [Martinez91]. FoodWeb3D users visualize the structure and nonlinear dynamics of empirical and model food webs, rotate the image, highlight food chain paths, delete species, and adjust the color and size of the nodes and links.

surrounding their focal systems.

Visualization and simulation allow concepts regarding complex networks to be more clearly and compellingly explored. The interactive display of networks in response to user inputs that manipulate model properties and visualization characteristics helps researchers gain new insights into the structure and dynamics of complex food webs. 3D visualization of is particularly valuable because 2D visualizations of such complex networks are usually overwhelmed with too much information, becoming cluttered and visually confused [Winemiller90]. Also, 3D visualization embraces users' intuitive connection between physical quantities and visible volumes, which are spatially more compact than 2D areas because volume varies as the cubed root of the spheres' radii whereas area only varies as the square root of circles' radii.

Our project develops information technology needed to greatly increase the quality, sophistication, accessibility, and pedagogical effectiveness of ecological network data, analysis, and visualization. We are pursuing these aims by developing a WWW demonstration/prototype web site that provides database, analysis, and visualization tools for research and education goals related to food web research. Our current prototype, FoodWeb3D, allows users to visualize empirical and model food webs, rotate the image, highlight food chain paths, delete species, and adjust the color and size of the nodes and links. Figure 1 presents a FoodWeb3D visualization of the food web of Little Rock Lake, Wisconsin [Martinez91], a network with 92 nodes and 997 links.

Part two discusses the value of these tools within the food-web research community and then reviews relevant research on network visualization, with a focus on web-based visualization and 3D formats on the web. Part three explains the algorithms used for food-web visualizations, the flexible architecture design of the integrated and collaborative tools, the WWW prototype site design, and the on-going implementations and results. Finally, we conclude with a discussion of future directions.

## 2. BACKGROUND

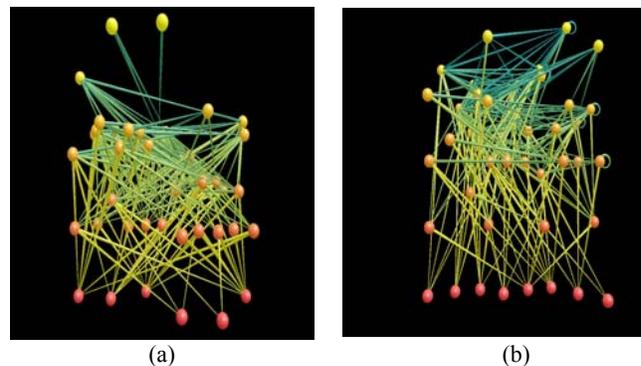
### 2.1 Uses within the Food-web Research Community

Structural studies of networks including food webs depicting co-occurring species and their feeding relations frequently focus on whether networks display "small-world" characteristics (short path lengths and high clustering [Watts99]) and "scale-free" degree distributions (distribution of nodes among classes of linkage frequencies [Barabasi00]). Two recent studies have examined food webs for these types of

characteristics and have come to very different conclusions. Montoya and Solé [Montoya02] examined 4 food webs and concluded that food webs, like many other networks, display small-world and scale-free characteristics. Camacho et al. [Camacho02], however, looked at a set of 7 food webs and concluded that they do not display small-world characteristics (due to low clustering) and have exponential, rather than scale-free, degree distributions.

These conflicting results were resolved by examining a larger array of data. Dunne, Williams, and Martinez studied 16 high-quality food webs including the previously analyzed webs [Dunne02]. Their results show that while some food webs have small-world and scale-free structure, most do not if they exceed a relatively low level of connectance, the number of links within a food web that are realized (links/species<sup>2</sup>). Path lengths, clustering, and degree distributions are sensitive to size and complexity of networks, which becomes apparent when a large number of networks are compared. If a centralized food-web database was available, it is less likely that the first two studies would have made the mistake of over-generalizing results from a small number of food-web data sets and this research could have proceeded more quickly and efficiently.

Visualizations have obvious value as an educational tool, but also have great potential to facilitate novel research findings. Comparison of visualizations of some widely-studied empirical data sets and food webs constructed using the niche model [Williams00] quickly made clear some significant disparities between the empirical data and the model (Fig. 2a & b). Figure 2b shows an example of a model web built using the same



**Fig. 2** – Visualization of an empirical food web (a) and a food webs constructed using the niche model (b) illustrated both known and previously unrecognized disparities between the empirical data and the model. For example, it was known that the niche model overestimated food-chain length (note the greater number of nodes at higher trophic levels in (b) than in (a)). However, it was not known that the niche model underestimated the fraction of species that are herbivores (note the 10 nodes at the 2<sup>nd</sup> “herbivorous” trophic level above the 1<sup>st</sup> “basal” trophic level in (a) compared to the 4 herbivores in (b)).

basic parameters (size and connectance) as the empirical food web shown in figure 2a. Visualization suggested that fewer herbivores (trophic level = 2, red-orange nodes) occurred in the model webs than in the empirical data. Before this suggestion, herbivores were largely overlooked in network analyses of food webs. However, subsequent statistical tests motivated by visualizations demonstrated that the visual discrepancies represented a systematic failing of the niche model.

## 2.2 Network Visualizations on the WWW

Information visualization and Human Computer Interface research groups have done intensive research on visualizing network data on diverse subjects including telecommunication networks [Koutsofios99] and monitoring WWW browsing activities [Eick96], [Gershon96]. Node and link diagrams, although natural choices to display this class of data, are easily overwhelmed with too much information, becoming cluttered and visually confused. Three solutions (1. Dynamic interaction and parameter focusing, 2. Clever node positioning, 3. 3D visualization) help solve these problems [Eick96]. Recent network visualization applications have been developed with these solutions in mind. However, these functionalities are mainly supported for offline research purposes and then the resulting 2D images are captured and published on the Web as a separate process. Not only is this a tedious process when posting more than a few images, static 2D images may obscure important findings of the original user.

Social network researchers share and publish papers on the WWW. For the effective presentation of complex networks in online journals, several online network visualization programs have been made available. Pajek [Pajek] and UCINET [UCINET] use 2D interactive visualization and Mage [Mage] provides 3D network visualization. These approaches focus on placing nodes using simple geometry in 2D/3D spaces and then providing simple interactions such as rotation, translation, and zooming. They do not offer integrated support of simultaneous analysis, visualization, and interactive simulation along with sophisticated database interfaces.

Providing interactive 3D network visualization on the WWW is complicated beyond similar visualizations offline by client-server architectural requirements including the 3D formats supported by WWW browsers. All three major approaches for WWW 3D visualization have problems that have prevented dominance by one format. For example, the Web3D Consortium approved VRML as a standard WWW 3D format that supports complex 3D primitives and features [VRML]. However, VRML typically needs to be combined with Java through Script node or EAI (External Authoring Interface) to implement non-trivial animation and user interfaces like

slides, buttons, etc. This combination occasionally causes VRML to be unstable and have compatibility problems between different VRML players such as Cosmo player, Cortona and OpenWorld [Walsh99][Marti97][Deihl00]. X3D is an XML application and a successor of VRML. X3D and MPEG4 inherit the VRML scene graph structure and attempt to resolve problems of VRML such as scalability, compatibility, streamability, and stable combination with 2D & 3D, but specifications are not finalized yet.

Another ubiquitous format, Java Applet, is more stable for supporting graphical user interfaces. But JVM (Java Virtual Machine) embedded in both IE (Microsoft Internet Explorer) & NS (Netscape Navigator) is jdk 1.1 and doesn't support any advanced features like SWING (Advanced and more stable Graphics User Interface Packages supported from jdk1.2). Java applets can be used for 2D or 3D visualization, but it is a general purpose programming approach and may not be a suitable approach for 3D visualizations with complex structures and sophisticated graphics properties such as shading, texture and transparency. The lack of support for 3D graphics features forces such features to be implemented from scratch, and may heavily oversize the class file's byte code that needs to be transmitted over network. Java3D was developed to resolve these issues, but Java3D is another huge size library and only supported as a Plug-in and is not directly supported by the JVM of the WWW browsers.

Proprietary formats require their own plug-in to be installed in the user's WWW browser. Plug-ins allow sophisticated graphics and full use of the local machine's computation power but require downloading. Users avoid such downloads unless they have a strong interest in the plug-in application. However, users with much more serious research interests consider the more powerful and responsive user interface and 3D graphics of stand-alone/plugin applications well worth the effort of buying and/or downloading them.

Due to the advantages and disadvantages of these three different approaches, WWW users have developed their own preferences and this has prevented 3D visualization from being very widely spread among researchers or students. One of the design goals of our project is to increase the use of 3D network visualization by employing a flexible underlying XML structure and pipeline architecture that provides diverse solutions (options of different formats such as VRML, java applet or plugin) suited to a wide range of users.

Recent development of XML applications on the WWW extends the scope of WWW usages in depth and breadth. For example, MathML [MathML] and Scalable Vector Graphics (SVG) [SVG] add versatility to the WWW for communities of specific interests. Chemical Markup Language (CML) is a good example of a XML

application for scientific visualization [CML]. It is called "HTML plus molecules" and provides capabilities far beyond the limited confines of conventional HTML documents. Molecular documents often contain thousands of different, very detailed objects. CML supports interactive 2D/3D molecular structures displayed online using a CML browser, java applet or plug-in.

XML allows the definition of DTDs or schema for specific data, and so is also widely used as a database system or an effective addition to a database system. For example, Metacat is an XML-enabled DB that provides more flexibility than relational DB systems but still utilizes a robust RDBMS for its underlying storage [Jones01] for better performance. We have designed a new XML application, FoodWebML, for describing food-web networks to allow both their storage and visualization on the WWW.

### 3. WOW ARCHITECTURE DESIGN

The WOW architecture focuses on providing a flexible database and 3D visualization format on the WWW (FoodWebML), a pipeline architecture that supports the flexibility of FoodWebML, graphical user interfaces for interactive analysis and visualization, and an efficient framework for a WWW demonstration site. It also includes improving, expanding, and reorganizing existing FoodWeb3D visualization software, a stand-alone application built by one of the authors (RJW) using OpenGL, into the new design.

In section 3.1, we describe the importance of the pipeline architecture and key algorithms of each component in the pipeline. In section 3.2, we discuss the design of FoodWebML, and in section 3.3 we focus on the web site implementation, and its results in terms of performance and visualization.

#### 3.1 Visualization Pipeline Design

The WOW design supports several visualization formats rather than using one fixed format like VRML or JavaApplet. To support multiple formats with minimal overhead, flexible architectures such as pipeline architecture become essential. Pipeline architecture uses component-based modular implementation and a simple interface for organizing such components to configure a pipeline as needed [AVIS]. This highly flexible pipeline architecture allows users to easily configure a new pipeline for specifically desired analyses and visualizations. The current pipeline includes a few core components working as a prototype of the whole pipeline architecture. Currently implemented components are a format converter, trophic level calculator, connectivity

calculator, visual node calculator, VRML-mapping translator, and aggregation animation generator.

**Format Converter:** converts .web and other food-web data formats to FoodWebML file format, validated with the FoodWebML DTD.

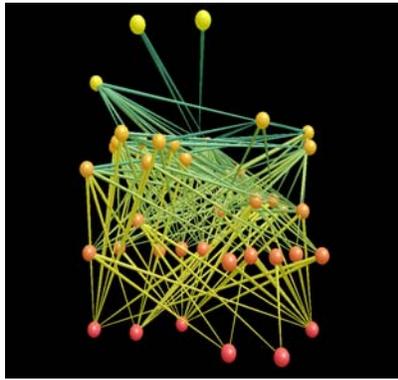
**Trophic level calculator:** calculates the trophic "distance" between each species and basal species such as plants within a given food web. Trophic level serves as an important cue for analysis and node placement during visualization. Many methods for computing trophic level exist in the ecological literature. We chose to use the prey-averaged trophic level recently shown to be a computationally efficient algorithm for use with binary food webs [Williams03].

**Connectivity calculator:** the total number of predators and prey of the species in question. This value is also used in analysis and visualization.

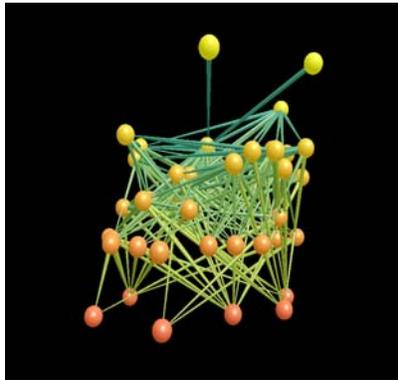
**Visual node calculator:** Nodes (species) are drawn as spheres and links are drawn as cones, with the cones tapered starting from the predators and pointing to the prey. Node color varies with the trophic level of the node. Link color also varies with the trophic level of the prey species. This means that omnivores, or species that consume prey from more than one trophic level, are visible because links of various colors originate at the omnivorous node. When species biomass or abundance data is available, node size is proportional to species abundance. Similarly, when the magnitude of the flows along the links is known, link diameter is used to visualize the flow magnitude. Most empirical data sets simply record presence or absence of species and feeding relationships, in which case nodes and links are all the same size.

Node placement is one of the most critical aspects of 3D network visualization [Eick96], [Gershon 96], [Graham00]. We currently use two algorithms to place nodes, or groups of organisms, in the three-dimensional space. One is based on a rectangular coordinate system (with coordinates  $x$ ,  $y$ ,  $z$ ) and the other is based on a cylindrical coordinate system (with coordinates  $r$ ,  $\theta$ ,  $y$ ). Figure 3a shows a visualization of a 42 species Caribbean island food web [Goldwasser93] with the nodes placed using the rectangular coordinate system. Figure 3b shows the same network drawn using cylindrical coordinates. Both visualizations are of a binary food web, and so all nodes and links are the same size.

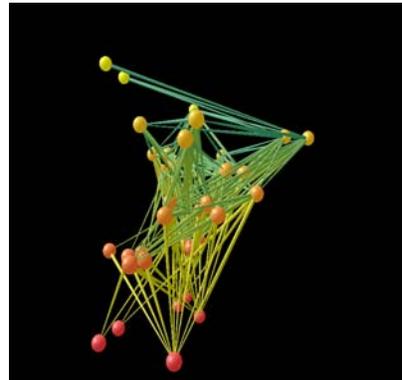
In both cases, the vertical ( $y$ ) axis is the trophic level of the species. The depth ( $z$ ) dimension or radius (in the rectangular and cylindrical projections respectively) is one of three parameters relating to the number of connections attached to the node. These parameters are the generality (the number of prey that the species consumes), vulnerability (number of predators that consume the species in question) or the connectivity (the total number of predators and prey of the species in



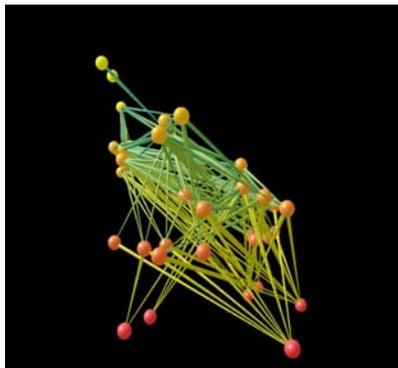
a) The visualization is viewed from the front, nodes are placed in a rectangular coordinate system and the depth dimension is based on the connectivity of nodes.



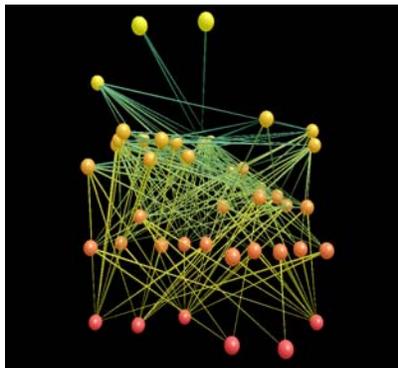
(b) The same food web as figure 1 but viewed in cylindrical coordinates.



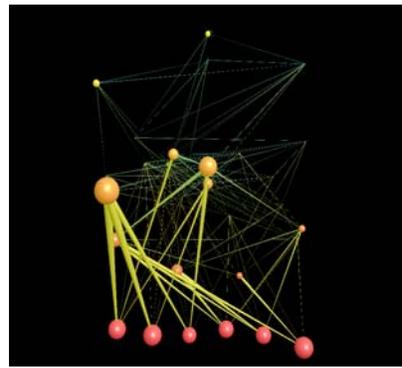
(c) The same food web as in figure 1 viewed from the right.



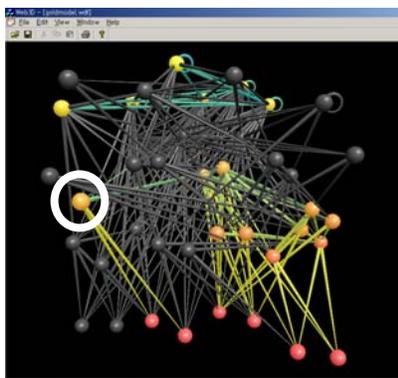
(d) The same food web as in figure 1 viewed from the right and using vulnerability (number of predators) as the depth dimension.



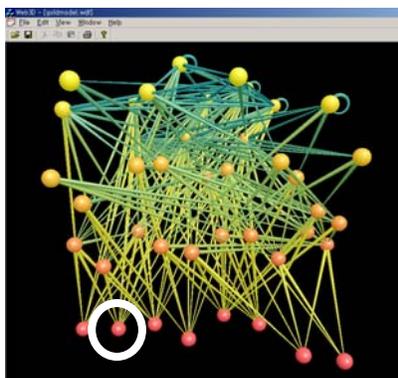
(e) The same food web as in figure 1 with the links half as large.



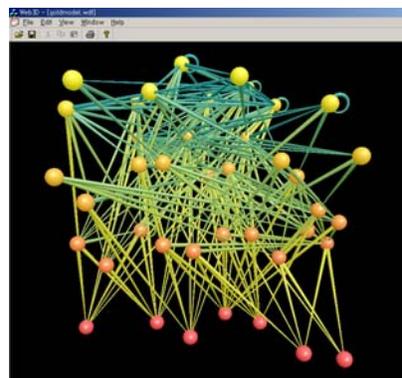
(f) Visualization from a 30-species dynamical model.



(g) When user clicks on a white-circled node, it allows user to see only prey, only predator, or both of the species (the current picture). Other nodes and links are gray-scaled.



(h) Simulation of more finely resolved dynamics such as the impacts of adding or deleting particular species or links within food webs – deleting the white-circled node.



(i) Result of deleting a node simulation from (h). It removes related links. If there are species that depend only the removed node, then that depending node is also deleted.

**Fig. 3** – Various visualization techniques applied to a 42 species food web from St Martin Island in the Caribbean [Goldwasser93] (a-e), and various model food webs (f-i).

question). This choice of depth or radius places nodes that are less highly connected near the front (rectangular) or periphery (cylindrical) of the visualization, while more highly connected nodes are toward the rear or core of the visualization.

The left-right or angular dimension is determined as follows. Trophic level values are rounded to the nearest integer and species are grouped into sets of species with the same integer value of trophic level. Within each trophic level group, species are evenly placed in the range  $x = [0,1]$  or  $q = [0,180]$  in the order they appear in the original data set. If the network was constructed with the niche model [Williams00], this preserves the niche ordering of the species. In empirical data sets, species are often grouped phylogenetically and so species that are in close proximity in the visualization are often closely related phylogenetically. In Figure 3a, the visualization is being viewed from the front and the depth dimension is the node connectivity. Figure 3c shows the same visualization viewed from the side and the most highly connected species are to the right. In Figure 3d, the depth dimension is now the node vulnerability, and the visualization is being viewed from the side, as in Figure 3c. The more highly preyed-upon species tend to be at lower trophic levels.

In systems with a large number of links, placing less connected nodes towards the front of the visualization allows more of the network structure to be seen. Placing more connected nodes in front causes the nodes' many links to obscure the parts of the network that are further back. Drawing the links with a smaller diameter can also make visualizations of highly connected networks clearer. In Figure 3e, the links are half the diameter of the links in Figure 3a. This opens up the visualization and allows nodes and links that are in the back of the visualization to be seen more easily.

Currently, the FoodWeb3D standalone version using OpenGL is being decomposed into each component and reassembled into the WOW infrastructure explained in detail in the next section. Some FoodWeb3D features are not yet implemented in WOW. One of these FoodWeb3D features displays the variable abundances of different species as variable volumes of spheres that are proportional to species' abundances (Fig. 3f). Another such feature visualizes the energy flow along a link as the cross-sectional area of the link.

**VRML Mapping Translator:** translates the FoodWebML, including all the visual information, into the VRML format. By using an XSL (Extensible Stylesheet Language) translator, FoodWebML can be easily converted to VRML/X3D. As partially shown at figure 7, XSL is an XML application itself, and used for transforming XML documents to other formats. Later we will extend the current translation to VRML to generate

```
<aggregation type="taxonomy">
  <group level="kingdom" name="Plantae">
    <group level="phylum" name="Anthophyta">
      <group level="class" name="Angiospermae">
        <group level="order" name="Fabales">
          <group level="family" name="Leguminosae">
            <group level="genus" name="Cytisus">
              <group level="species" name="scoparius">
                ...
            </group>
          </group>
        </group>
      </group>
    </group>
  </group>
</aggregation>
```

Fig. 4 – Aggregation design example in FoodWebML.

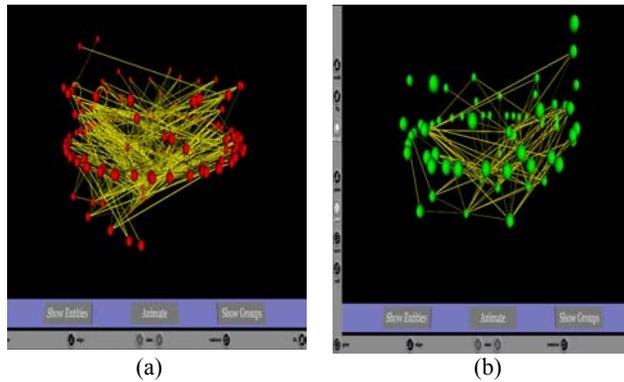
more diverse formats which FoodWeb3D JavaApplets and Plug-ins can read and render.

### 3.2 FoodWebML (FWML)

In designing WOW, we developed FoodWebML, an XML application that flexibly handles diverse food-web network data formats and visualization information efficiently, and can be easily translated into different formats like VRML, or data for Java Applets and Plug-ins. The core visualization information can be calculated upon request or stored in the FoodWebML for future reuse, thus saving significant computation time.

The FoodWebML allows a wide range of food web data to be flexibly represented, including various parameters that are associated with nodes and links. Parameters that describe nodes include taxonomic and functional similarities, body sizes, and other bioenergetic parameters [Williams01]. Parameters that describe properties of the links may include relative diet preferences, absolute flows, prey preferences and maximum ingestion rates. In addition to describing individual species and the links between them, FoodWebML allows the representation of system-wide properties, such as environmental parameters.

FoodWebML is also designed to handle hierarchical aggregation of nodes. Visualizations using simple nodes and links can often obscure information when there is a high number of nodes or density of links. Network data can deliver more meaningful information by embedding its hierarchical information. For example, each node will be identified taxonomically according to sub-species, species, genus, family, etc. (Fig. 4). The number of nodes could be systematically reduced by taxonomic or functional similarity aggregation.[Martinez93b][Martinez96]. This could hide overwhelming degrees of complexity to give additional information in a very intuitive way [Kundu]. FoodWebML allows the definition of different types of aggregations using group and level elements. Links between the aggregated groups can be calculated in various different ways. The current implementation calculates the group node link value as a decimal value from 0.0 to 1.0. A zero value implies "maximal" linkage

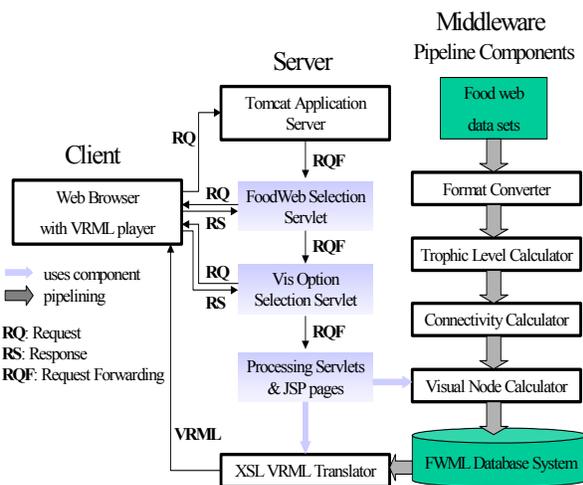


**Fig. 5** – Broom Lake’s food web viewed in the cylindrical coordinate system; (a) shows nodes resolved to the species level and (b) shows nodes grouped to the family level. At the demonstration site, the VRML animation of the aggregation processing of (a) to (b) is available.

- a link exists between two groups if there is at least one link between two entities, one from each group. A value of 1 implies "minimal" linkage - a link exists between two groups if every member within a group must be linked to every member of the other group [Martinez91]. The process of aggregation can be visualized by using animations of collapsing nodes into a higher level node. Figures 5a and 5b show a food web visualized aggregated to the species level and the family level respectively. The animation is available at temporary hosting site at <http://unicorn.sfsu.edu:5080/wow>.

### 3.3 Web Application Implementation

The current WOW implementation is for prototyping and studying the design for building flexible visualizations using pipelining, FoodWebML, VRML and its related database components that will be easily extended to full implementation of infrastructure for



**Fig. 6** – WOW Architecture Design

Data	Num of Nodes	Num of Links	FWML with visual node info (size) [KB]	FWML visual node generation time [sec]	VRML (size) [KB]	VRML generation time [sec]
Grass	75	113	107	3.0	198	15
Broom	154	370	285	7.9	517	19
Elverde	156	1510	715	27.7	1,676	148
Little Rock	181	2375	1,101	42.5	2,575	250

**Table 1** – Data Size and related execution time. FWML stands for FoodWebML. Performance was measured at a PC with Pentium II, 833 MHz with 128Mbyte main memory. (Grass:Grasslands in England and Wales, Broom:Scotch Broom – *Cytisus scoparius*, Elverde:El Verde Rainforest, LittleRock:Little Rock Lake)

collaborative research and education. Figure 6 presents the current WWW architecture. The WWW user interface allows users to choose one food-web data set from the database and then choose from a range of visualization options. Upon requests from the client, WOW serverlets invoke jsp pages to retrieve a FoodWebML file from the XML database system (Xindice) and process selected options to create VRML on the fly. Table 1 shows the size of FoodWebML at different stages, generation time, and the number of nodes and links when executed on a relatively slow PC (Pentium III, 833 MHz with 128MByte main memory).

FoodWebML and VRML increase their size radically when number of links increases. As data size increases, computation time proportionally increases. Due to the computation time and possibly frequent requests, caching and reuse of VRML would be greatly beneficial for improving user services and will be added in near future.

Figure 7 shows a portion of XSL that translates FoodWebML with visual node information into the corresponding VRML. This will be extended to translate FoodWebML into other formats.

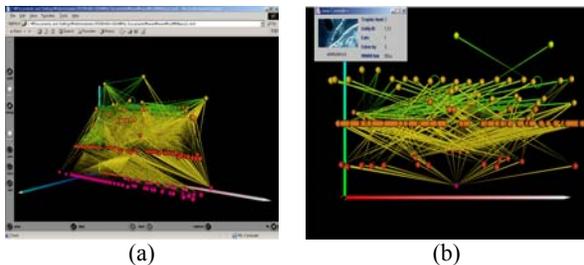
Figure 8 shows the generated VRML visualizations. We added XYZ axis to give better depth cue and clearer location information to the nodes (Fig. 8a). Upon clicking on the node, users can get descriptions of the node such as taxonomy, tropic level, images of the species and hyperlinks to pages on, for example, FishBase ([www.FishBase.org](http://www.FishBase.org)) or Google (Images.Google.com), where more information is available (Fig. 8b).

```

<xsl:template match="node">
  DEF NODE_<xsl:value-of select="@id"/> FWNode {
  translation <xsl:value-of select="node_visual/position/@x"/>,
  <xsl:value-of select="node_visual/position/@y"/>, <xsl:value-of
  select="node_visual/position/@z"/>
  <xsl:if test="boolean(node_visual/rotation)">
  rotation <xsl:value-of select="node_visual/rotation/@x"/>,
  <xsl:value-of select="node_visual/rotation/@y"/>, <xsl:value-of
  select="node_visual/rotation/@z"/>, <xsl:value-of
  select="node_visual/rotation/@angle"/>
  </xsl:if>
  diffuseColor <xsl:value-of
  select="node_visual/appearance/color/rgb/@r"/>, <xsl:value-of
  select="node_visual/appearance/color/rgb/@g"/>, <xsl:value-of
  select="node_visual/appearance/color/rgb/@b"/>
  <xsl:if
  test="boolean(node_visual/appearance[@transparency])">
  transparency <xsl:value-of
  select="node_visual/appearance[@transparency]"/>
  </xsl:if>
  <xsl:choose>
    <xsl:when test="boolean(node_visual/geometry[sphere])">
    geometry Sphere { radius <xsl:value-of
    select="node_visual/geometry/sphere/@radius"/> }
    </xsl:when>
  </xsl:choose>
}

```

**Fig. 7** – Example of using XSL to generate VRML; positioning of nodes



**Fig. 8** – Results from the FoodWebML to VRML translation.

#### 4. CONCLUSION

The work in progress aims to develop a range of data management, analysis and visualization tools to facilitate easy access of food web data and other relevant information through the WWW. The flexible system design is planned to accommodate a range of users with different levels of interest, including the interested lay public, students, researchers, and managers. FoodWebML and the pipelining architecture provide a flexible framework that is capable of being automatically validated, thereby greatly enhancing their utility as collaborative research and educational tools. The tools will eventually allow the visualization of empirical and model food webs, and permit the user to interactively manipulate both the visualization parameters and

properties of the underlying data and models. When fully implemented and available to a wide audience, these tools could profoundly affect ecological and network research and education, perhaps even as much as molecular visualization has altered chemistry research and education.

#### ACKNOWLEDGEMENT

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

#### REFERENCES

- [AVS] <http://www.avz.com>
- [Batagelj98] Batagelj, V., and A. Mrvar. 1998. Pajek.Program for large network analysis. *Connections* 21:47-57.
- [CML] <http://www.xml-cml.org>
- [Crosby97] Crosby, A. W. 1997. *The Measure of Reality: Quantification and Western Society, 1250-1600*. Cambridge: Cambridge University Press.
- [Diehl00] Diehl, S., and J. Keller. 2000. VRML with constraints. *Proceedings of the Web3D-VRML 2000 Fifth Symposium on Virtual Realist Modeling Language*.
- [Dunne02] Dunne, J.A., R.J. Williams, and N.D. Martinez. *In preparation*. Food webs aren't small worlds: unique aspects of ecosystem network structure. To be shortly published in the *Santa Fe Institute Working Papers Series* and submitted to *Proceeding of the National Academy of Sciences USA*.
- [Eick96] Eick, S. G. 1996. Aspects of network visualization. *IEEE Computer Graphics and Applications* 16:69-72.
- [Freeman00] Freeman, L. C. 2000. Visualizing social networks. *Journal of Social Structure* 1: <http://www.heinz.cmu.edu/project/INSNA/joss/vsn.html>.
- [Gershon96] Gershon, N., K. Andrews, S. G. Eick, J. Foley, And W. Ruh. 1996. Visualizing the Internet. *Proceedings of the CHI '96 Conference Companion on Human Factors in Computing Systems: Common Ground* April 1996.
- [Goldwasser93] Goldwasser, L. and Roughgarden, J. Construction of a large Caribbean food web. *Ecology* 74: 1216-1233 (1993).
- [Graham00] Graham, M., J. B. Kennedy, and C. Hand. 2000. A comparison of set-based and graph-based visualisations of overlapping classification hierarchies. *Proceedings of the Working Conference on Advanced Visual Interfaces*, May 2000.
- [Jones01] Jones, Matthew B., C. Berkley, J. Bojilova, M. Schildhauer. 2001. Managing Scientific Metadata. *IEEE Internet Computing* 5 (5): 59-68.
- [Koutsofios99] Koutsofios, E. E., S. C. North, R. Truscott, and D. A. Keim. 1999. Visualizing large-scale telecommunication networks and services (Case study). *Proceedings of the Conference on Visualization '99: Celebrating Ten Years*.
- [Kundu] Kundu, K., Sessions, C., desJardins, M., and Rheingans, P., "Three-Dimensional Visualization of Hierarchical Task Network Plans," <http://www.csee.umbc.edu/gavl/handouts/finalDraft.pdf>
- [Mage] <http://kinemage.biochem.duke.edu/kinemage/kinemage.php>

- [Marti97] Marti, J. 1997. Viewing IGES files through VRML. *Proceedings of the Conference on Visualization* October 1997.
- [Martinez93] Martinez, N. D. 1993b. Effects of resolution on food web structure. *Oikos* 66:403-412.
- [Martinez96] Martinez, N. D. 1996. Defining and measuring functional aspects of biodiversity. Pages 114-148 in *Biodiversity: A Biology of Numbers and Difference*, ed. K. J. Gaston. Blackwell Scientific.
- [MathML] [www.w3.org/Math](http://www.w3.org/Math)
- [Montoya02] Montoya, J. M., and R. V. Solé. In press. Small world patterns in food webs. *Journal of Theoretical Biology*.
- [Newman01] Newman, M. E. J. 2001. The structure of scientific collaboration networks. *Proceedings of the National Academy of Sciences* 98:404-409.
- [Pajek]<http://vlado.fmf.unij.si/pub/networks/pajek/pajekman.htm>
- [Pimm91] Pimm, S. L., J. H. Lawton and J. E. Cohen. 1991. Food web patterns and their consequences. *Nature* 350:669-674.
- [Polis96] Polis, G. A., and K. O. Winemiller (eds.). 1996. *Food Webs: Integration of Patterns and Dynamics*. New York: Chapman and Hall.
- [Strogatz01] Strogatz, S. H. 2001. Exploring complex networks. *Nature* 410:268-276.
- [SVG] <http://www.w3.org/Graphics/SVG/overview.html>
- [UCINET] [http://www.analytictech.com/ucinet\\_5\\_description.html](http://www.analytictech.com/ucinet_5_description.html)
- [VRML] <http://www.cs.brown.edu/research/graphics/research/vrml>
- [Walsh99] Walsh, A. E., and M. Bourges-Sevenier. 1999. *Core Web 3D*. Prentice Hall.
- [Williams00] Williams, R. J., and N. D. Martinez. 2000. Simple rules yield complex food webs. *Nature* 404:180-183.
- [Williams01] Williams, R. J., and N. D. Martinez. 2001. Stabilization of chaotic and non-permanent food web dynamics. *Santa Fe Institute Working Paper* 01-07-37.
- [Williams03] Williams, R. J., and N. D. Martinez. 2003. Trophic levels in complex food webs: theory and data. In press at *American Naturalist*.
- [Wilbur97] Wilbur, H. M. 1997. Experimental ecology of food webs: complex systems in temporary ponds. *Ecology* 78:2279-2302