



VBI Hosts First Annual Research Symposium

The Virginia Bioinformatics Institute (VBI) hosted its very first annual research symposium on March 23-24. The event, which was organized to share scientific ideas, showcase research efforts and stimulate new collaborations with research colleagues, included over 20 oral presentations from students, post-graduates and other scientists working at VBI. It also included over 30 poster presentations on topics spanning bioinformatics, genomics, metabolomics, proteomics and systems biology.

Reactome's website maps the interactions that take place for many metabolic pathways as well as some of the molecular events that take place in diseases like HIV/AIDS and influenza. "Each section contains a diagram that demonstrates the molecular reactions involved and allows the user to navigate to different molecular pathways and parts of pathways," Stein said. "Reactome connects different pathways, links diseases to genomic data and can be used as a 'Cliff Notes' of human biology. It's open source and freely available to the scientific community."



Dr. Lincoln Stein

The symposium was a great opportunity for scientists at different stages of their careers to give presentations not only to their colleagues but also to a wider scientific community at Virginia Tech. "The first symposium will serve as a platform for an annual event designed to make VBI research widely accessible to a broad audience" said Bruno Sobral, executive and scientific director of VBI. "We very much want to open up our research to the Virginia Tech community and beyond. The research symposium is the ideal forum for this purpose."

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Lincoln Stein, a renowned scientist at the Cold Spring Harbor Laboratory, NY, was the keynote speaker in VBI's conference center on the first day of the symposium. Stein's pioneering work in the field of bioinformatics has spurred the development of several powerful computer-based methods for analyzing a wide variety of biological data.

During his talk, Stein discussed the Reactome project, an open-source database of biological pathways which has been developed through a joint collaboration between Cold Spring Harbor Laboratory, The European Bioinformatics Institute, and the Gene Ontology Consortium.

Reactome is a database that models biological pathways and reactions in humans. It consists of a compilation of research data authored and peer reviewed by many scientific experts in different fields. Stein started Reactome because he found many limitations with some of the current biological databases. "We were missing a comprehensive pathway database that was curated and evidence-tracked," said Stein. He wanted a database that was computable and had detail down to the molecular level not only for small molecules but also for more complex molecules involved in events like cell signaling.

About Reactome (www.reactome.org)

- A curated resource of core pathways and reactions in human biology
- Information in the database is authored by biological researchers with expertise in their field
- Information is maintained by the Reactome editorial staff and cross-referenced with PubMed, GO, and the sequence databases at NCBI, Ensembl and UniProt
- Inferred orthologous events in 15 non-human species such as mouse, fugu fish, worms, fly, yeast and *Escherichia coli* are also available
- Reactome is a free on-line resource and Reactome software is open-source

Core Laboratory Facility Achieves National Custom Array Center Status

VBI has signed an agreement with Affymetrix, Inc. (Nasdaq: AFFX) for the not-for-profit use of Affymetrix' GeneChip(R) technology. Under the terms of the new, non-exclusive agreement, the Institute's Core Laboratory Facility (CLF) has been granted the status of National Custom Array Center for custom microarray design, sample processing and analytical services.

Dr. Bruno Sobral, VBI's executive and scientific director, commented: "We are excited by this opportunity to build further upon our successful relationship with Affymetrix. The GeneChip technology is a popular resource at VBI's Core Laboratory Facility and a proven tool for whole-genome analysis worldwide."

He added: "Our status as a National Custom Array Center means that we can expand our offerings of Affymetrix technologies and services to include new custom Affymetrix microarrays integrating further breakthrough genomics tools with experimental and bioinformatics expertise. This is a win-win situation for Affymetrix, the Virginia Bioinformatics Institute and our growing customer base."

Affymetrix custom microarrays offer researchers the flexibility to design arrays that can analyze the genome sequence of any organism. The custom arrays use the same high-quality design and manufacturing technologies used to create GeneChip catalog arrays.

The GeneChip technology platform consists of high-density microarrays and tools to help process and analyze microarrays. GeneChip microarrays consist of small DNA fragments that are chemically synthesized at specific locations,

referred to as features, on a coated quartz surface; millions of features can be contained on one array. By extracting and labeling nucleic acids from experimental samples, and hybridizing those prepared samples to the array, the amount of label can be monitored at each feature, enabling a wide range of applications on a whole-genome scale. Typical applications include gene- and exon-level expression analysis, novel transcript discovery, genotyping, and resequencing.



New Affymetrix Scanner Joins the Team

VBI's Core Laboratory Facility (CLF) has introduced the upgraded Affymetrix GeneChip(R) Scanner (GCS) 3000 7G as part of its services for gene expression and DNA analysis applications.

The original GCS 3000 scanner was designed to permit an upgrade for use with the next generation of high-density GeneChip microarrays reaching the market. The upgraded GCS 3000 7G, which offers advanced design improvements and high-resolution scanning capabilities, provides peak scanning performance for all applications including RNA expression and DNA analysis.

The new scanner allows analysis of microarrays that feature 500% more data than previous generations. Higher resolution scanning at pixelations from 2.5 microns to 0.51 microns is now possible.



The new upgraded instrument supports the latest high-density GeneChip microarrays for tiling, all-exon and single nucleotide polymorphism (SNP) genotyping research.

VBI e_Connections

VBI e_Connections is a quarterly publication of the Virginia Bioinformatics Institute produced by the Public Relations & Education and Outreach team. The newsletter includes feature articles, technology updates as well as interviews that may be of interest to VBI's audiences. Contributions are welcomed.

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Dr. João Setubal

New Deputy Director at VBI

The Virginia Bioinformatics Institute at Virginia Tech has announced the appointment of João Setubal as the Institute's deputy director. Setubal will act on behalf of VBI's executive and scientific director, Bruno Sobral, handling internal administrative functions as well as scientific decision making.

Source: Collegiate Times

VBI and the College of Agriculture and Life Sciences at VT Award Research Fellowships to Undergraduates

VBI and the Virginia Tech College of Agriculture and Life Sciences (CALS) have each awarded one systems biology summer research internship to an undergraduate student poster presenter at the Society for Advancement of Chicanos and Native Americans in Science (SACNAS) Annual Conference. These awards will give the students the opportunity to work side by side with Virginia Tech researchers for ten weeks during the summer of 2006.

Source: VBI press release

NSF to Support Cyberinfrastructure Education and Outreach Initiative

Bluefield State College, WV, the Galileo Magnet High School in Danville, VA, and VBI at Virginia Tech, received a \$250 000 grant to support a forward-looking initiative for education in cyberinfrastructure. The funds from the National Science Foundation (NSF) will be used over a period of two years to develop and implement the new course, broaden access of high school and undergraduate students to computer-related technologies, and to encourage trained students to pursue careers in informatics-related projects.

Source: VBI press release

Calendar of Forthcoming VBI Sponsored Events

- April 26-29, Alpha-Proteobacteria Symposium
- June 14-16, VBI Faculty Retreat
- October 28-31, 9th Conference on Computational Genomics

See calendar of events at: www.vbi.vt.edu

Folkerts and Whyte Join Institute

Otto Folkerts has been named associate director of technology development for VBI at Virginia Tech. Barry Whyte has been appointed to lead its communication efforts.

Source: Blue Ridge Business Journal

VBI Scientific Publications

High-efficiency transformation of the diploid strawberry (*Fragaria vesca*) for functional genomics.

Oosumi T, Gruszewski HA, Blischak LA, Baxter AJ, Wadl PA, Shuman JL, Veilleux RE, Shulaev V.

Planta. 2005 Dec 1:1-12 [Electronic publication ahead of print]

Researchers at the Virginia Bioinformatics Institute (VBI) and the Department of Horticulture at Virginia Tech have developed a new procedure for the efficient transfer of specific DNA sequences into the genome of strawberry. The scientists have used *Agrobacterium tumefaciens*, nature's genetic engineer, to introduce DNA into the woodland or alpine strawberry *Fragaria vesca*. By helping researchers establish the function of large numbers of strawberry genes, this method could, in the long term, be extremely useful in enhancing the nutritional value of these plants as well as the amount of health-enhancing antioxidants that they may contain. The work was funded by a VT ASPIRES grant

A new type of sulfite reductase, a novel coenzyme F₄₂₀-dependent enzyme, from the methanarchaeon *Methanocaldococcus jannaschii*.

Johnson EF, Mukhopadhyay B.

Journal of Biological Chemistry 2005 Nov 18; 280(46): 38776-86.

Biswarup Mukhopadhyay and Eric Johnson from the Virginia Bioinformatics Institute at Virginia Tech have discovered a novel enzyme that represents an ancient detoxification system and provides a clue to the development of early metabolism on earth. The newly discovered enzyme links biological methanogenesis and sulfate reduction, two most ancient respiratory metabolisms, in a unique way. Professor Rolf Thauer, professor and head of the Department of Biochemistry at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany, and a noted authority on anaerobic microorganisms, commented: "The finding of a novel sulfite reductase in a methanogenic archaeon is an important discovery. It may prove to be directly relevant to the anaerobic oxidation of methane with sulfate, a process in which archaea, closely related to methanogenic archaea are intimately involved."



Interview with Albert-László Barabási

Albert-László Barabási is the Emil T. Hofman Professor of physics at the University of Notre Dame, USA. His research focuses on the study of scale-free networks and their relationships to biological and communications systems. Dr. Barabási obtained an MSc in physics in 1991 from Eötvös Loránd University, Budapest, Hungary and a PhD in 1994 from Boston University in the United States. He is the author of *Linked: The New Science of Networks*.

“I tell my students not to wait until all the data are available to make the important discoveries in network science. The time to do this is now.”

How did a physicist become involved in the study of networks?

My early work and research were in statistical physics. This involved using statistical methods to solve problems related to materials science and complex systems. During my postdoc at IBM, I developed an interest in the properties of real networks, like those that are the foundation of the Internet, social networks, and biological systems. My group’s work has shown that real networks have a strict architecture that cannot be explained by models that rely on random connections. The focus of our work has been seeing how real networks emerge, what they look like and how they evolve.

Could you explain to us what you mean by a scale-free network?

Networks have a range of properties. One of them is that the probability that a particular node in the network has a certain number of links obeys a “power law” relationship. This means that if you were to look at the histogram showing the number of nodes with a certain number of links for a typical network, you will find that most nodes have only a few links, but there are a few hubs that are connected to a large number of other nodes. Thus the average node is not typical in the network, which is the source of the scale-free name. There is no intrinsic or typical degree in these systems.

How useful are scale-free networks for the study of biological phenomena?

It’s not really a question of utility. I would place more emphasis on the observation that they appear to be so widespread. Indeed, most biological networks have been found to be scale free. Researchers have looked at protein networks, gene networks, metabolic networks, in each case documenting a scale-free topology. And this feature is not limited to selected or-

ganisms: the scale-free nature of the metabolic network has been seen in over 200 organisms, and the scale-free nature of the protein-interaction network has been documented for humans, the fruit fly *Drosophila*, *Helicobacter pylori* — the bacterium that leads to peptic ulcers — yeast, and the worm *Caenorhabditis elegans*. Based on these observations, and the increased understanding that gene duplication leads to the observed scale-free topology, I would be extremely surprised if someone discovers an organism that does not have scale-free metabolism or a scale-free protein-interaction network.

VBI has a strong focus on transdisciplinary research or team-based science. What do you see as the key ingredients and challenges in putting together a successful collaborative group of multidisciplinary researchers?

A successful collaboration should include a combination of experienced people with complementary expertise. The excellence of the research domain and the willingness to work with others are more important than familiarity between individuals — the fact that we have worked with somebody in the past is not always an asset. In the current climate, it is often overlooked that interdisciplinarity could be a personal property of a single investigator — in general, small groups with a few collaborators that have the flexibility to change direction quickly and pursue new leads could be more successful than large teams. However, today there are clearly projects that demand large collaborative groups and which will not yield to the single investigator approach.

You asked about challenges. I think today’s funding system poses a serious problem for interdisciplinary science in general and for young scientists in particular. Most funding agencies permit only one principal investigator on a grant and I think this poses serious constraints on career

development, particularly for younger scientists.

What do you consider to be the biggest scientific finding of your career to date?

It is not the discovery of the scale-free nature of networks in itself but rather the recognition that scale-free networks are generic, emerging in a wide range of systems. It’s exciting when you discover something that seems to be so widely entrenched.

What work in progress by your peers do you consider to be truly groundbreaking in the study of biological or other networks?

The list is endless. Some of the work on the real-time monitoring of network and single molecule behavior in biological systems is truly exciting. Studies of sub-networks are also bringing new dimensions to the way network science is done, indicating that the “bottom up” and “top down” approaches to complex networks are not only complementary, but can be also equivalent in some sense.

Systems biology has many definitions, some of them grandiose. How realistic do you think it is to map, understand and model the whole cellular network of an organism, for example the regulatory, metabolic, and spatial relationships?

I think it will happen but I have no idea how long it will take. What I can say is that in the next five years or so we will have sufficient amounts of data to systematically address the organizing principles of biological networks. I tell my students not to wait until all the data are available to discover the basic features of real networks. The time to do this is now. By the time the data will be complete, most discoveries of importance will already have been made.