OoR News

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INSIDE THIS ISSUE:

First Word

Terry Magnuson, PhD, Vice Dean for Research

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Completed this month and with many thanks to the faculty for their comments on the early draft, the new strategic plan for the School of Medicine recognizes the strength of our basic sciences and the importance of maintaining and improving the current infrastructure. We are also focusing on taking that strength and moving it into the clinical realm via translational research.

On another front, good progress is being made with the university on a large-scale plan to build our school's relations with industry. We're gathering a complete inventory of research projects that includes the schools of medicine, pharmacy, public health and the College of Arts and Sciences. Barbara Entwistle, the vice-chancellor for research is helping to bring it all together, as is Mark Mears in the university development office and Joyce Tan of TraCS.

Our High-Throughput Sequencing Facility (the focus of this issue's Core Resources article) working with Renaissance Computing Institute (RENCI), Research Computing, LCCC, Genetics and the Genome Science Center has allowed us to be more competitive and obtain several large clinical sequencing grants. Indeed, we're fast becoming one of the leaders in genome-wide sequencing, thanks largely to the work of Jim Evans, Jonathan Berg, Pat Sullivan, Kirk Wilhelmsen, Chuck Perou, Neil Hayes, Ned Sharpless and all their co-workers. Finally, congratulations to Mike Cohen whose research in HIV transmission prevention was named by the journal Science as the 2011 "Breakthrough of the Year."

Nota Bene

Dede Corvinus, PhD, Director, Office of Research

As it says in Latin, this column will carry announcements, reminders and other items of importance to take note of, to "note well."

N.B. Applications for a NIH Shared Instrumentation Grant (SIG) are due at NIH by March 22, 2012. Up to the amount of $600 no cost-share is required. But above that amount a commitment to the price of the instrument is required. Our office will help write biosketches and create additional support tables. We also have boilerplate copy if the instrument is going into a Core Facility.

(Continued on page 2…)

Nota Bene Continued...

Please note that SIGs require at least 3 NIH-funded P.I.'s who have RO1 or Program Project Grants.

Typically, we have six to eight researchers who will be using at least 75 percent of the instrument time initially. I recommend six to eight because of the 75 percent usage time that is required. Our office also can give applicants examples of successful SIG applications.

For more details, click this link: http://www.ncrr.nih.gov/biomedical_technology/shared_instrumentation/

Cheers,
Dede Corvinus

Patents

This section contains the titles of patents recently issued to SOM faculty members.

Elizabeth Bullitt: U.S. Patent No. 8,090,164, entitled "Systems, Methods, and Computer Program Products for Analysis of Vessel, Attributes for Diagnosis, Disease Staging, and Surgical Planning."

Thomas H. Fischer, et al**:** Mexican Patent No. 288478, entitled "Delivery of Compounds with Rehydrated Blood Cells."

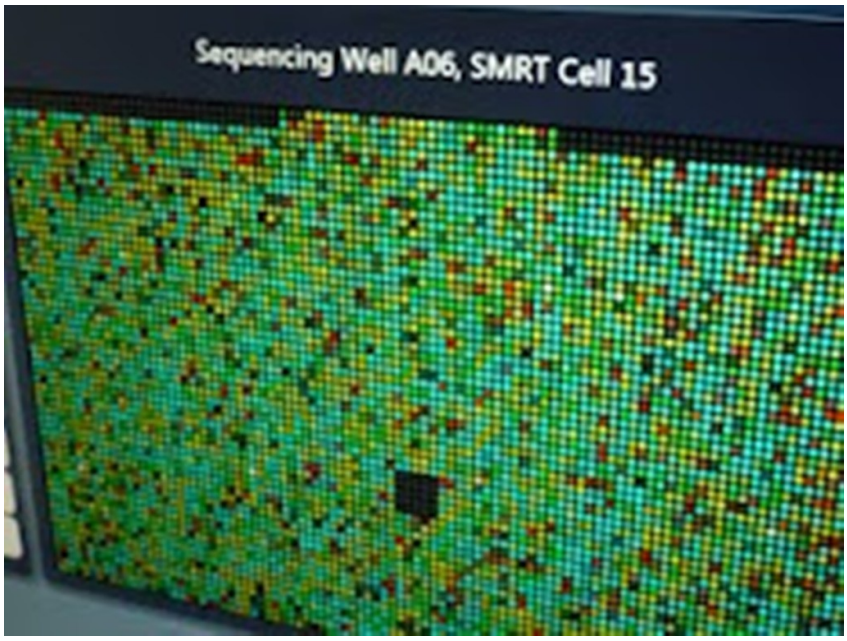
Robert E. Johnston, et al**:** Canadian Patent No. 2,220,964, entitled "Alphavirus RNA Replicon Systems." Australian Patent No. 2006302794, entitled "New Live Virus Vaccines."

Jude Samulski, et al: Japanese Patent No. 4860886, entitled Duplexed Parvovirus Vectors."

Richard Tidwell, et al**:** U.S. Patent No. 8,101,636, entitled "Linear Dicationic Terphenyls and their AZA Analogues as Antiparasitic Agents."

Core Facilities Report

Our column in this issue highlights out High-throughput Sequencing Facility (HTSF). Managing Director Piotr Mieczkowski, along with Faculty Director Corbin Jones, provided the following summary of their facility.



HTSF PacBio RS sequencing activity.

The UNC High-throughput Sequencing Facility (HTSF), which is supported by the School of Medicine and the Lineberger Comprehensive Cancer Center, operates state-of-the-art next generation sequencing instruments, and provides sample preparation and initial bioinformatic services for NextGen sequenceing. Our technologies are helping PIs screen for new genetic and chromosomal anomalies in tumors and other tissues, identify natural and induced mutations in model systems, and profile the genetic variation, transcriptomes, and metagenomes of a broad range of samples. HTSF supports whole genome shotgun sequencing, transcriptome analysis (RNAseq), exon capture, ChIP-seq, FAIRE-seq, and a host of other applications. We are also happy to consult on new application development.

The HTSF has eight Illumina HiSeq 2000s, two Genome Analyzer II machines (Illumina), a Pacific Biosciences SMRT Sequencing System, and a Life Technologies Ion Torrent. We are among the very first commercial machines from Pacific Biosystems, which was installed in Q3 2011. HTSF also has associated equipment necessary for efficient operation, including four cBot cluster generators, three older Cluster Stations, a particle counter, a capillary electrophoresis system - Experion (Biorad), a nanodrop ND-1000 (Thermo Electron), DNA shearing devices, and a host of other equipment. All sequencers are associated with on-board computers for real-time data processing, with one server dedicated for data analysis. Eight full-time personnel, in addition to the Managing Director Piotr Meiczkowski, staff the HTSF.

The UNC Center for Bioinformatics, led by Hemant Kelkar, has provided Information Technology and Bioinformatics analysis support for the UNC-HTSF since its inception in fall 2007. Center for Bioinformatics staff are responsible for data processing, data management, initial analysis and distribution of all data generated at UNC HTSF.

(Continued on page 4)

Core Facilities Report Continued...

They work in conjunction with Research Computing to provide community access to NextGen analysis software (454 newbler assembler/mapper, Bowtie, MapSeq, BWA, SOAP2, MAQ, QIIME etc.). In addition to these open source software programs, there are two network licenses for CLC Genomics Workbench.

In 2012 we anticipate the arrival of an Illumina miSeq and an automated system for exon capture using the SureSelect system. Additionally, we will be releasing our online sample submission and tracking system in the next couple months. This will allow investigators to know where their samples are in the process at all times.

The most common question we receive is "how long will my sample take?" Unfortunately, the answer is seldom simple. The number of samples, nature of the samples, and the amount of sequence needed all affect the time a sample takes to run. Typically, a 2x50 RNAseq run with an already prepared library will be done in less than a month. Longer and more esoteric libraries and samples may take several months.

suggest consulting with the HTSF staff to estimate how long your samples will take. If you have a few samples (<5) that need very rapid turnaround, we have implemented a quick queue. However, PIs are limited to at most four such samples per year.

The HTSF is part of a larger collection of genomic oriented cores (LCCC Genomics Core, Genome Analysis Facility, Vironomics, and Microbiome core) and works closely with these other cores to provide an integrated solution for your genomics needs. See https://sites.google.com/site/htsfunc.

For details on each and more, visit our new website: http://www.med.unc.edu/corefacilities

--Mike Topal