NRC *newsletter*

Neuroscience research with bioinformatics approaches in the post-genomic era

By Yin Liu, Ph.D.

Liu

Abstract: Over the past two decades, advances in genomics technology have opened the door for rapid biological data acquisition and have revolutionized many aspects of neuroscience research. Given the complex nature of brain systems and the noisy nature of large-scale biological data, it is becoming increasingly important to develop sound analytical tools, together with computational models for the analysis, integration, and interpretation of experimental data in order to aid new discovery of brain system function. Here, using Traumatic Brain Injury (TBI) as a case study, we demonstrate how the computer-assisted approaches developed in our lab can help identify functional gene networks involved in TBI. An understanding of these genes will provide insights on the pathological processes in TBI, including memory loss, poor attention, and visual disturbances.

Experimental advances in high-throughput technologies have provided neuroscientists with a wealth of information that spans multiple levels of the nervous system. The rapid accumulation of genomic and proteomic information has provided valuable resources that motivate us to study how the genome as a whole contributes to the development, structure and function of the nervous system. We are now in the post-genomic era, with complete genome sequences of human and many other organisms available, and the application of bioinformatics in the neuroscience domain goes far beyond traditional bioinformatics research such as DNA sequence analysis. The intersection of bioinformatics

How bioinformatics is shaping and influencing neuroscience research: development of bioinformatics in clinical research

By: Georgene W. Hergenroeder, MHA BSN RN CCRC and John Redell, Ph.D.

Hergenroeder

Redell

Abstract: According to the CDC, traumatic brain injury (TBI) is a contributing factor in over 30% of all injury-related deaths in the U.S., with the direct and indirect costs associated with TBI estimated to exceed $75 billion. Although improvements in personal safety devices (e.g. increased seat belt use, air bags) and emergency medical care have greatly improved the initial survivability of TBI, a lack of objective diagnostic/prognostic tools are available to help identify TBI patients at risk for developing potentially devastating secondary pathologies. In addition, adherence to established and effective clinical guidelines for the car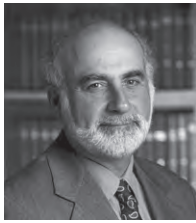e and treatment of TBI patients is inconsistent. Our research focuses on both clinical and translational aspects of TBI diagnosis and treatment. Bioinformatics is instrumental in this research through its use in biomarker discovery, in the collection of clinical/physiological data to evaluate responses to interventions, and to support quality of care improvement efforts. The ultimate goal of our bioinformatics effort is to improve healthcare and patient outcomes at both the individual and systems levels.

An international movement is currently directed at standardizing health information and employing electronic health records (EHR) to more efficiently and accurately utilize clinical data, with the goal of improving

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Bentsen Stroke Center

From the Director, John H. Byrne, Ph.D.

In the United States, there are approximately 800,000 new or recurrent stroke cases each year, with stroke being the leading cause of long-term disability and the third-leading cause of death. Progressive, ongoing research is crucial to help those affected by stroke. The Neuroscience Research Center is pleased to report on significant progress underway at the Senator Lloyd and B.A. Bentsen Center for Stroke Research at UTHealth. January 2009 marked the opening and dedication of the Center, which aims to promote research and collaboration in stroke prevention, treatment and care. The Center was named after the four-term U.S. Senator from Texas and Secretary of the Treasury, Lloyd Bentsen, Jr. and his wife, B.A.. Together, along with the help of others, they created this research center and program which is now a major component of The Brown Foundation Institute of Molecular Medicine for the Prevention of Human Diseases (IMM).

In just three years, the Center has already established seven funded Bentsen Investigators working on six research projects. In 2011 and 2012, the Bentsen Stroke Center grants were awarded to UTHealth faculty members to develop cell-based therapies to lesson injury progression, reduce overall brain injury and enhance recovery. A summary of these projects is below.

Following hemorrhagic stroke, scavenging cells (e.g., microglia, macrophages, phagocytes) help remove the excess blood that has created a toxic environment and inhibited proper brain function. Professor Jaroslaw Aronowski of the Department of Neurology will conduct a clinical trial to examine whether genetically or pharmacologically modified scavenging cells can act more efficiently to remove that blood. A faster process could lesson injury progression, reduce brain damage and improve neurological recovery.

Associate Professor Qilin Cao of the Department of Neurosurgery is developing novel strategies to turn the skin cells of stroke patients into neural stem cells.

These neural stem cells could then be transplanted back into the patient to replace nerve cells damaged or killed by the stroke injury and hopefully promote functional recovery. Dr. Cao is testing the therapeutic efficacy and long-term safety of patient-specific neural stem cells in a clinically relevant animal model of stroke injury.

Assistant Professors Ying Liu and Jiaqian Wu of the Department of Neurosurgery are also working to create replacement cells, however this process is generally slow and inefficient. Their goal is to identify differences in gene expression and regulatory mechanisms between two cell types derived from human induced pluripotent stem cells (hiPSC); hiPSC-derived neural stem cells (NSCs) and hiPSC-derived neuronal restricted progenitors (NRPs). Understanding the genetic and molecular mechanisms of differentiation could lead to more efficient regeneration of replacement cells and ultimately better treatment strategies for stroke victims.

A surgical procedure performed on babies born with congenital heart disease can lead to reduced blood flow in the brain, resulting in neurological injury similar to stroke. Professor Charles S. Cox, Jr. of the Department of Pediatric Surgery is conducting a preclinical test to determine if stem cell therapy, using stem cells derived from amniotic fluid, can treat and lessen the neurological injury. Using the patient's own stem cells could decrease risk of rejection and increase the success rate.

Stroke and traumatic brain injury both lead to inflammation which results in further neurological damage. Professor Pramod Dash of the Department of Neurobiology and Anatomy is examining the cellular and molecular mechanisms underlying brain injury-induced inflammation to develop novel treatment strategies. Using a combination of intravenously administered adult stem cells as well as pharmacological and molecular techniques, his goal is to decrease stroke-induced cognitive impairments.

Using animal models, Professor Sean Savitz of the Department of Neurology was one of the first to use stem cells in stroke treatment. His group is currently identifying potential biological targets of stem cell therapies in stroke patients using neuroimaging techniques. These studies examine the extent to which stem cells reduce brain damage and repair white matter injury in the brain of stroke patients.

These projects, as well as others conducted at the Center, will result in important advancements in stroke prevention and treatment. But, the Center is designed to be more than an assembly of individual projects. Dr. Brian Davis, Associate Professor and Director of the IMM's Center for Stem Cell and Regenerative Medicine, which is the academic and administrative home of the Bentsen Stroke Center, has instituted steps to encourage synergistic collaborative interactions that will lead to new and greater research advances. To foster these collaborations, the Center holds monthly meetings of the group to discuss research updates and to host invited speakers to share their expertise with members of the Center. Collaborations and interactions are also facilitated by physical location of many of the research laboratories in the Sarofim Research Building of the IMM. Shared equipment is available to all Bentsen Investigators. The generosity from the Bentsen family extends to their son, Lan Bentsen, who is working to maintain and continue the success of the Center with his mother B.A..

New research laboratory space at the Senator Lloyd and B.A. Bentsen Center for Stroke Research

news&information

Terri Armstrong, Ph.D., Professor at the UTHealth School of Nursing, has been awarded a Research Project Grant to study toxicity profiling by the National Institute of Nursing Research (NINR).

Michael R. Blackburn, Ph.D., and **Yang Xia, Ph.D.,** from the Department of Biochemistry and Molecular Biology, are two of three recipients of Program Project Grant (PPG) awarded by the National Heart, Lung and Blood Institute of the National Institutes of Health. Dr. Blackburn's project focuses on adenosine signaling in lung disease, while Dr. Xia's project explores the role of adenosine signaling in sickle cell disease.

Raymond J. Grill, Ph.D., Assistant Professor in the Department of Integrative Biology and Pharmacology was awarded a grant from the Craig H. Neilsen Foundation to explore the use of a dual cyclooxygenase and 5-lipoxygenase inhibitor in improving motor function following spinal cord injury.

Jair C. Soares, M.D., Chair of the Department of Psychiatry and Behavioral Sciences, is Principal Investigator of a National Institute of Mental Health R01 study to determine whether brain differences observed in people with bipolar disorder are due to hereditary-dependent genetic alterations.

Congratulations to NRC Members:

Michael R. Blackburn, Ph.D., Gerard E. Francisco, M.D., Cynthia W. Santos, M.D., and their fellow UTHealth colleagues for being elected to the UT Academy of Health Science Education.

Michael R. Blackburn, Ph.D., Dean of the Graduate School of Biomedical Sciences and Professor Biochemistry, was awarded the UTHealth's President's Scholar Award for Research.

Nachum Dafny, Ph.D., John McMahon, Ph.D., Merrill Overturf, Ph.D., Gary C. Rosenfeld, Ph.D., George Stancel, Ph.D., and **Anthony Wright, Ph.D.,** were honored with the UTHealth 2013 Star Award for 40 years of service.

Pamela M. Diamond, Ph.D., Associate Professor in the Division of Health Promotion and Behavioral Sciences at UTHealth School of Public Health has been awarded the 2012-13 John P. McGovern Award for Outstanding Teaching.

Andrew Harper, M.D., Chief Medical Officer of the UT Harris County Psychiatric Center, Assistant Dean for Educational Programs and Professor of Psychiatry and Behavioral Sciences, has been elected president-elect of the Texas Society of Psychiatric Physicians (TSPP).

Nneka Ifejika-Jones, M.D., Assistant Professor of Neurology, has been selected as one of ten from a national pool for the inaugural class of the American Academy of Physical Medicine and Rehabilitation's Academy Leadership Program.

Vineeth John, M.D., M.B.A., led a team of Psychiatry residents to win the Mind Games Trophy at the annual meeting of the American Psychiatric Association in San Francisco. Team members were Drs. Garima Arora, Marsal Sanches, and Ashley Toutounchi.

Pedro Mancias, M.D., Associate Professor of Pediatrics and Neurology, and Assistant Dean of Diversity and Inclusion, has been awarded the John P. McGovern Outstanding Teaching Award for exceptional clinical teacher.

Ponnada Narayana, Ph.D., Professor in the Department of Diagnostic and Interventional Imaging and Director of Magnetic Resonance Research, was a recipient of the 2013 Distinguished Investigator Award of the Academy of Radiology Research.

Philip R. Orlander, M.D., Professor and Director of the Division of Endocrinology, Diabetes, and Metabolism in the Department of Internal Medicine, was awarded the UTHealth's President's Scholar Award for Teaching.

Philip R. Orlander, M.D., Professor of Medicine, and **Gary C. Rosenfeld, Ph.D.,** Assistant Dean for Educational Programs, received the Regent's Outstanding Teaching Award that recognizes faculty members at UT System institutions who have demonstrated dedication to innovation and for the advancement of excellence in the classroom and laboratory.

Han Zhang, M.D., Associate Professor of Neurobiology and Anatomy, is this year's winner of the John H. Freeman Faculty Teaching Award. This is the fourth time Dr. Zhang has received the award. Thirty-five NRC members were recipients of the 2012-2013 Dean's Teaching Excellence Awards.

Antonio Tito, a student in the lab of **Sheng Zhang, Ph.D.,** received the 2013 Federation of American Societies for Experimental Biology (FASEB) MARC Travel Award.

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and neuroscience research in the past 10 years has focused on the following areas: microarray, next-generation sequencing and proteomic techniques applied in brain diseases for disease biomarker identification; tools and methods to study gene expression and sequencing; methods for network analysis connecting molecular pathways to disease mechanisms and nervous function; and the development of user-friendly genome-scale resources such as the Allen Brain Atlas and BrainMap databases. With large-scale genomic and proteomic information available, the "omics" or discovery-based approaches aim to extend the scope of brain research from individual genes or pathways to a systems-level understanding of brain circuit function. Traditionally, omics-based approaches focus on hypothesis generation, rather than hypothesis testing. These approaches have led to a revolution in the field of neuroscience research, by allowing high-throughput hypothesis generation, that is unique compared to the single hypothesis-testing approaches utilized in traditional neurobiology laboratories. One area in which the omics-based approaches have been promising is in the detection of biomarkers for neurological and psychiatric diseases. In this case, the focus has been on generating novel hypotheses regarding genetic signatures. A gene signature is the combined expression pattern of a group of genes that is distinctly characteristic of a disease, or the specific state of a disease. By using this information, researchers can use genetic signatures to better understand the underlying disease mechanisms, leading to the discovery of new therapeutic interventions.

In recent years, the strength of applying bioinformatics approaches combined with genomic and proteomic experimental techniques has been demonstrated across different areas of neuroscience research. For example, a recent study, published in Nature Neuroscience (2008) by Emes et al. from the Wellcome Trust Sanger Institute, combined genomic and bioinformatic approaches to successfully identify synaptic proteins that have changed during evolution and investigate how these proteins might relate to brain anatomy and function. Another study, published in Proc Natl Acad Sci (2005) by Nagasaka et al., applied bioinformatic approaches to identify a unique gene signature that distinguishes familial Alzheimer's disease mutation carriers from their normal siblings. While the power of omics-based approaches has been clearly demonstrated in these studies, the adoption of these approaches remains a challenge in the field of neuroscience. This is mainly due to the extreme heterogeneity and complexity of brain systems relative to other non-neural tissues. Another challenge is the generation of high-throughput genomic and proteomic datasets. The complexity and the volume of the information available has posed enormous challenges in data sharing and modeling, making it necessary to develop sophisticated bioinformatics tools for facilitating data mining and integration. How can we investigate brain functions in health and disease by integrating data simultaneously gathered at multiple levels of the nervous system? What new tools are required for encompassing these levels to allow us to both find patterns in

the data and to test specific hypotheses? How can signaling or metabolic networks inferred by these tools help to guide the diagnosis and treatment of neurological diseases? These are exciting and challenging questions that we need to address in order to advance the field of neuroscience in the post-genomic era.

While closely collaborating with experimental neuroscientists, the primary research focus of my lab is in the area of computational systems biology. We develop and apply computational approaches to integrate information across multiple levels of genomic, proteomic, epigenetic, and phenotypic data in order to reconstruct gene and protein interaction networks. Recent application projects have been aimed at the problems of understanding brain disease and injury. The long-term goal in my lab is to develop a software package for investigating the mechanisms used by neural cells to accomplish signal transduction processes through computational modeling and integration of different types of information. At the current stage, we are specifically interested in identifying signaling networks through the integration of functional genomic datasets such as whole-genome gene expression profiles and proteomic data including protein-protein interaction information. The protein-protein interaction data provides direct information on specific protein relationships occurring along the backbone of the signaling network, while the whole genome expression profiles are currently the largest source of high-throughput genomic information available. The whole genome expression profiles provide gene expression information on thousands of genes in different cells, tissues or pathological specimens under various conditions. The software will be offered in an open source format to facilitate user modifications and extensions.

To demonstrate how this software tool can be applied to large-scale genomic and proteomic datasets to study brain disease and injury, we have undertaken a systematic and quantitative study of Traumatic Brain Injury (TBI), a leading cause of death and disability in industrialized countries, with approximately 1.7 million people sustaining a TBI in the United States each year (TBI statistics provided by the Centers for Disease Control). TBI results from an external force causing immediate damage to brain tissue, followed by secondary pathogenic events which ultimately give rise to neurodegeneration. Dependent on the context of the primary injury, different cell responses are initiated that can exacerbate the injury to varying degrees. Cell death resulting from the initial impact on the brain tissue is irreversible so treatments normally focus on minimizing the secondary injury due to these cell responses. To date, these secondary injury responses have not been well characterized, leaving molecular classification of TBI cases difficult. TBI subtype classification is an important step towards the development and selective application of novel treatments. We have aimed to improve the identification of biomarkers that can distinguish two different classes of TBI in rodent animal models; the mild Cortical Contusion Injury (mCCI) and the mild Fluid Percussion Injury (mFPI), representing focal and diffuse TBIs, respectively. We developed and

applied a network-based approach on gene expression profiles from the entire rat genome, generated from Dr. Pramod Dash's lab in the UT Medical School at Houston. Typically, in traditional expression profiling studies, genes that are not significantly differentially expressed between TBI classes (i.e., genes that are not associated with a class of TBI at a significance threshold) are neglected. These discarded genes' modest association may represent false negatives and may be important biomarkers of TBI. We hypothesize that these genes may be identified within functional units of genes that in aggregate have a significant association to a TBI class. To test this hypothesis, we identified biomarkers not as individual genes but as gene sub-networks by incorporating the gene expression profiles from mCCI and mFPI insults and the protein-protein interaction information from existing databases. We expect the resulting sub-networks to provide novel hypotheses for testing the role(s) of pathways involved in different TBI classes.

Unlike traditional expression profiling methods, our network-based analysis can identify genes that are not differentially expressed and are often neglected to determine if such genes are essential for maintaining the integrity of a sub-network whose overall expression is discriminative between samples. An example of the resulting discriminative sub-network is shown in Figure 1. The genes interferon-γ (IFNG) and myc-interactor (NMI) did not show significant differentiated expression between CCI and FPI samples, but they played an important role in the discriminative sub-network by interconnecting many differentially expressed genes, such as JAK1, JAK2, JAK3, STAT1 and STAT3. Given the fact that both IFNG and NMI genes are well-known players in the cytokine signaling pathway involved in inflammatory response, our results suggest they can serve as potential targets for intervention.
Another advantage of our network-based analysis demonstrated from our preliminary study is that the list of identified significant gene sub-networks achieves higher sensitivity and specificity in classifying the heterogeneous responses corresponding to different classes of TBI, compared to a conventional analysis using an individual gene list. We therefore believe that effectively incorporating gene expression profiles into protein interaction information can identify functional subnetworks that better classify different classes of TBI and are more reproducible across related studies than individual genes selected without network information. We understand that translating the knowledge gained from an animal model to molecular biomarkers identification in patients is practically challenging, simply because the brain tissue in TBI patients is rarely available. However, the use of peripheral tissues such as lymphoblast or blood could be a potential solution. If successful, these identified biomarkers could be used to better direct the diagnosis and treatment to TBI patients, and more optimistically, they could help to develop rationale-based therapies for treating the millions of Americans who suffer from TBI.

Neuroscience has no doubt provided a rich application area for informaticians. A decade after the human genome sequencing was completed there is a high demand for bioinformatics tools to explore a wealth of neuroscience information at multiple levels of the nervous system, spanning from molecules to behavior. Our work provides an example on how bioinformatics approaches can be applied in neuroscience research by performing a genome-wide data analysis to gain a better understanding of interacting signaling pathways. The developed approaches will enable the generation of hypotheses subject to experimental validation. The resulting experimental data will, in turn, be used to generate more refined models that will advance our understanding of brain function.

Figure 1. *An example of discriminative sub-network. The overall expression activity of the sub-network is different between the mild Cortical Contusion Injury (mCCI) and the mild Fluid Percussion Injury (mFPI) samples. Nodes and edges represent proteins and protein interactions, respectively. The circle-shaped nodes indicate the corresponding genes are significantly up-regulated in mFPI samples (FDR controlled q-value <0.05), but not in mCCI samples. The diamond-shaped nodes indicate the corresponding genes are not differentially expressed*
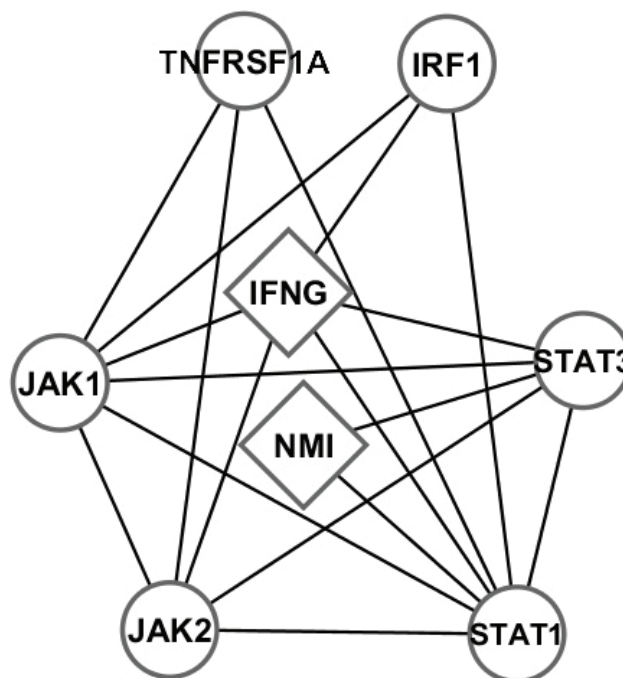
About the Author
Dr. Yin Liu received her Ph.D. in Computational Biology and Bioinformatics from Yale University Scool of Medicine. Subsequently, she joined the Department of Neurobiology and Anatomy at the University of Texas Medical School at Houston as an Assistant Professor in 2007. Her laboratory develops computational and statistical methods to analyze and integrate heterogeneous data sources for understanding brain circuit function at a systems level. For more information, please visit: **http://nba.uth.tmc.edu/homepage/liu/**

patient care. In addition to utilizing electronic clinical documentation to obtain automated responses to specific research questions, research efforts analyze care patterns and patient outcome data to identify best practices, determine strategies to promote quality and allocate resources. It is increasingly clear that a uniform standard for collecting and disseminating electronic clinical data is needed in order to more effectively communicate across a variety of systems. The American Recovery and Reinvestment Act of 2009 authorized the creation of incentive programs to speed "meaningful use" documentation utilizing EHRs. These meaningful use standards coincided with an increased movement of healthcare payers toward refining uniform procedural and diagnostic medical coding for reimbursement of patient care costs while promoting improved access to information. Likewise, many research granting agencies, including several NIH Institutes and Centers, are actively encouraging the recording and use of standardized common data elements (CDEs), which can be used by investigators to more easily collect, analyze, compare, and share data collected across different studies. Together, these shifts toward standardized electronic data entry and collection provide more opportunities for clinical and biomedical researchers to easily integrate clinical information with bioinformatic resources, and present opportunities for the development, testing, and evaluation of new treatments and therapeutics to improve patient care and outcome. Working with partners at the Mischer Neuroscience Institute, Memorial Hermann Hospital System, and ClearPath Solutions, our bioinformatic efforts currently focus on sample analysis for biomarker discovery, developing database systems for interventional studies, and clinical care quality analysis, with the ultimate goal of improving healthcare at both the systems and individual patient levels (Figure 1).

Protein biomarkers can be used clinically to screen for, diagnose, or monitor the state of a physiological or pathological condition/disease. We have used a combination of proteomic and bioinformatic analyses of patient serum/plasma samples in our biomarker discovery research. For example, we have used proteomics in our traumatic brain injury (TBI) research to identify relative changes in protein abundance with the goal of discovering protein biomarkers to facilitate diagnosis and treatment. In this study, TBI patient serum samples were first immuno-depleted to remove highly abundant proteins (e.g., albumin, IgG), which can be present at milligram per milliliter quantities and interfere with the detection and quantification of lower abundant (pg/ml) circulating proteins that may be more diagnostically informative. The remaining serum proteins were digested and labeled with unique mass-balanced isobaric tags (iTRAQ). These labeled peptides were then identified, and their relative quantities determined, using a liquid chromatography-tandem mass spectrometry (LC-MS/MS). The resulting MS data then underwent obligatory bioinformatics analyses to filter the MS spectra data, identify peptide sequences, quantify their relative abundance, and map the peptides back to their parent proteins. This analysis identified 31 candidate TBI biomarkers, and relied upon the integration of two related data sets: clinically collected patient data, which enabled the accurate classification of TBI patients into appropriate analysis groups, and the LC-MS/MS data, which enabled the identification and quantification of changes in serum proteins.

We have since performed follow-up studies on some of the putative biomarker candidates, including the copper-containing, acute phase response protein ceruloplasmin. We found that serum ceruloplasmin was significantly decreased within the first 36 hours post-injury in a subset of TBI patients who later developed elevated intracranial pressure (ICP). We found a similar decrease in retinol binding protein-4 levels in a subset of TBI patients who developed elevated ICP. Elevated ICP is a significant secondary pathology associated with TBI, and contributes to increased TBI patient morbidity and mortality. The development of clinically useful biomarkers that are able to accurately predict the development of elevated ICP could be used to more efficiently allocate resources, optimize patient care (e.g., placement of an extraventricular drain or transportation to a center with neurosurgery expertise), and improve patient outcomes.

In a separate project on subjects with devastating neurological injury, protein biomarker analysis utilizing enzyme-linked immunosorbent assay (ELISA) of inflammatory markers measured the effect of an anti-inflammatory nutritional intervention. The possible benefits of immunomodulating nutrition include: reduced intestine-to-liver bacterial product translocation that may contribute to multi-organ failure; provision of antioxidants and vitamins that lower oxidative stress, cytokine levels and apoptosis; and improved neutrophil (a type of white blood cell) response to infection and inflammation. In this study, indirect calorimetry was performed on organ donors to quantify energy expenditure. Additionally [13]carbon-labeled uracil breath analysis was performed using infrared spectrophotometry to measure gastrointestinal function. The results indicated that a third of the subjects metabolized the tracer indicating that the gastrointestinal tract as the route for delivery of anti-inflammatory nutrition is safe and absorption is possible for some of these patients.

The Brain Trauma Foundation introduced clinical practice guidelines for the management of TBI in 1996. Although adherence to these guidelines has been shown to decrease mortality, improve outcome, and reduce length of hospital stay and health care expenditures, they are not always consistently applied in practice. Improving adherence to these guidelines could potentially

Figure 1. The relationship of bioinformatics with human subject samples and research.
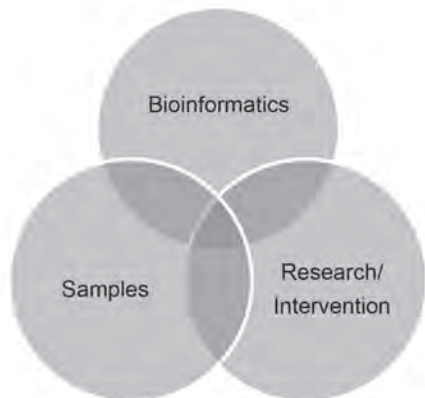
significantly impact patient care and outcome, and is a focus of our quality improvement initiative. It is expected that fostering the delivery of safe and effective healthcare, improving compliance with care guidelines, and improving patient outcomes can be accomplished by incorporating patient care protocols founded on the Brain Trauma Foundation guidelines into electronic clinical decision support using a neuro-specific EHR that is in development. The Institute of Medicine's (IOM) report Crossing the Quality Chasm identifies information technology as being central to improving health care quality by providing timely and readily accessible data to aid in clinical decision making. The IOM defined clinical decision support as "software that integrates information on the characteristics of individual patients with a computerized knowledge base for the purpose of generating patient-specific assessments or recommendations designed to aid clinicians and/or patients in making clinical decisions". For example, decision support systems incorporating data from hospital information systems have been shown to improve antibiotic treatment choice and reduce patient adverse events. Similarly, electronic reminders have been shown to increase preventive care (e.g., influenza vaccination, venous thromboembolsim prophylaxis, myocardial infarction/stroke prophylaxis). Through the implementation of electronic decision support utilizing evidence-based clinical practice guidelines like those of the Brain Trauma Foundation for TBI patients, we aim to augment clinical decision making. Bioinformatics can influence quality of care by offering clinical decision support as an adjunct to the EHR to alert or recommend care according to agreed upon clinical best practice guidelines.

About the Author

Georgene W. Hergenroeder, MHA BSN RN CCRC is an Assistant Professor in the Department of Neurosurgery and the Director of the Neuroscience Research Repository and the Director of the HOPES Trial. She received her undergraduate and graduate degrees from Duke University, Durham, NC. She has directed the implementation of a neurosurgery-specific electronic health record. She is involved in designing, developing, and implementing translational and clinical trials. Her primary research focus has been on protein biomarkers in traumatic brain injury, spinal cord injury and organ donors. In addition, she was a member of the UT Committee for the Protection of Human Subjects (IRB) 2006-2012.

About the Author

Dr. John Redell received his Ph.D. from the University of Washington, working in the laboratory of Dr. Bruce Tempel. He received his post-doctoral fellow training in the laboratory of Dr. Pramod Dash at the University of Texas Health Science Center at Houston, where he is an Assistant Professor. At UT-Houston, his work has focused on the pathological molecular changes initiated by traumatic brain injury. Most recently, his research has been directed toward investigating the

Figure 2. Flow of information and samples for research to improve healthcare and ultimately patient outcomes.
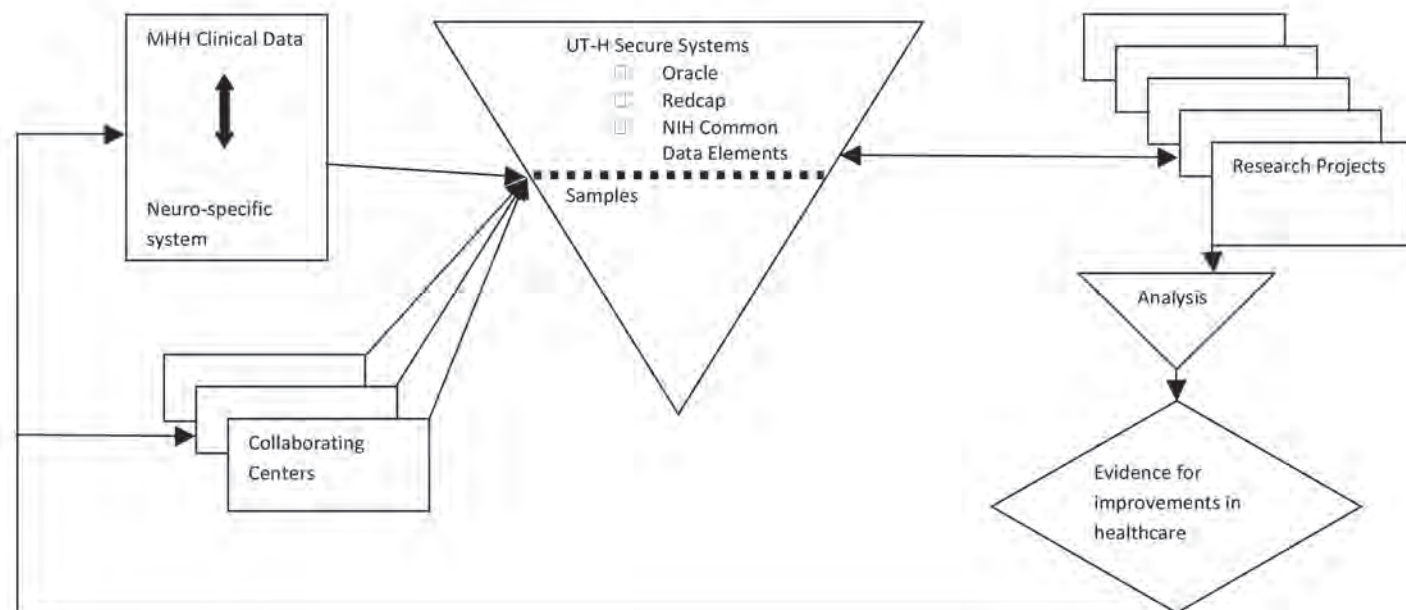
Brain Awareness Week 2013

With support from the Society for Neuroscience and Dana Alliance for Brain Initiatives and the TIRR Foundation & Mission Connect, the NRC hosted two events in association with Brain Awareness Week 2013. Special thanks to our many volunteers and public advocacy groups that were involved.

Brain Night at The Health Museum - March 14, 2013

Over 40 volunteers and more than 500 local community members joined us during Spring Break to learn about the brain. Sixteen activity booths allowed children to build a neuron out of pipe-cleaners, hold a real human brain, see real nerve cells under a microscope, test their reflexes, and challenge their senses.

18th Annual Public Forum - February 23, 2013
"Concussions: Advances in Prevention, Diagnosis and Treatment"

Left Side Photo: Former NFL Offensive Lineman, Dr. Mark Adickes (top, center) moderated a timely discussion on concussions. Expert UTHealth Panelists included (counterclockwise from Adickes) Drs. James McCarthy, Pramod Dash, Summer Ott and Nitin Tandon. Dr. Jack Byrne, Director of the NRC, welcomed everyone to the event.

Upcoming Events

Neurobiology of Disease Seminar Course: Progress and Challenges in Understanding Brain Disorders.
Wednesdays from Noon to 1:00 pm, from August 28 to December 11, 2013

This course will explore grand challenges in understanding the underlying mechanisms and future treatments of a variety of neurological diseases and disorders. Lectures will be given by UTHealth faculty with a special guest lecture. Course contacts: Anne.Hart@uth.tmc.edu or John.H.Byrne@uth.tmc.edu. Held at the UTHealth Medical School Building, Room 7.037.

Neurobiology of Disease Course Guest Lecture.
Wednesday, August 28, 2013

Dr. Tom Jacobs, Assistant Vice Chancellor For Federal Relations, U. T. System. UTHealth MSB B.645 from Noon to 1:00 pm. A special Q&A session with Dr. Jacobs will be held from 4:00 – 5:00 pm for all of the Gulf Coast-Houston neuroscience community, postdocs and students about the future of neuroscience research and training at NIH. UTHealth MSB 2.103.

Neuroscience Poster Session.
Saturday, December 7, 2013, 9:00 am to Noon

UTHealth Cooley University Life Center, 7400 Cambridge St., Houston, TX.

Brain Night at The Health Museum.
Thursday, March 20, 2014, 6:00 to 8:00 pm

The Health Museum, 151 Hermann Drive, Houston, TX. Free event and open to the public.

Distinguished Lecture Series.
Thursday, March 27, 2014, 4:00 to 5:00 pm

UTHealth Medical School Building, Room MSB 3.001, Dr. Huda Y. Zoghbi, Baylor College of Medicine

19th Annual Public Forum: MS Update: Advances in Diagnosis and Management of Multiple Sclerosis.
Saturday, April 5, 2014, 10:30 am to Noon

UTHealth Cooley University Life Center, 7400 Cambridge St., Houston, TX. Co-moderators for this event are country singer, Clay Walker, and UTHealth MS Specialist, Dr. Jerry Wolinsky. Expert UTHealth panelists include: Drs. Flavia Nelson, J. William Lindsey, Nneka Ifejika, and John Lincoln. Free event and open to the public.

The 2nd annual UTHealth Stroke Festival of Life.
will be held on May 3, 2014 at Discovery Green

This is a family-friendly event featuring stroke education, brain health, health screenings, nutrition, fitness & lifestyle education and activities, giveaways, door prizes and family entertainment. The event is open to the public- no admission fee.

Please contact Dr. Elizabeth Noser at Elizabeth.noser@uth.tmc.edu if you would like to volunteer or for further information.

The NRC is able to host events free to the public because of the continued support and generosity of individuals in the community.

Please support us by making a tax-deductible donation online at: http://giving.uthouston.org/nrc

Welcome New Executive Committee Members!

Welcome New Executive Committee Member Dr. Joy Schmitz! The NRC would like to welcome Joy M. Schmitz, Ph.D., of the UTHealth Department of Psychiatry & Behavioral Sciences to the UTHealth NRC Executive Committee.

The NRC would also like to thank Dr. Frederick Gerard Moeller, M.D., for his years of dedicated service to the Committee.

UTHealth | **Neuroscience Research Center**

The University of Texas
Health Science Center at Houston

6431 Fannin St., MSB 7.046
Department of Neurobiology & Anatomy
Houston, TX 77030

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Questions? Comments?
Contact us at 713-500-5538
or E-mail: nba-nrc@uth.tmc.edu

Check out of Neurofax calendar of neuroscience events on-line! The Neurofax includes seminars, grand rounds, research colloquia, symposia, and local or national conferences that are sponsored by UTHealth, the Texas Medical Center, and other Houston area universities and research institutions. To submit your event to this calendar, please send an email to nba-nrc@uth.tmc.edu and include the Event Name, Contact, Date, Time and Location.

This Newsletter is distributed by mail to individuals and groups engaged in neuroscience research within the TMC and worldwide and features research , neuroscience accomplishments and outreach efforts performed at UTHealth. Past issues are available on the NRC website.

If you prefer to receive a digital copy through email, please contact nba-nrc@uth.tmc.edu with your information.