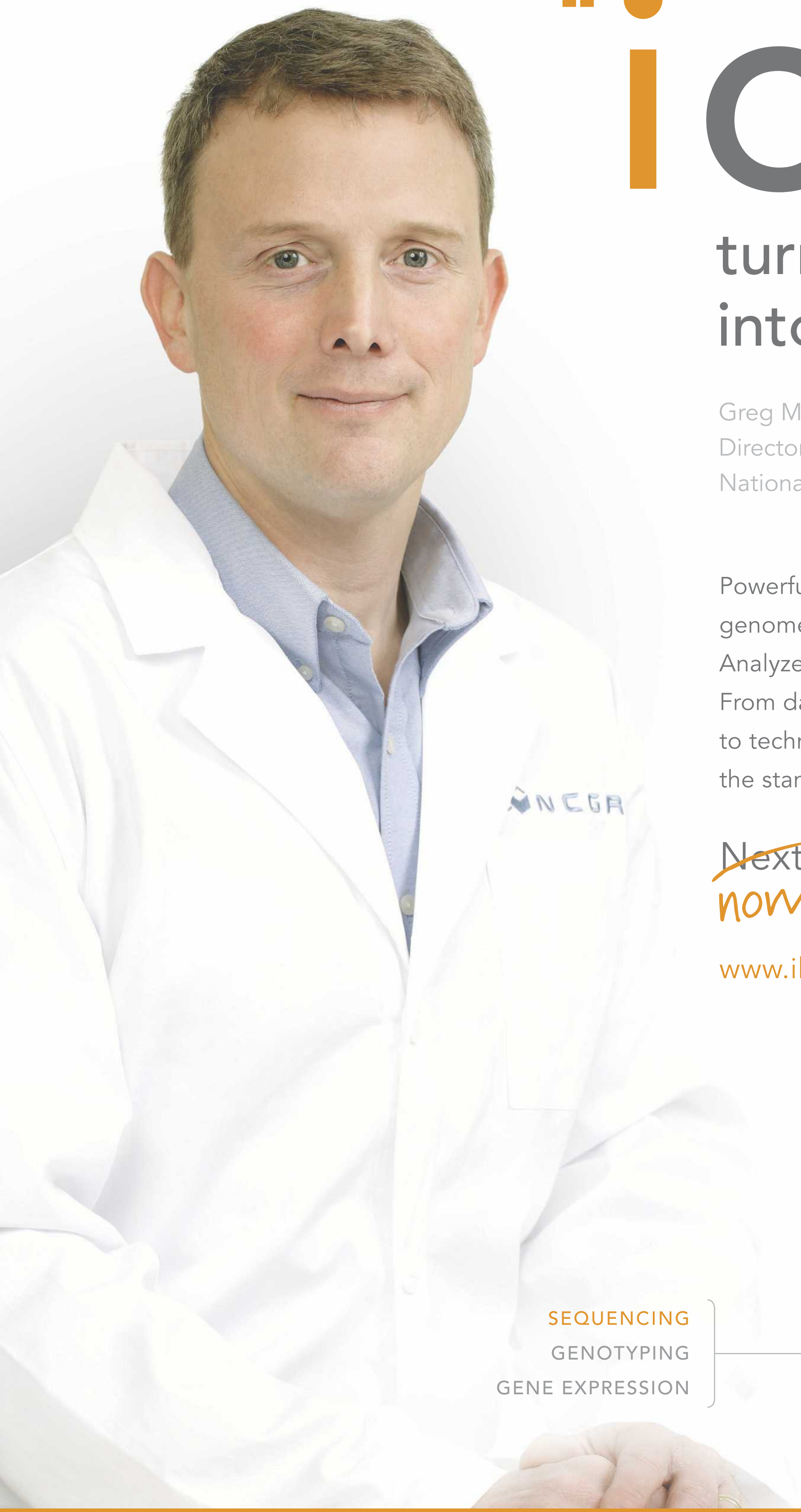
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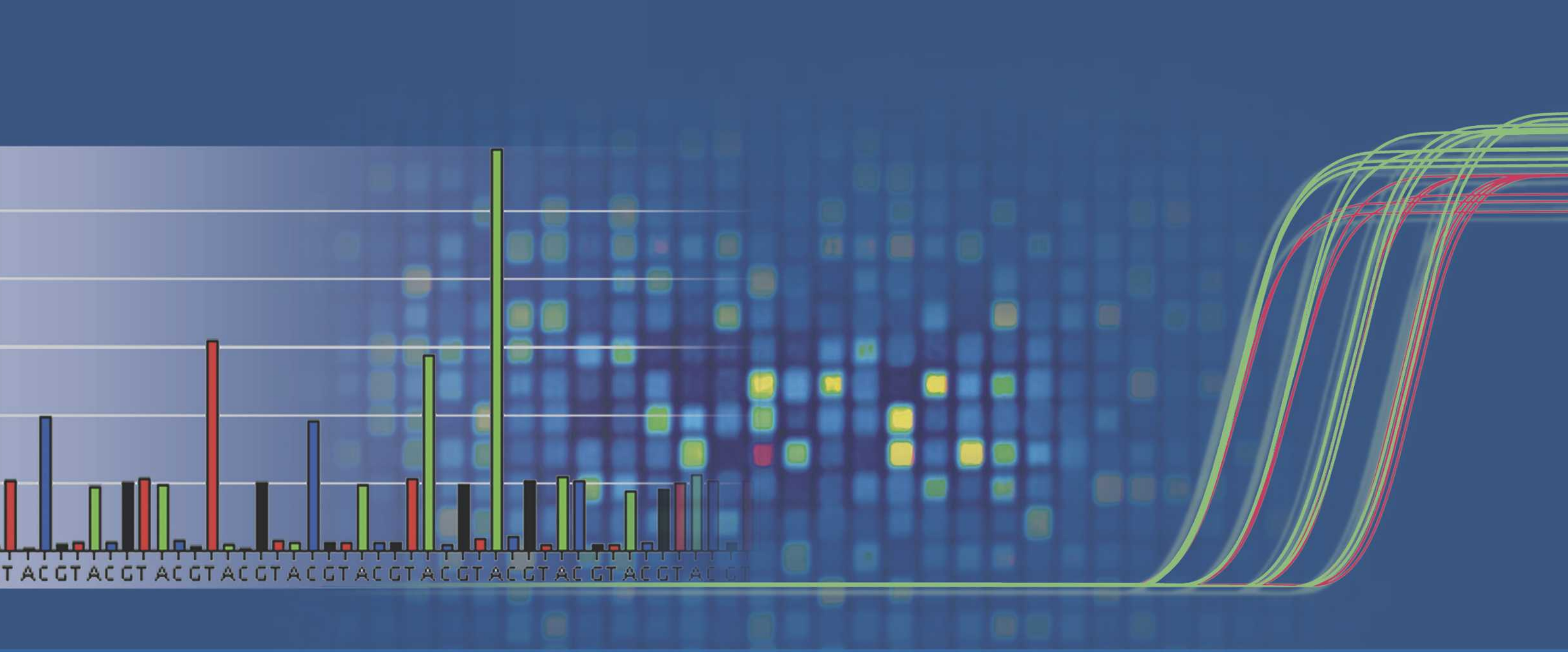


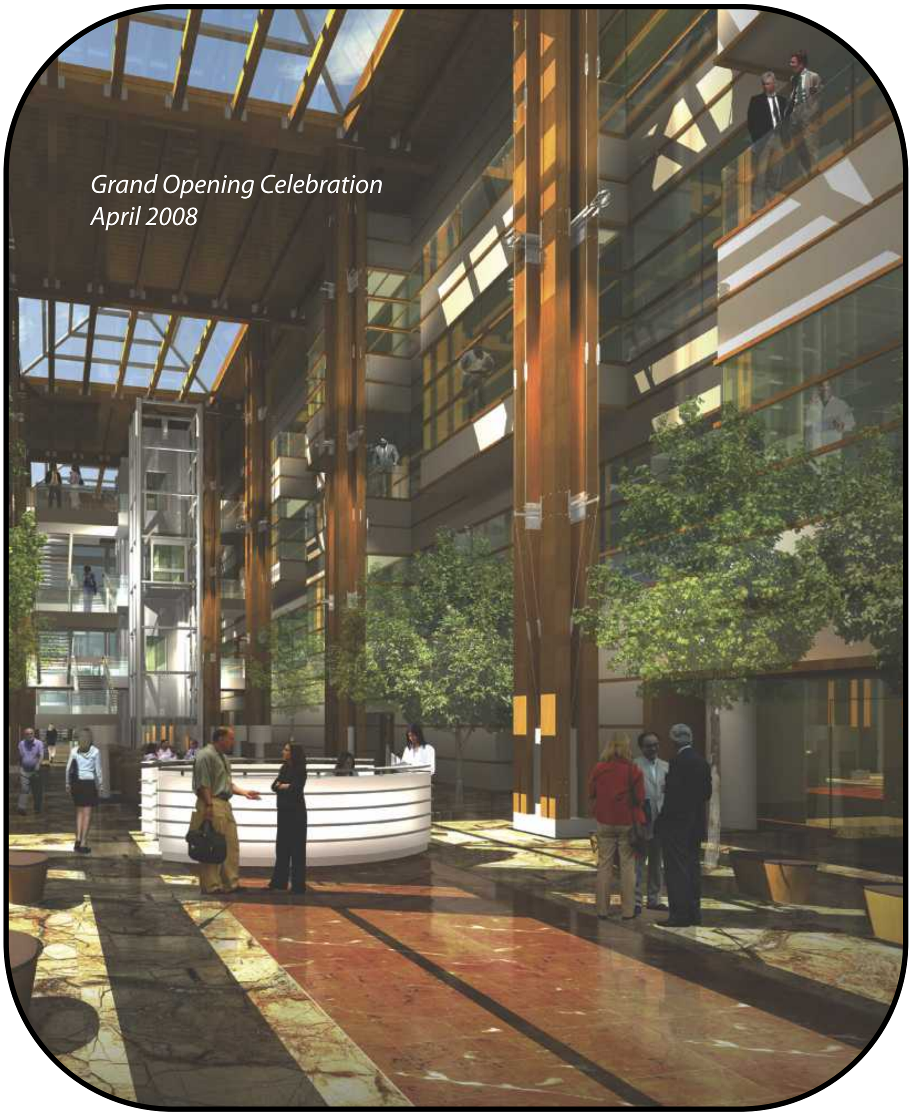
Applying genome-scale technology to human diversity and disease

HudsonAlpha: A fresh perspective for research and discovery

- Close alliance of a non-profit human genomics research institute with biotechnology community
- Open architecture and entrepreneurial spirit
- Rich intellectual environment for collaboration, discovery and innovation

> *Advances in genomic technology are generating an exponential increase in what we know about genome sequences and genetic variation. Our goal is to develop and apply this information to increase the quality and health of our lives.*
>
> — Dr. Richard M. Myers
> Director
> HudsonAlpha Institute

> *New insights and opportunities will result from combining genome-scale research with innovative, small business ventures.*
>
> — Jim Hudson
> Founder and President
> HudsonAlpha Institute



Grand Opening Celebration
April 2008

HudsonAlpha is the cornerstone of the 150-acre Cummings Research Park Biotech Campus. Huntsville, Alabama is home to the NASA Marshall Space Flight Center and the nations's second largest research park. Per capita, Huntsville has the highest percentage of scientists and engineers in the nation. Proximity to the University of Alabama in Huntsville, the University of Alabama at Birmingham, Auburn University and Vanderbilt University provides an ideal environment for genomics research and biotechnology.

Accepting resumes
for a variety of positions, including:

Faculty-level Investigators
Senior Scientists
Postdoctoral Fellows
Computational Biologists
Statistical Geneticists
Senior and Junior Research Technicians

HudsonAlpha
INSTITUTE FOR BIOTECHNOLOGY
Huntsville, Alabama

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At NEB, we make transformation as simple as selecting the best strain for your experiment. Our expanded line of competent cells includes a variety of strains for cloning and expression, as well as strains with unique properties (see chart). For added convenience, we offer a choice of efficiencies, formats and customized packaging. Choose the superior performance and quality of competent cells from New England Biolabs.

Advantages:

- Extremely high transformation efficiencies
- Phage T1 resistance (*fhuA2*) preserves clone integrity
- Choice of protocols: high efficiency or 5 minute transformation
- Nonspecific endonuclease activity eliminated, resulting in highest quality plasmid preparations
- Express difficult or toxic proteins with T7 Express strains containing $lacI^q$ and/or a novel lysY variant
- Obtain colonies faster than any other commercial strain with NEB Turbo
- SOC Outgrowth Media and pUC19 Control Plasmid included
- Free of animal products

Cloning strain characteristics	Strain	NEB #
Obtain colonies faster than any other commercial strain (6.5 hours)	NEB Turbo Competent *E. coli* *	C2984H/I
Versatile cloning strain	NEB 5-alpha Competent *E. coli* † *	C2987H/I
Cloning of toxic genes	NEB 5-alpha F´ I^q Competent *E. coli*	C2992H/I
Cloning of large plasmids and BACs	NEB 10-beta Competent *E. coli* *	C3019H/I
Growth of unmethylated plasmids	dam^{-}/dcm^{-} Competent *E. coli*	C2925H/I

Expression strain characteristics	Strain	NEB #
Most popular non-T7 protein expression strain	NEB Express Competent *E. coli*	C2523H/I
Added control of IPTG induced expression with non-T7 plasmids	NEB Express I^q Competent *E. coli*	C3037H/I
Most popular T7 protein expression strain	T7 Express Competent *E. coli*	C2566H/I
Reduced basal expression	T7 Express I^q Competent *E. coli*	C3016H/I
Tight control of protein expression by inhibition of T7 RNA Polymerase	T7 Express *lysY* Competent *E. coli*	C3010H/I
Highest level of protein expression control	T7 Express *lysY*/I^q Competent *E. coli*	C3013H/I
For crystallography experiments/SeMet labeling	T7 Express Crystal Competent *E. coli*	C3022H/I

† *Available as subcloning efficiency* * *Available as electrocompetent cells*

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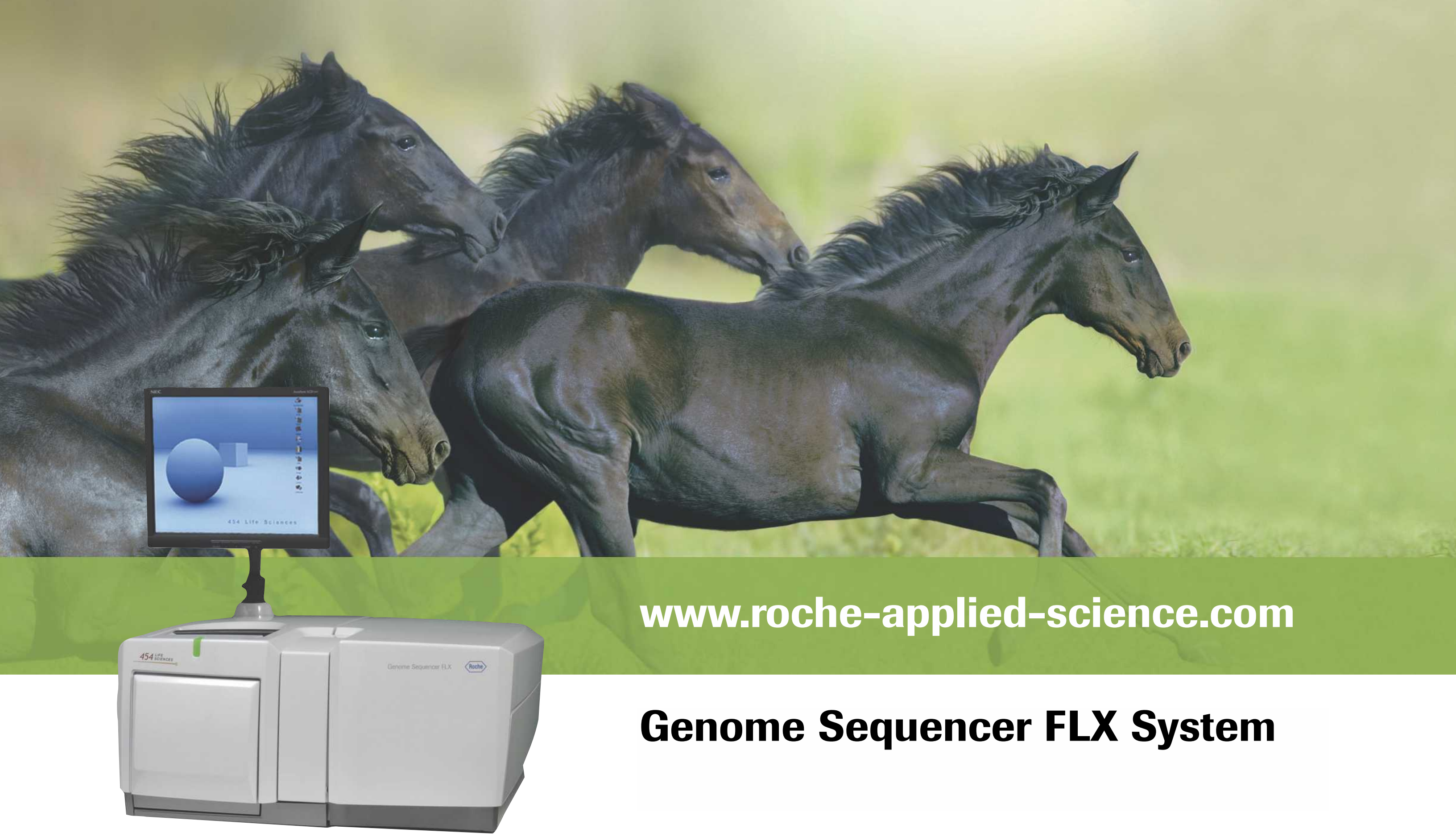

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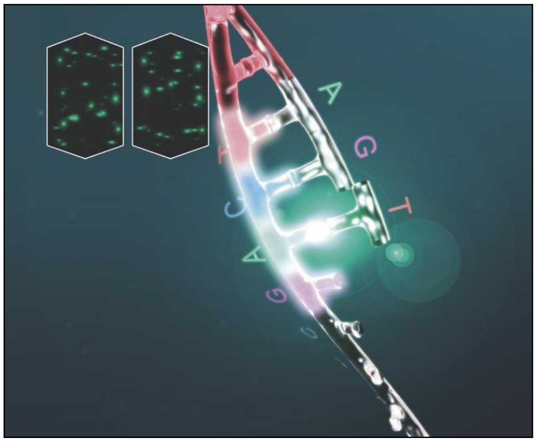
Genome Sequencer FLX System

Longer sequencing reads mean more applications.



Sequencing-by-Synthesis: Using an enzymatically coupled reaction, light is generated when individual nucleotides are incorporated. Hundreds of thousands of individual DNA fragments are sequenced in parallel.

In 2005, the Genome Sequencer 20 System was launched
- Read length: 100 bases
- 20 million bases in less than 5 hours

In 2007, the Genome Sequencer FLX System was launched
- Read length: 250 to 300 bases
- 100 million bases in less than 8 hours

Available in 2008, the Genome Sequencer FLX with improved chemistries
- Read length: >400 bases
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Director, Biomedical Genomics Research Center
University of Minnesota

Applications are invited for the position of Director, in the Biomedical Genomics Research Center (BMGC) at the University of Minnesota (www.bmgc.umn.edu). The BMGC is a dynamic center currently managing facilities that provide comprehensive, cost-effective, cutting edge instrumentation, as well as infrastructure and technical expertise for biological research to the entire University as well as the extended local scientific community, including: DNA sequencing and analysis, genotyping, oligonucleotide and peptide synthesis, protein sequencing, microarrays, and RNAi libraries. Facilities are staffed by highly experienced academic and technical personnel. We are seeking an established leader in providing genomics and genetic analysis services, to oversee the development and expansion of the Center, which currently has an operating annual budget of approximately $2 million. The candidate should have a doctoral level degree in the life sciences, chemistry or engineering, and extensive experience in a variety of genomic analysis methodologies. Five or more years relevant research and laboratory-based management experience is desirable. This will be a Professional & Academic, Director appointment. Generous benefits and salary commensurate with experience.

To apply, please go to **http://employment.umn.edu**, search for **Job Requisition #153017** for application instructions and links. All applications must be submitted on line, and should include names of references. Review of completed applications will begin immediately, and will continue until the position is filled. For questions regarding this position, contact Dr. Brian Van Ness at 612-624-9944 (vanne001@umn.edu)

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APBC2009

The Seventh Asia Pacific Bioinformatics Conference
Beijing, China, 13-16 January 2009

Conference co-chairs:
- Michael Q. Zhang, CSHL, USA and Tsinghua University, China
- Yanda Li, Tsinghua University, China
- Xuegong Zhang, Tsinghua University, China

Program Co-chairs:
- Michael S. Waterman, University of Southern California, USA
- Michael Q. Zhang, CSHL, USA and Tsinghua University, China
- Xuegong Zhang, Tsinghua University, China

Confirmed Invited Speakers:
- **David J. Lipman, Director of NCBI, USA (Keynote)**
- **David Botstein, Princeton University, USA (Keynote)**
- Martin Vingron, Max-Planck Institute for Molecular Genetics, Germany
- John Mattick, University of Queensland, Australia
- Michael B. Eisen, Lawrence Berkeley National Lab and UC Berkeley, USA
- Bailin Hao, Fudan University and CAS, China
- Chunting Zhang, Tianjin University, China

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- Mark Ragan, Australia
- Michael Q. Zhang, China & USA

Call for Papers
Call for Posters
Call for Tutorials
Call for Industry Sponsors

The Asia Pacific Bioinformatics Conference (APBC) series, founded in 2003, is an annual international forum for exploring research, development and applications of Bioinformatics and Computational Biology. The Seventh Asia-Pacific Bioinformatics Conference, APBC2009, will be held in Beijing, China in January 13-16, 2009, following the 2008 Olympic Games.

APBC2009 invites high-quality original papers and posters on any topic related to Bioinformatics and Computational Biology. Accepted papers will be invited for publication in the journal of *BMC Bioinformatics*, and abstracts of accepted posters will be published in the conference proceedings.

APBC2009 invites scientists and professionals working in the fields of bioinformatics and computational biology to submit proposals for high quality tutorials.

Industry sessions will be hosted at APBC2009 and we invite industry partners to participate in this great conference.

bioinfo.au.tsinghua.edu.cn/apbc2009 www.apbc09.org

Sponsors: Tsinghua University, Beijing, China
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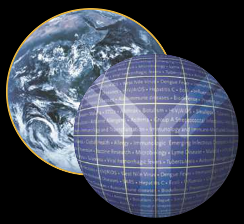

Help Us Help Millions

Tenure Track/Tenure Investigator Positions in Systems Immunology and Infectious Disease Modeling

The National Institute of Allergy and Infectious Diseases (NIAID), Division of Intramural Research (DIR) is seeking several outstanding individuals for its new Program in Systems Immunology and Infectious Disease Modeling (PSIIM).

Modern technology allows the analysis of immune responses and host-pathogen interactions at multiple levels - from intracellular signaling networks, to individual cell behavior, to the functioning of a tissue, organ, and even the whole organism. The challenge is not only to collect the large amounts of data, but also to organize it in a manner that enhances our understanding of how the immune system operates or how pathogens affect their hosts. To do this, it is necessary to develop detailed quantitative models that can be used to predict the behavior of a complex biological system. These models can help explain the mechanisms underlying physiological and pathological responses to infection or vaccination, which can then be employed to design better therapies or vaccines.

Achieving these goals requires an interdisciplinary effort and for this reason the PSIIM is organized as an integrated team of scientists and support staff. Within the PSIIM, there will be groups with expertise in the areas of computational biology, bioinformatics, proteomics, genomics, cell biology, immunology, and infectious diseases. These teams will have access to the latest technology for gene expression profiling, high content screening of RNAi libraries for the discovery of pathway components, imaging tools, genomic and proteomic analysis, cores for the genetic manipulation of animals, and a substantial computer infrastructure. They will also have access to BSL3 facilities for working with infectious agents of high priority for human health and biodefense. Although the PSIIM has been established within NIAID and has an immune / infectious disease focus, it is also expected to play a major role in fostering the growth of systems biology efforts throughout the NIH and involving diverse biomedical areas.

Current teams in the PSIIM include Immunology, Computational Biology – Modeling and Simulation, and Molecular / Cell Biology – High-throughput screening. The PSIIM is now recruiting for tenure track or tenure level team leader appointments in the following areas:

Bioinformatics / Biostatistics: the incumbent will lead a group focused on developing and implementing computational tools and statistical methods for the analysis of genomic and proteomic data. The ideal candidate will have a strong background in statistics, mathematics, programming, and modeling biological systems as well as a strong interest in collaboration with biologists for the elucidation of biological mechanisms. The group will include expertise in software development (C++, Java, Perl, SQL etc.), knowledge of bioinformatic tools, databases and algorithms, and experience with heterogeneous computer environments (UNIX, Windows, Mac).

Proteomics: the incumbent will lead a group involved in the development and application of new methods for the determination of protein number, binding affinities, post-translational modification, and other qualitative and quantitative aspects of protein expression and behavior that are necessary for computer modeling and simulation. Tools such as mass spectrometry and microfluidic-based multiplexed binding assays are expected to be key elements in the efforts of this group. A strong background in protein biochemistry and the relevant instrumentation needed for high-throughput, high-sensitivity analysis is required.

Genomics: the incumbent will be responsible for developing novel approaches to the systems-wide analysis of such issues as transcription factor and epigenetic control of gene expression, the effects of allelic polymorphism on gene expression and function, quantitative measurement of gene expression, and the role of non-coding regions and transcripts such as miRNAs in regulating gene/gene product expression patterns. Knowledge of modern methods in high-throughput analysis of gene transcription, transcription factor binding site identification, analysis of epigenetic modifications, and analysis of gene regulatory circuits is required; bioinformatics experience is desirable.

These positions and the research activities they conduct are fully funded by the intramural research program of NIAID. Each team leader is expected to build a working group consisting of postdoctoral fellows, students, technicians, and staff scientists. The team leaders will work with the Program Director to help set the goals for the PSIIM and to determine how best to reach these goals as an integrated group. To ensure appropriate career trajectories for those joining the PSIIM team effort, the NIH has modified its tenure policies to take specific account of contributions made in such a team science setting. Applicants should be seeking a difficult challenge in which creativity, technical expertise, and a strong desire to achieve in a team setting will be critical for success.

Interested candidates may contact Dr. Ronald Germain, Program Director, PSIIM, DIR, NIAID at (301) 496-1904 or email (rgermain@niaid.nih.gov) for additional information about these positions.

To apply, submit your curriculum vitae, bibliography, and a detailed statement of how your expertise can contribute to the success of the PSIIM program, to Wanda Jackson at NIAID.DIR.Search@niaid.nih.gov. In addition, three letters of reference must be sent directly from your three referees to Dr. Robert Hohman, Chair, NIAID Search Committee, c/o Wanda Jackson at NIAID.DIR.Search@niaid.nih.gov or 10 Center Drive, MSC 1356, Building 10, Room 4A22, Bethesda, Maryland 20892-1356. Email is preferred. Completed applications MUST be received by Friday, May 23rd. Please refer to ad #019 for bioinformatics/biostatistics, #020 for proteomics, and #021 for genomics on all correspondence. Further information regarding the DIR laboratories is available at: **http://www3.niaid.nih.gov/about/organization/dir/default.htm** and information on working at NIAID is available on our website at: **http://healthresearch.niaid.nih.gov**

For more information about the NIAID systems biology program, please visit **http://www.nih.gov/catalyst/2006/06.09.01/page1.html**

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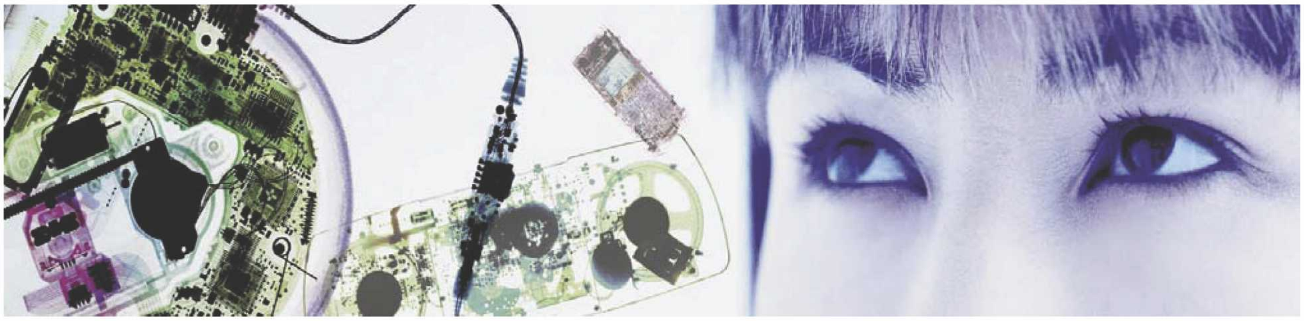

Research Staff Positions at Institute for Infocomm Research (I^{2}R)

I^{2}R is Singapore's premier Information, Communications and Media (ICM) research institute. We are currently located on a wooded ridge, amid tropical greenery, and overlooking the sea. I^{2}R currently employs over 300 researchers coming from many nationalities and working in diverse areas including digital wireless, embedded systems, security, media and signal processing, networking, data mining, speech and natural language processing, automated video analysis, radio systems and fibre optics.

I^{2}R provides a vibrant research environment with strong support for patenting and publications and has close links with local and international universities and research institutes. Through industry programs, I^{2}R helps local companies in the industry to upgrade technologically. Please see our website http://www.i2r.a-star.edu.sg for more information.

We are looking for PhD holders to join us in our Data Mining Department and Assistive ICM for Health Monitoring & Rehabilitation (AIM) Programme. The positions are for up to three years and may lead to a long-term position. Successful applicants will receive a competitive salary and a comprehensive benefits package. They may also be provided with assistance for relocation.

The Data Mining Department in I^{2}R, focuses on the effective mining of complex patterns from both structured and unstructured data, as well as the innovative uses of such techniques to discover new knowledge for a wide range of application domains. With a unique history of starting out as a bioinformatics group more than a decade ago, the Department excels in cross-disciplinary data mining research, and it is expanding its success in bioinformatics to other challenging domains such as financial data analysis, business analytics, and social network mining.

The Assistive ICM for Health Monitoring & Rehabilitation (AIM) Programme aims to develop Infocomm & media technologies for healthcare applications. The programme focuses on health monitoring & rehabilitation, especially for chronic disease patients (for example, CVD, stroke) and elderly. The programme explores systems and solutions for physiological and physical monitoring, as well as for sensorimotor and cognition rehabilitation. The programme will also develop technologies to enhance safety and independent living.

Interested applicants, please fill up the online application form in the career section of our website. Look for the position with this reference number: GENOME 2008/01

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