I presented the article:

Alpi, Kristine. "Bioinformatics Training by Librarians and for Librarians: Developing the Skills Needed to Support Molecular Biology and Clinical Genetics Information Instruction." *Issues in Science and Technology Librarianship.* Spring 2003.

on September 9, 2003. Due to technical difficulties with UNC's server, which is still struggling with multiple viruses on campus, I was unable to demonstrate some of the tutorials available that were initially part of my presentation, but the main content of the article was covered regardless.

The major debate was over whether librarians should be involved in bioinformatics, and if so, in what capacity. This centered around the hierarchy of a question's complexity, defined by Yarfitz and repeated in this article. The categories were:

I. Basic Questions
II. Technical Questions
III. Analytical Questions

Basic questions were defined as pointing to a suite of tools that a graduate student could utilize in a particular discipline such as molecular biology or genomics, and this level was expected of all librarians, regardless of specialties in bioinformatics or other disciplines.

Technical questions were a more in depth explanation of particular databases, such as knowing what the database included or excluded, and which would be most appropriate for someone searching an EST vs. a protein sequence. This level of questions would require specialized knowledge, and the majority of the room thought that this should be the accepted level of expertise for a bioinformatics librarian.

Analytical questions involved interpreting the data and actually find the homologs for a particular protein, or identifying the gene sequence across different species, and the group thought that specific research groups are the ones who should have this domain knowledge and should provide local help to those who have question on how to use these tools.

However, I believe that a bioinformatics librarian should have the knowledge to include analysis and synthesis of the information that is presented to them, and that in addition to knowing which database, they should be familiar with its particular features that allow a proper analysis of the particular gene. We should be able to construct a phylogeny tree from the data provided by the scientist, as well as perform more complicated queries, and make ourselves an extra resource that is a constant for the campus outside of the rapid fluctuation of research group's knowledge, focus, and personnel.

Ultimately, we agreed to disagree on the role of a bioinformatics librarian, and only used the article as a jumping-off point for debating the role of librarians in bioinformatics.