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The Bioinformatics Program at Washington University's Bernard Becker Medical Library: Making it Happen

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Main Results:

Class attendance exceeded expectations. A total of 220 people attended classes offered in the first semester. Student backgrounds reflected a broad spectrum of academic rank (figure 1). The course evaluation forms (figure 3) were divided into two categories: "Teacher Evaluation" and "Students Knowledge Gained." The form allowed students to rate the course as excellent, good, fair or poor. The courses were highly rated. All of the evaluations fell into the excellent or good category. The data showed that Post-docs exhibited the most interest in the bioinformatics courses (figure 2). Due to the increased demand for bioinformatics services at the Medical School, hiring an additional Bioinformatics Specialist became a priority. The Becker Library recruited Kristi Holmes, a PhD in biochemistry. She will join Dr. Lili Wang, MD, MS in June 2006, and focus on developing new courses.

Abstract:

The need for a Bioinformatics Program became apparent after repeated requests from researchers for bioinformatics resources, and the University's announcement of BioMed 21, a 300 million dollar biomedical science initiative to bring "new knowledge of the human genetic blueprint to the patient's bedside and change how illnesses are understood, diagnosed and successfully treated." A Bioinformatics Specialist with a strong background in the fields of Molecular Biology and Biostatistics was hired. Program development started in 2002. Initially, three core courses were developed, Sequence Similarity Search, Genetic Variation and Human Genome Resources. Each of these courses was offered twice per semester. Additionally, partnerships were established within the University Medical School Community (e.g., Genome Sequencing Center) to license and teach Spotfire, a software package used to analyze microarray data. From March through May of 2005, seven Spotfire classes were taught. Each Spotfire class consisted of seven hours of classroom work. Also, in-depth consultations were scheduled with faculty and researchers to address their specific needs. They suggested other software packages for Becker Library to purchase and manage, including Lasergene and CSD (Cambridge Crystal Structure Database). Efforts to reach outside of the University Community were made through the development of a Bioinformatics website.

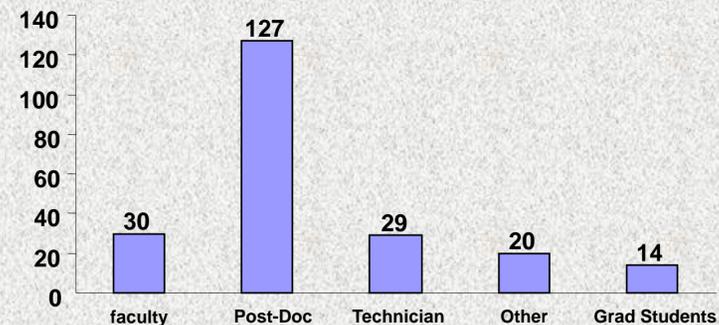


Figure 1: Number of Students by academic rank

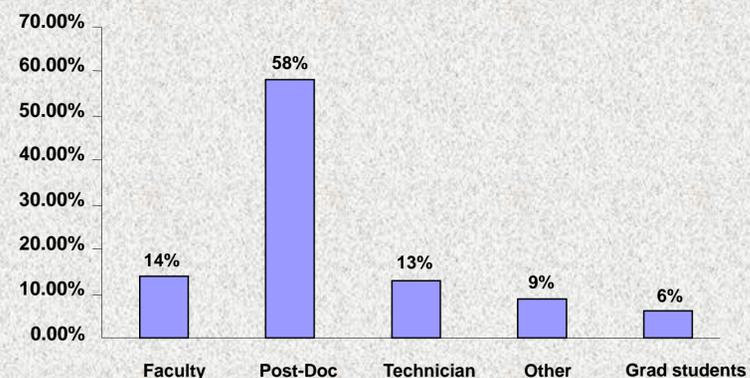


Figure 2: Percent of Students by Academic Rank

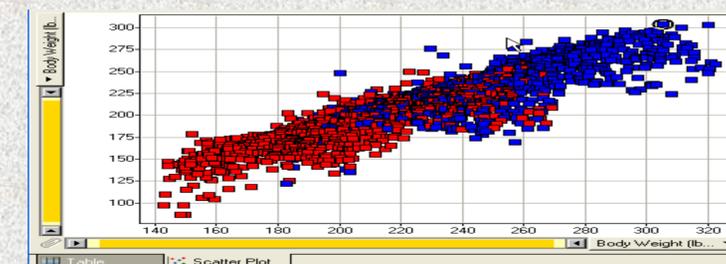
Figure 3: Evaluation Form



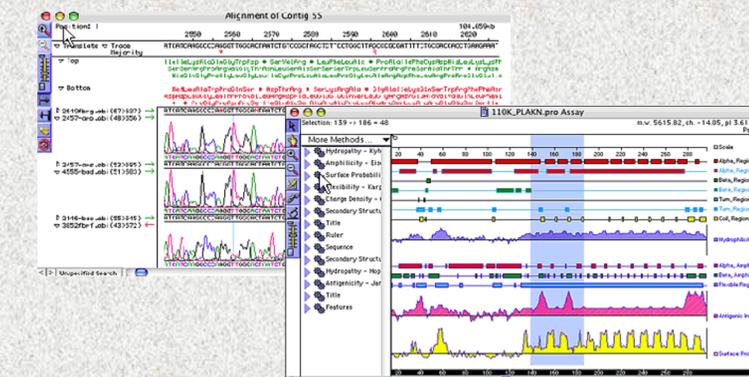
NCBI, a national resource for molecular biology information including Entrez, the integrated, text-based search and retrieval system for the major databases, including PubMed, Nucleotide and Protein Sequences, Protein Structures, Complete Genomes, Taxonomy...



Spotfire offers an interactive, visual approach to data analysis that empowers individuals to quickly and easily see trends, patterns, outliers and unanticipated relationships in Microarray data.



Lasergene is a comprehensive Software for DNA & Protein Sequence Analysis, Contig Assembly and Sequencing Project Management



Conclusion:

According to Dr. Seth Crosby, Director, Microarray Facility, Genome Sequencing Center "Providing a trainer for complex data analysis tools is exactly the kind of thing a medical school library ought to be doing. The Becker Library's decision to accept the challenge, facilitated the ability of science at Washington University to be stronger and more independent." Creating the Bioinformatics program transformed library services and provided greater opportunity for meeting the University's goal of bringing "new knowledge of the human genetic blueprint to the patient's bedside and changing how illnesses are understood, diagnosed and successfully treated".