Medical College of Wisconsin uses cutting-edge technologies to speed results from proteomics research.

Overview

- ***Challenge***
  Conducting proteomics research on a mixed hardware platform and 32-bit operating system was slowing the pace of discovery for academic researchers
- ***Solution***
  A high-performance Linux® on POWER® computing environment from IBM built on an IBM @server® BladeCenter™ chassis containing eight IBM BladeCenter JS20 blade servers running 64-bit SUSE LINUX Enterprise Server Version 8.0 technology; each blade server has two IBM PowerPC® 970 processors and 4GB memory
- ***Key Benefits***
  Faster analysis of experimental data using a leading-edge computing platform designed to push technology to the limit

Researchers at Milwaukee's private Medical College of Wisconsin dared to ask the hard questions when they applied for a highly competitive proteomics research grant from the National Institutes of Health (NIH) in 2002. Their visionary proposal related to improving the technologies life sciences researchers use to make new discoveries about the human body.

"We really stuck our necks out as we saw there were major advances that could be made by reinventing technology and doing things in completely different ways," says Dr. Andrew Greene, professor and director of the Biotechnology and Biomedical Engineering Center at the Medical College of Wisconsin. The risk paid off. Being awarded this prestigious seven-year NIH grant seems to represent a trend at the college, which received US$118.9 million in external support for research and training in 2003–04 and is

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among the nation's fastest-growing medical schools in terms of increased research funding. The faculty here conducts 1,500 medical research studies annually. And the Department of Physiology, the academic home for faculty involved in Greene's project, ranks number one in the United States for NIH dollars received.

Greene, principal investigator at the college's NIH-funded National Center for Proteomics Research and Technology Development, and his research staff use an instrument called a mass spectrometer to detect proteins. Altogether, ten programs in the U.S. are funded by NIH National Heart, Lung and Blood Institute grants. The programs focus on techniques that range from building instrumentation to performing computational analysis—and all are aimed at developing transformational technology to assist researchers studying proteins.

Learning how technology can be refined to improve academic research

Greene's researchers conduct experiments to identify proteins involved in angiogenesis, a biological process that causes blood vessels to grow. Understanding the fundamental triggers that regulate blood vessel growth has broad implications. For example, if researchers discover a protein that is released only by tumor cells, technicians could use a mass spectrometer to detect that protein in a patient's blood sample—creating an early diagnostic for the presence of tumor cells. And if researchers like Greene could develop ways to interfere with the blood vessel growth factor process, they could potentially stop blood vessels from growing into cancer cells and developing into tumors.

The two overall goals of the NIH research program are to discover novel proteins that are markers for disease and to improve technologies used to detect these proteins. "We're driving toward increased sensitivity and resolution of instruments that will allow the application of proteomics to very small samples with very rapid analysis," Greene explains.

But proteomics researchers are hindered by time-consuming computation and analysis processes—bottlenecks that force researchers to spend a majority of their time working on a computer to understand experimental results and verify them computationally. "The whole technological aspect of it is a real headache," says Dr. Simon Twigger, assistant professor in the Department of Physiology and director of the bioinformatics component for the college's National Center for Proteomics Research and Technology Department.

Mass spectrometry generates a huge amount of data that is analyzed through algorithms in database searching software. Typically, algorithms compare each experimental protein sample to every known protein in a database—generating many potential hits. The traditional hardware environment researchers use to analyze proteomics experiments is a single PC that's provided with the mass spectrometer machine. Running complex analyses against a huge database on that type of platform can take many days. "This really hampers your ability to quickly run an analysis, get a result, go back and

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change your hypothesis or run a slightly different experiment, and then re-analyze your data," Twigger says. "Speeding up and improving that process is one of the major goals of the bioinformatics part of this project."

When researchers at the college initiated their proteomics research program, they used a mixture of hardware platforms that were slow and required extensive IT support. Among their key software applications was a database searching tool supported only on 32-bit Microsoft® Windows® and Linux operating systems. "We needed to run this application on a hardware platform that gave us the best chance of running it as quickly as we could," Twigger says. The college also wanted to move to a newer, 64-bit Linux operating system—preferred by most academic researchers.

Taking the leap to deploy a leading-edge computing infrastructure

To speed its research efforts, the Medical College of Wisconsin needed a fast, reliable hardware platform. But, explains Greene, "It was not a hardware solution alone that we were looking for." The college's long-term proteomics research project demanded winning technology supported by an industry-leading vendor. "From our initial meeting with IBM, we understood that they had a real commitment to help us implement a solution that would actually meet our needs and our timetable," Greene says.

To improve mass spectrometry techniques and overall technology development, the college was prepared to establish a computing environment using several new-release technologies. So the Medical College of Wisconsin participated in an early support program from IBM, building the heart of its high-performance computing environment on an IBM **@server** BladeCenter chassis with eight IBM BladeCenter JS20 blade servers running 64-bit SUSE LINUX Enterprise Server Version 8.0 technology.

The industry's first blade system based on IBM Power Architecture™ platform, each JS20 blade server contains two IBM PowerPC 970 processors. The Power Architecture is a robust processor technology developed in collaboration with chip manufacturers, device designers and many IBM clients to support demanding computing environments. In conjunction with this new technology deployment, the college also implemented a new version of the SUSE LINUX operating system and ported IBM Business Partner Thermo Electron Corporation's Sequest database searching software to the 64-bit platform.

"We've been very happy about the way our people, IBM and Thermo Electron have all been able to attack this problem together and come up with a solution that's really working and will continue to get better," Greene says. A team of IBM specialists worked closely with Thermo Electron to port its Sequest software to the new platform. And IBM Business Partner Berbee assisted in setting up the chassis and initial Linux implementation. IBM continues to work with these partners to optimize configuration and boost performance.

With the new cluster-based platform, researchers say the popular Sequest software from Thermo Electron Corporation runs much more efficiently. “We can get results back much faster, so our entire group of experiments speeds up dramatically as a result,” Twigger says. And since it’s very affordable to expand the IBM BladeCenter technology, he says the college can just add more nodes to the cluster when it needs additional computing capacity.

Leveraging new tools to deliver faster, better results

For laboratory researchers, the new IBM Linux on POWER platform at the Medical College of Wisconsin drastically improves day-to-day activities. “When you do an experiment, you don’t want to sit down for five days in a row waiting on the results,” Greene says. “The IBM platform has really pushed things forward.” Now, researchers can quickly conduct several different iterations of an experiment and fine-tune their analyses to boost the chances of discovering real-life medical applications.

Working hand-in-hand with IBM’s life sciences experts gives researchers an opportunity to provide ongoing feedback that can be used in subsequent technology developments. Knowledge experts from IBM and IBM Business Partner software vendors are easily accessible for support, Twigger says, and have provided valuable training to the college’s own IT staff—which should help keep support costs low in the future.

By working with technology leaders to hone proteomics technologies today, researchers hope to make faster progress as techniques mature. “It will take a lot of work to get this program up to speed so that we can take the information that came out of the human genome project and start to capitalize on it for research and possibly healthcare benefits,” Greene states. Working in collaboration with leading technology firms like IBM and Business Partner Thermo Electron is a major advantage—amplifying academic researchers’ efforts and helping to speed exciting medical breakthroughs that promise vast improvements to our quality of life.

For more information

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