Introduction Microarrays are one of the latest breakthroughs in experimental molecular biology, which allow monitoring of gene expression for tens of thousands of genes in parallel and are already producing huge amounts of valuable data. Analyses and handling of such data is becoming one of the major bottlenecks in the utilization of the technology. Before reaching the analysis stage of a microarray experiment, a researcher has to go through a variety of steps that include patient information collection, sample tissue collection, specimen retrieval from the tissue, cell line information, DNA/RNA preparation, clone generation, microarray printing etc. Gene expression data derived from analysis software applications are not meaningful unless they are linked to patient's clinical information and histology and pathology of the tissue specimen.

We describe an online integrated database management and analysis system called Microarray Laboratory Information Management Systems (M-LIMS). We have developed a system that is accessible to the collaborating labs via the World Wide Web (WWW). Each laboratory can access our system online and enter, retrieve, modify and query experimental data.

Background Researchers at Ellis Fischel Cancer Center at the University of Missouri, Columbia are using microarray technology to study methylation patterns in breast tissue. Our goal was to develop a system that will allow scientists to run interactive queries of the database through a convenient and widely accessible Web interface.

Methods We are using SQL Server 2000 Database Management System (DBMS) as our back end. Active Server Pages (ASP) connects the DBMS to the WWW. ASP together with ActiveX Data Objects (ADO) can bring about this access to myriad of heterogeneous data sources.

Data Collection Data are collected at every step of the microarray experiments. Some of the important steps involved in the data generation are as follows: 1. Patient/Tissue/Specimen/Cell-lines 2. DNA Preparation 3. Amplicon Generation 4. Slide Preparation for Printing 5. Clone, Sequence and restriction Enzymes Information 6. Microarray Printing. 7. Analyzers Output Management.

Results Our site takes the users to the main entry page that is the login page. Users log under their respective user names and passwords. The main entry page is centralized in a way that all the functions can be performed from this page.

Data Entry and Update
After clicking the link to insert the data, users will be presented with data entry forms. For example, after filling the experiment data entry form, they will have the option of going back or go to tissue data entry form and from there to array, clone or sequence data entry forms. Users can either go to the update pages after filling the data entry forms or they can go directly to the update screen.

Interactive Query Environment
M-LIMS provides the users with a flexible query interface. Users can input query parameters and search the database based on those parameters. The users are given a wide range of query options. They can perform queries based on experiment data, clone values, array type, relevant clone and sequence data, and specific microarray image and analyses data.

In the near future, we plan to open a socket form our database to perform searches through the powerful search engines like PUBMED, GENBANK and BLAST. The purpose would be to provide users access to all the information related to genetics and molecular biology, which is not possible to store in our database.