The University of Oklahoma Health Sciences Center Laboratory for Genomics and Bioinformatics

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The University of Oklahoma
HEALTH SCIENCES CENTER

In this issue

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OUHSC COBRE

Acknowledgements

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Free DNA sequencing!

As noted on page 2 of this newsletter (Faculty Advisory Committee for the Core Laboratory Facilities), we are trying to get a better understanding of your needs and how our core facility can more effectively meet these needs. So, we have included in this issue of our quarterly newsletter a short user survey for you to fill out (page 3). As an incentive to encourage you to fill out and return this survey, we will be holding a drawing for $50 of free DNA sequencing. If you return your survey with your name and email address, we will put your name in the running for this free service. Joe Waner (Vice-President for Research) will pull one name out of this pot in late December or early January, and the recipient will get $50 of free DNA sequencing that can be redeemed any time. Please understand that we are always open to suggestions for ways to improve our services. And, if you have any suggestions for new technology that you think should be incorporated into our core facility, please don't hesitate to let us know. Thanks for your support!

-Dave Dyer & Allison Gillaspy

Featured project: Interactive Web-based Program for Smoking Cessation

Tobacco use is widely recognized as the most preventable cancer in the United States. Furthermore, tobacco use is responsible for 30% of all cancer-related deaths in the United States. Dr. Stephen Gillaspy (Assistant Professor of Pediatrics) is developing and testing an interactive web-based computer program to facilitate motivation and readiness to cease tobacco use and engage in smoking cessation services.

The web-based program is designed to provide an assessment of current smoking behavior and deliver personalized feedback. Parents will enter information about their smoking habits into the program and will be presented with a series of graphs and normative feedback regarding their smoking behavior and associated parental and child health risks. Dr. Gillaspy's central tenet is that proper and efficient delivery of assessment and personalized feedback will increase smokers' readiness and motivation to engage in smoking cessation services. Jeremy Zaitshik, a senior-level Bioinformatics Specialist from the OUHSC Laboratory for Genomics and Bioinformatics, worked with Dr. Gillaspy on the design and development of the web-based program. The program was developed using LAMP (Linux, Apache, MySQL and Perl). A randomized controlled comparison of the web-based program versus treatment as usual is now being conducted. Parents of children presenting to a general pediatric outpatient clinic, who self-report as current smokers, will complete measures of motivation and readiness to cease smoking. They will then be randomly assigned to complete the computer program or receive treatment as usual. One month later, they will again complete measures of motivation and readiness to engage in smoking cessation. Dr. Gillaspy hypothesizes that exposure to this brief intervention will increase smokers' readiness to cease tobacco use and engage in smoking cessation services. The successful completion of the proposed project will result in the development of a smoking cessation intervention that can be easily and consistently delivered, in a host of different settings, with little burden to existing staff. Dr. Gillaspy is aided on this project by co-investigators Mary Anne McCaffree, M.D. (Professor, Neonatal-Perinatal Medicine), Julie Lee, M.D. (Clinical Assistant Professor, Pediatrics) and Thad Leffingwell, Ph.D., (Assistant Professor, Oklahoma State University). These studies are supported by a College of Medicine Alumni Association Research Grant.

Contributed by Stephen Gillaspy, Ph.D.

INBRE News *by Edgar Scott, M.S.*

http://okinbre.org/

This fall I lectured to Dr. Jenna Hellack's Molecular and Population Genetics class to expose her students to some available bioinformatics resources that can be used in their research. The lecture focused on using NCBI resources for exploring genes and their related diseases.

The students were first exposed to the Books database, which provides several published textbooks online that cover a variety of topics, such as molecular biology, genetics, and biochemistry. The students were introduced to the "Genes and Disease" book, where they could search for introductory information concerning human-related disease. For more detailed information, we then explored the Online Mendelian Inheritance in Man (OMIM) database. OMIM is a literature database that contains short and complete summaries of genes and related Mendelian diseases.

We then explored Entrez Gene, which is NCBI's gene-centered sequence database. The goal of Entrez Gene is to provide a well-curated resource for the public that contains a comprehensive description of the genes and gene products of mammals, plants, fungi, bacteria, archea, and viruses. We then used links available in Entrez Gene database entries to explore the Single Nucleotide Polymorphism database (dbSNPs), which stores SNPs for many genes identified from the human genome project and other projects. Since Dr. Hallack's course is focused on population genetics, the students learned how to obtain the genetic population data for the different alleles caused by SNPs.

Lastly, the students explored sequence similarity search techniques. BLAST was covered as the main sequence similarity search tool available to the public, followed by Blink. Blink is a link associated with most sequences at NCBI that provides curated results of a BLAST search with the sequence in question. If any of you are interested in this lecture, or other lectures like this, please feel free to contact me and I'll be glad to provide you with the lecture material, or present this lecture to your class.

Faculty Advisory Committee for the Core Laboratory Facilities

UNIVERSITY OF OKLAHOMA HEALTH SCIENCES CENTER
office of research administration

http://w3.ouhsc.edu/ORA/

The Laboratory for Genomics and Bioinformatics, The Molecular Biology-Proteomics Facility and The Flow and Image Cytometry Laboratory are core institutional facilities located in BRC II that provide state-of-the-art services and intellectual content to the scientific missions of the OUHSC. Paradoxically, they also are among the best-kept secrets of the OUHSC. Some faculty do not utilize the resources available. The core labs often do not interact sufficiently with investigators to anticipate their needs in a rapidly changing technology-driven environment. This also leads to lack of timeliness in introducing new technologies and inefficient use of institutional resources.

To address these issues, a Faculty Advisory Committee was appointed to bridge the gap between the core labs and the active research faculty. The committee represents research-oriented departments and centers; the members of the committee are Muayyad Al-ubaidi, Jimmy Ballard, Doris Benbrook, Patrick McKee, Ann Olson, Ricardo Saban, Joe Zhao and Ming-Hui Zou. The laboratory directors, Dave Dyer, Allison Gillaspy, Ken Jackson, and Jim Henthorn also serve on the committee. Initially, the committee will familiarize themselves with the operation and resources of the core lab and become an informational resource for their colleagues. They will provide feedback to the directors on how the core labs may be better postured in the OUHSC research structure. The vital and continuing mission of the committee will be advising the directors and, in turn, the administration on the technology needs of OUHSC investigators. This is intended to be a two-way street, however, and the directors will in turn be an intellectual resource for new technologies and their applications. Additionally, the role of satellite core labs that may be associated with departments or individual investigators will be addressed. The result of this effort will be a more vigorous research establishment at OUHSC. Faculty are encouraged to interact with the core directors and/or the other committee members to inquire about the resources available or to offer suggestions as to how the core facilities can meet the needs of their research.

Contributed by Joseph Waner, Ph.D.
Vice-President for Research

OUHSC LGB User Survey *(Please fold in half and tape or staple for campus mail.)*

1. Are you aware of our web site and how to access submission and pricing information? Yes No

1a. Have you used the services of the LGB in the last six months? Yes No

1b. If ‘yes’, what services have you used? (please check all that apply)

- DNA sequencing, small-scale
- Microarray hybridization and scanning
- Real-time quantitative PCR
- Other (please describe)
- DNA sequencing, large-scale
- Microarray data analysis
- Bioinformatics support

1c. If ‘no’, would you provide a brief explanation?

2. Several potential users have indicated to us that they don’t bring their DNA samples to us for sequencing because we require that you submit your samples in 96-well plates, rather than Eppendorf tubes. Is this true for you? If we were to provide these 96-well plates for you, would that make you more likely to bring your DNA samples to us for sequencing?

3. We have begun to sponsor technology seminars to interest the OUHSC user community in new technology in our core facility, or that is being considered for acquisition. Have you attended the technology seminars sponsored by the LGB this semester? (please check all that apply)

- Biacore surface plasmon resonance
- Combimatrix microarray platform
- Beckman Proteomelab PF2D

3a. If ‘yes’, did you find these seminars useful? Have you considered using these technologies in your own research? How would you change the format of these seminars to make them more useful? Please explain.

3b. Are there other technology-related seminars that you would be interested in seeing in the future?

Thanks for your time!

If you're interested in being entered in our drawing to win $50 of free DNA sequencing, please provide your contact information (e-mail address) below. Good luck!

Please mail to:

OUHSC Laboratory for Genomics and Bioinformatics
Stanton L. Young Biomedical Research Center
Room BRC1106
OUHSC Campus

COBRE News

by John Iandolo, Ph.D.

One of the goals of the COBRE program is to establish itself as a stand-alone center that promotes research by sponsoring the formation of Program Project Grants (PPG), research symposia and conferences. At this time, we are attempting to stimulate the formation of research groups that could prepare a competitive PPG. The program project grant mechanism is designed to support research in which the funding of several interdependent projects as a group offers significant scientific advantages over support of these same projects as individual regular research grants. Eligible principal investigators include any individual with the skills, knowledge and resources necessary to carry out the proposed research. With respect to strengthening biomedical research, our theme of functional genomic and proteomic analysis of host-pathogen interactions is central to understanding the impact of gene expression on pathogen survival and innate host resistance. To continue this development, we are offering to provide administrative support to foster the preparation and submission of one or more program project proposals focusing on the general area of applied and functional genomics. This area may be broadly interpreted in order to attract the interest and inclusion of a qualified group of investigators. Interested potential PIs are invited to contact Dr. John Iandolo, the COBRE PI (john-iandolo@ouhsc.edu), to discuss plans for such a proposal and the type and extent of funding required to prepare a competitive application.

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Combimatrix microarrays

On October 30, Mr. Charles Greaves presented a seminar on the new Combimatrix microarray platform that we are currently considering for our core facility. The availability of genome sequence of many organisms commonly used for scientific research has opened a doorway to advance basic science on many horizons. CombiMatrix CustomArrays allow scientists to tap into this genomic information and develop innovative custom-made DNA microarrays. With free online tools and access to bioinformaticists, building a custom array has never been easier.

To build a commercial-grade custom-content DNA microarray, the CombiMatrix CustomArray™ Synthesizer is the manufacturing solution. The fully automated CustomArray™ Synthesizer is a semiconductor based oligonucleotide microarray synthesizer. In-situ synthesis occurs on a blank CombiMatrix CustomArray™ slide, which allows researchers to manufacture high quality commercial grade microarrays to exact specifications with complete control over the content while improving design-to-results turnaround. Investigators now are able to rapidly manufacture high-quality, commercial grade microarrays to exact specifications while maintaining complete control over the DNA sequence information. Investigators also can create novel microarray focusing on specific pathways or organisms not addressed by other vendors.

With the CustomArray Synthesizer, probes are created in-situ, eliminating the need to buy and maintain large libraries of oligonucleotides. In addition, there is no need to store oligonucleotides that are made obsolete by design and experiment changes. Simply changing a design file allows a researcher to make rapid, iterative design changes as often as they wish. With several microarray formats from which to choose (2,200, 12,000 and 90,000 feature arrays) there is a density available to help answer you microarray needs. These arrays can be stripped and re-hybridized, cutting costs dramatically versus other microarray platforms. CombiMatrix also offers pre-designed CatalogArrays that can be used for many applications.

In summary, CombiMatrix CustomArrays and the CustomArray Synthesizer open the door to many microarray experimental applications and is truly a platform for discovery. To learn more about CombiMatrix technology and how they can help create a CustomArray for you, visit www.CombiMatrix.com.

Contributed by Charles Greaves
Sales Support Specialist
CombiMatrix Corp.

http://www.combimatrix.com/

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We're on the Web!

See us at:

microgen.ouhsc.edu

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Rate structure *(partial listing; please check our web page for details)*

DNA sequencing (<96 samples)	\$5/reaction	Library construction	*contact us*
DNA sequencing (≥96 samples)	\$3/reaction	Human genotyping	\$500/sample
DNA fragment analysis	\$3/sample	Membrane array fabrication	\$11/array
HLA DNA sequencing	\$400/locus	Microarray scanning	\$20/slide
DNA normalization, 96 samples	\$10.60	Bioinformatics support	\$45/hour

Bioinformatics support

We offer bioinformatics support through our Informatics Core, directed by Jeremy Zaitshik. The rate for support is \$45/hour with a one-hour minimum charge. **Please note: we do not provide Tier 1 IT support.** For inquiries or work requests contact:

Jeremy Zaitshik (Jeremy-zaitshik@ouhsc.edu)
Perl programming (for sequence analysis, manipulation, etc.)
UNIX/Linux system administration
Security issues
Sequence analysis software questions
Data acquisition/automation
Database design (MySQL/PostgreSQL)
Web design (HTML/CGI)

Tim Schmidt, M.S. (Timothy-schmidt@ouhsc.edu)
Phylogenetic analysis (PAUP, PHYLIP, MEGA, PAML, etc.)
Comparative genomics (alignment, promoter analysis, etc.)
Perl programming (data manipulation, data mining, etc.)
Proteomic analysis (localization, structure, display with spdv, Rasmol, etc.)
Web design/HTML

INBRE Multicampus Bioinformatics Specialist

The INBRE MBE Specialist is responsible for fostering the development of bioinformatics education on 14 undergraduate campuses in the state of Oklahoma, and coordinating INBRE-related bioinformatics activities with the INBRE Bioinformatics Core. For inquiries and INBRE information, please contact:

Edgar Scott, M.S.
(edgar-scott@ouhsc.edu)
Bioinformatics education
Computational biology education
Sequence analysis software questions
Data acquisition/automation
Web design

About us…

The OUHSC Laboratory for Genomics and Bioinformatics is a full-service genomics facility offering DNA sequencing (small- and large-scale projects), microarray design and hybridization and other services. The Director of the Laboratory for Genomics and Bioinformatics is David Dyer, Ph.D., a Professor in the Department of Microbiology and Immunology at the University of Oklahoma Health Sciences Center. Allison Gillaspy, Ph.D., is the Associate Director of the Laboratory for Genomics and Bioinformatics and a Research Assistant Professor in the Department of Microbiology and Immunology. The University of Oklahoma is an equal opportunity institution. This publication, printed by OU Printing services, is issued by the University of Oklahoma. 150 copies have been prepared and distributed at no cost to the taxpayers of the State of Oklahoma.