GENNOVATIONS

Genomics Core Newsletter *Volume 1, Issue 1*

Meet the SOM Genomics Core Personnel

Dr.Judy Crabtree

The Director of the newly created SOM Genomics Core is Dr. Judy Crabtree, Assistant Professor of Genetics, who assumed this position beginning October 1, 2013. Dr. Crabtree's first introduction to genomic technologies took place during her graduate work in the laboratory of Dr. Bruce Roe at the University of Oklahoma. Oklahoma's Advanced Center for Genomic Technology was one of the original ten laboratories funded by the NIH to sequence the human genome. Dr. Crabtree's graduate efforts resulted in the production and annotation of over 0.8Mb of sequencing data from portions of human chromosomes 9, 11 and 22. Additional efforts contributed to technology development resulting in higher throughput and accuracy of DNA sequencing data. Dr. Crabtree has first-hand experience in the rapidly evolving field of genomic technology, from manual radioactive Sanger sequencing to the first automated DNA sequencers to the Next Generation Sequencing available today. As Director of the SOM Genomics Core, Dr. Crabtree is available for advising and consulting, along with Dr. Chris Taylor (see below), to assist LSUHSC faculty with genomics projects, experimental design and appropriate methodology. She is also responsible for establishing agreements with outside institutions to expand the available genomics services available to LSUHSC researchers. Dr. Crabtree will be visiting each department, both clinical and basic science, in the coming year to present a seminar on the utility of genomics technology and to describe the application of genomics to the current research conducted by our LSUHSC faculty.

Core Services

LSUHSC faculty have access to many resources for genomic analysis both on campus and off. On campus, a MiSeq instrument available for small genome sequencing projects (for example microbial genomes) managed by Drs. David Welsh and Meng Luo. Through collaboration with the LCRC Illumina Core, larger genome projects can be run on the Illumina Genome Analyzer IIx directed by Jovanny Zabaleta. Off campus, the SOM Genomics Core is establishing contracts with outside commercial vendors and genomics core facilities at regional institutions to obtain competitive pricing for services including whole genome sequencing, exome sequencing for clinical or research applications, miRNA-sequencing, ChIP-sequencing, transcriptome analysis, and more. Contact us for details.

Dr. Chris Taylor

Dr. Chris Taylor is the Bioinformatics Manager for the SOM Genomics Core and Associate Professor in the Department of Microbiology, Immunology, and Parasitology. Dr. Taylor has been working in the field of bioinformatics and productively collaborating with biologists for more than a decade. During his graduate studies, he spent nearly 5 years working in a molecular biology lab focusing on DNA replication and chromatin structure in the human genome working with genome-tiling microarrays, an early precursor of high-throughput DNA sequencing. Dr. Taylor has an educational background in mathematics and computer science that complements his current research focus in genomics and high-throughput sequencing. Dr. Taylor has developed analysis methods for a variety of experimental data sets using high throughput sequencing including data produced on the 454 Genome Sequencer FLX, Illumina's GA IIe, and the newer Illumina MiSeq and HiSeq instruments. This work has included RNA sequencing studies and studies of microbial communities (microbiome), ultimately leading to the development of an entire distributed software system for RNA sequence analysis and a computational framework for metagenomic sequencing. As the Bioinformatics Manager, Dr. Taylor advises and directs LSUHSC faculty on the analysis and interpretation of data from large scale genomics projects in addition to designing and developing software for visualization, analysis and storage of high-throughput genomics data.

Want to do large scale genomic analysis?
Where to start?

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Consult Drs. Crabtree, Taylor or Zabaleta

MiSeq
small genomes
exomes

Outsourced Contract Vendors

Genome Analyzer IIx
large genomes
RNA-seq
ChIP-seq

Judy Crabtree, Ph.D.
Director
CSRB 748D
jcrabt@lsuhsc.edu
504-568-2963

LSU Health New Orleans
HEALTH SCIENCES CENTER
School of Medicine
Genomics Core

Chris Taylor, Ph.D.
Bioinformatics
CSRB 7605
ctay15@lsuhsc.edu
504-568-2215