

ISICR Officers

President

Kathryn Zoon

President-Elect

Keiko Ozato

Secretary

Sidney Pestka

Treasurer

Sam Baron

June 2001

Volume 8, No. 2

Future ISICR Meetings

Oct. 7 - 11, 2001

Cleveland, OH

<http://www.isicr2001.org>

Oct. 6 - 11, 2002

Torino, Italy

Joint ISICR/ICS

2003

Melbourne

ISICR WWW Site

www.ISICR.org

ISICR Business Office

ISICR@faseb.org

TEL: 301-571-8319

FAX: 301-530-7049

ISICR Newsletter Editors

Howard Young

youngh@mail.ncifcrf.gov

Fax: 301-846-1673

Pat Fitzgerald-Bocarsly

Bocarsly@umdnj.edu

Fax: 973-972-7293

Hannah Nguyen

nguyenh@cesmtp.ccf.org

Fax : 216-445-9769



ISICR Board of Directors:

Congratulations to the following members who are newly elected to the ISICR Board of Directors:

Ara Hovanesian

Ganes Sen

Tadatsu Taniguchi

ISICR International Council Members (2001-2003)

AUSTRALIA

AUSTRIA

Thomas Decker

Alternate:

Gunther Adolf

BELGIUM

Jan Tavernier

Alternate:

Hubertine Heremans

CANADA

Eleanor N. Fish

(1999-02)

Alternate: (1999-02):

John Hiscott

CHINA

Zhong-Tian Qi

FRANCE

Juana Witzerbin

Eliane Meurs

Alternate:

Bernard LeBleu

GERMANY

Peter Staeheli

Alternate:

Hansjoerg Hauser

ISRAEL

Ben-Zion Levi

Alternate:

Gideon Schreiber

ITALY

Antonina Dolei

Alternate:

Filippo Belardelli

JAPAN

Masayoshi Kohase

Kouji Matsushima

Alternates:

Jiro Imanishi

Yoshihiro Sokawa

POLAND

Ewa Zaczynska

Alternate:

Wojciech Rzeski

SWEDEN

Dan Grandér

SWITZERLAND

Jean-Michel Dayer

UNITED KINGDOM

Anthony Meager

UNITED STATES

Ernest Borden

Christine Czarniecki

Joan Durbin

Dhan Kalvakolanu

Michael Katze

Lawrence Pfeffer

Nancy Reich

Charles Samuel

Ganes Sen

Milton Taylor

Kathryn Zoon

Alternates:

Patricia Fitzgerald-

Bocarsly

W. Robert Fleischmann

Allan Lau

David Levy

Richard Pine

Margaret Sekellick

Gerald Sonnenfeld

Bryan Williams

ISICR COMMITTEES

The ISICR thanks all committee members whose efforts help improve our society

ARCHIVES COMMITTEE

Norman Finter (2001-2003)
Co-chairperson
 Robert Friedman (2001-2003)
Co-chairperson
 Ferdinando Dianzani(2001-2003)
 Yoshimi Kawade (2001-2003)
 Samuel Baron (2001-2003)
 Alfons Billiau (2001-2003)
 Ernest Knight, Jr (2001-2003)
 Edward De Maeyer (2001-2003)
 Charles Chany (2001-2003)

AWARDS COMMITTEE

Ara Hovanessian (2001-2003)
Chairperson
 Keiko Ozato (1999-2001)
 Paula Pitha-Rowe (2001-2003)
 Bernard Lebleu (2001-2003)
 Michael Katze (2001-2003)
 John Kirkwood (2001-2003)
 Robert Schreiber (2001-2003)
 Ian Kerr (2001-2003)

MEETINGS COMMITTEE

Christine Czarniecki(2001-2003)
Chairperson
 Joan Durbin (2001-2003)
 Allan Lau (2001-2003)
 Yu-ichiro Satoh (2001-2003)
 Santo Landolfo (2001-2003)
 Nancy Reich (2001-2003)
Ad Hoc Members
 George Stark (2001-2002)
 Huub Schellekens (2000-2001)
 Paul Hertzog (2001-2003)

NOMENCLATURE COMMITTEE

Erik Lundgren (1996-2001)
Chairperson
 Margaret Sekellick (1999-2001)
 Richard Pine (1999-2001)
 Jerome Langer (2001-2003)
 Antonina Dolei (2001-2003)

Isabelle Marie (2001-2003)
 Gideon Schreiber (2001-2003)
 Eleanor Fish (2001-2003)

FINANCE COMMITTEE

Samuel Baron (1999-2001)
Chairperson
 All Officers
 Members of the Finance
 Subcommittee
 All Officers

Gianni Garotta (2001-2003)
 Huub Schellenkens (2001-2003)
 Ernest Borden (2001-2003)
 Ferdinando Dianzani(2001-2003)
 Raymond Kaempfer(2001-2003)
 Masayoshi Kohase (2001-2003)
 Filippo Belardelli (2001-2003)
 Bryan Williams (2001-2003)
 Seng-Lai-Tan (2001-2003)

MEMBERSHIP COMMITTEE

Heinz-Kurt Hochkeppel
Chairperson (2001-2003)
 Bret Hassel (1999-2001)
 Steve Ralph (1999-2001)
 Howard Young (2001-2003)
 Mariano Esteban (2001-2003)
 Eliane Meurs (2001-2003)
 Robert Silverman (2001-2003)
 Ken Takeda (2001-2003)

PUBLICATION COMMITTEE

W. Robert Fleischmann, Jr.
Chairperson (2001-2003)
 Kurt Berg (1999-2001)
 Maria Capobianchi (1999-2001)
 Deborah Vestal (1999-2001)
 Yoshihiro Sokawa (1999-2001)
 Jeremiah Tilles (1999-2001)
 Philip Marcus *Ex Officio*

Sandra Pellegrini (2001-2003)
 Milton Taylor (2001-2003)

STANDARDS COMMITTEE

Sidney Grossberg (1997-2001)
Chairperson
 Norman Finter (1999-2001)
 Andrew Galazka (1999-2001)
 Wendy Jones (1999-2001)
 Masayoshi Kohase (1999-2001)
 Anthony Meager (1999-2001)
 Huub Schellenkens (1999-2001)
 Hanna-Leena Kauppinen
 (1999-2001)
 Ronald Bordens (2001-2003)
 Guido Antonelli (2001-2003)

*"If you don't know where
 you are going, how can you
 expect to get there?"*

Basil S. Walsh

*"To think too long about
 doing a thing often becomes
 its undoing."*

Eva Young

OOPS! I Goofed!!!

In the last issue, I forgot to acknowledge that the Membership Committee minutes were submitted by Dr. Heinz-Kurt Hochkeppel. My apologies to Dr. Hochkeppel for this oversight and many thanks to all the committee chairs for their outstanding jobs.

Two Day Symposium Honoring Sidney Pestka

By Patricia Fitzgerald-Bocarsly

A two-day symposium honoring Dr. Sidney Pestka was held at the Robert Wood Johnson Medical School on May 21 and 22nd. The symposium, entitled "From the Genetic Code and Protein Synthesis to Interferon and the New Age of Biology" was sponsored by an educational grant from Roche and featured approximately twenty speakers and chairs, all of whom had had significant interactions with Sid over his long and productive career. Many of the speakers had directly worked with Sid at some point, either as mentor, colleague, student or post-doc, and others have had long and fruitful collaborations with Sid or made substantial contributions to the field of interferon research. In the large audience were many past and present associates of Sid, as well as many friends and UMDNJ colleagues. These individuals had gathered literally from all over the world, with one speaker, Hsiang-fu Kung, coming all the way from Hong Kong and two from Japan, Kunimoto Hotta and Shuichiro Maeda. Each of the talks was punctuated with warm anecdotes about the interactions that the speakers had had with Pestka.

The symposium started with a session entitled "The Genetic Code and Protein Synthesis", chaired by Herbert Weissbach. It began with a view back to the early 1960's by Marshall Nirenberg, who had been Sid's post-doctoral advisor at the NIH. Marshall recounted how the genetic code was deciphered in his laboratory forty years ago. For the younger attendees who were not

even born (or, as in my case, were in elementary school) when the code was deciphered, it was eye-opening to recall how recent the origins of the field of molecular genetics really are and the magnitude of our progress since that point. Dolph Hatfield continued the session with his perspective on "Decoding Triplets and Novel tRNAs in Today's Age", with emphasis on his discovery of selenocysteine tRNA and its importance. The afternoon session the first day, chaired by Paul Fisher, was entitled "Beyond the Code: Cancer, interferon, signal transduction and HIV" and featured talks by Phil Leder, Bob Gallo, Waijen Soo, and ISICR luminaries, Ganes Sen and George Stark. The second day included sessions on "Antibiotics: the road to interferon as a therapeutic", "Biology of Interferon" and "Biology of Interferon: Signal transduction". Speakers and chairs in these sessions ranged from members of the original Roche Institute team (Shuichiro Maeda, Hsiang-fu Kung, Marian Evinger, and Nancy Chang) that purified and cloned interferon and have since moved on to other areas of research, to Ronald Herberman, Jeff Schlom and James Ihle, who have each had significant collaborations with Sid in the understanding of the biology of interferon or cytokine signaling. The chairs of these sessions were respectively, Mary Ann Liebert, William Hait and Idhaliz Flores.

Although Sid is best known for his team's cloning of the type I

interferons, Dolph Hatfield, chair of the introductory session, pointed out numerous other "firsts" from the Pestka laboratory including the discovery that the small ribosomal subunit (30S subunit in *E. coli*) was the site of decoding mRNA contrary to dogma that ascribed this to the large subunit, studies of antibiotic-induced miscoding, the use of HPLC for protein purification, the first large scale use of monoclonal antibodies for protein purification, functional YAC screening, the use of antisense RNA, the description of multi-chain cytokine receptors and studies of the differential biological effects of IFN subtypes.

At the conclusion of the symposium, Sid expressed his thanks individually to each of the speakers, and spoke specifically of his interactions with each of them. He also expressed his thanks to each of his three children and his wife Joan, the latter who was responsible for arranging the remarkable lunches and dinners for the occasion. The major organizers were Barbara Schwartz and Rick Wernoski, staff members of Sid's department, who began the organization of the Symposium on their own initiative. They then elicited Dolph Hatfield to help them contact the speakers. Although such symposia sometimes mark the end of a career, Sid made an emphatic point that the symposium did not signal his retirement, but rather that he fully intended to continue his career both at the Robert Wood Johnson Medical School and at his company, PBL.

New ISICR Members

The ISICR welcomes the following new members.
Contact information can be obtained from the Headquarters Office

Jesper B. Andersen Denmark
Jaya Bansal Jessup, MD
Judith A. Britz Columbia, MD
Alexandre Caillaud Paris, France
Maureen C. Dolan Blacksburg, VA
Xuan Feng Chicago, IL
Sarah L. Gaffen Buffalo, NY
Peter Huessy Switzerland
Joan C. Huff Columbia, MD
Nicholas F. Landolfi Fremont, CA

Joe Lau New York, NY
Mingjuan Liu Baltimore, MD
Xinrong Ma Baltimore, MD
Suneel D. Mundle Chicago, IL
Morten M. Nielsen Denmark
Signe E. Nielsen Denmark
Sarah Porteous Cleveland, OH
Jacques H. Theze Paris, France
Vadim Tsvetnitsky Ontario, Canada
Christina Ulane New York, NY

Students and Fellows Science of the Future

Cleveland ISICR Meeting and some useful Web Sites

I feel pretty privileged to be living in the host city of this year's the 2001 Annual Meeting of the ISICR! The Interferon and Cytokine gang here at the Cleveland Clinic Foundation's Lerner Research Institute are anxious and excited to welcome you to Cleveland this October. For those who haven't yet had the chance, bug your supervisors to let you go to this Meeting! It's really easy, you can register online. It's too late for abstracts, but definitely not too late for registration. All the information that you may need about the meeting is found on www.isicr2001.org. The list of topics and invited speakers is printed in this newsletter issue. Word is that a good number of abstracts have been submitted...it's going to be a great meeting! Not only is there going to be good science, Cleve-

land is wonderfully colorful in the fall and the weather is also usually pleasant in early October. There are various extracurricular events planned for one to get a taste of the city, and it is our pleasure to help you get efficiently acquainted with Cleveland. For those who love the arts, fine dining and varied culinary delights, Cleveland has much to offer in that regard. Everything is pretty decently affordable in Cleveland. And don't miss the chance to visit our new state-of-the-art Lerner Research Institute, where the Interferon and Cytokine gang hangs out - you may have to tolerate us bragging about it (just a teeny bit!). Hope to see you there!

Besides that, here are a few Web sites that I have found to be useful:

- The Scientist: www.the-scientist.com. The News Journal for the Life Scientist. Free Web subscription (gives you unlimited online access) to all and free print subscriptions to US residents who are active members in the life sciences community. Great articles on some of the latest research, science careers, lab consumer products, funding, and more.
- Genetic Engineering News: www.genengnews.com. Biotechnology News. Conditional free print subscriptions (Libraries, Venture Capitalists, Attorneys, Consultants, Investment Bankers and Students don't get complimentary subscriptions). Web site displays highlights and abstracts of articles. Describes the latest in biotechnology and drug development worldwide. Also serves as a great biotech company directory.

Clinical Trials

Study ID Numbers HALT C Long Term **Interferon** for Patients Who Did Not Clear Hepatitis C Virus with Standard Treatment Contact: Carol Craig, University of California-Irvine/VA Medical Center-Long Beach, Long Beach, CA. Tel: 562-494-5933

Study ID Numbers NIAID ACTG A5071 A Prospective, Multicenter, Phase II/III, Open-Label, Controlled, Randomized Trial Evaluating the Efficacy, Safety, and Tolerability of **Interferon-Alfa-2A** Plus Ribavirin Versus **Peginterferon-Alfa-2A** Plus Ribavirin for Chronic Hepatitis C Virus (HCV) Infection in Individuals Co-Infected with Human Immunodeficiency Virus-1 (HIV-1). Contact: Julieann Lewis, Univ of California San Francisco, San Francisco CA. Tel: 415-514-0550

Study ID Numbers 199/15216; NYU-9938; NCI-101. Thalidomide Plus **Interferon** alfa in Treating Patients With Progressive Liver Cancer That Cannot be Surgically Removed. Contact: Jonathan Schwartz, Mount Sinai School of Medicine, New York, NY. Tel: 212-241-3984

Study ID Numbers 199/14454; UT-H-HSC-MS-99-116; NCI-V99-1561 Cisplatin, Gemcitabine, **Interferon alfa**, and Hyperthermia in Treating Patients With Advanced Cancer. Contact: Joan M.C. Bull, University of Texas-Houston Medical School, Houston, TX. Tel: 713-500-6820

• The Chronicle of Higher Education: www.chronicle.com. Good source of information on colleges and universities (facts and figures, trends in higher education, career advice). Good source for advertised jobs in many areas in academia, such as “biological sciences” and “public health”. Subscription for access to everything The Chronicle has to offer costs money, but you have free access to a certain proportion of job listings and information even if you are not a chronicle subscriber.

More web sites to come, but feel free to let us know of your favorite science web sites too, so that we could spread the word!

Hannah

Reviews of Interest

Dupuis S, Doffinger R, Picard C et al. Human interferon- γ -mediated immunity is a genetically controlled continuous trait that determines the outcome of mycobacterial invasion. *Immunological Rev.* 178: 129, 2000.

Hiscott J, Kwon H, Genin P. Hostile takeovers: viral appropriation of the NF- κ B pathway. *J. of Clin. Invest.* 107: 143, 2001.

Garcia-Sastre, A. Inhibition of interferon-mediated antiviral responses by influenza A viruses and other negative-strand RNA viruses. *Virology* 279: 375, 2001.

Geijsen N, Koenderman L, Coffey PJ. Specificity in cytokine signal transduction: lessons learned from the IL-3/IL-5/GM-CSF receptor family. *Cytokine & Growth Factor Reviews* 12: 19, 2001.

Heyman D, Rousselle AV. gp130 cytokine family and bone cells. *Cytokine* 12: 1455, 2000.

Horvath CM. STAT proteins and transcriptional responses to extracellular signals. *TIBS* 25: 496, 2000.

Luther SA, Cyster G. Chemokines as regulators of T cell differentiation. *Nature Immunol.* 2: 102, 2001

Ottenhoff THM, de Boer T, Verhagen CE et al. Human deficiencies in type 1 cytokine receptors reveal the essential role of type 1 cytokines in immunity to intracellular bacteria. *Microbes and Infection* 2: 1559, 2000.

Shannon MF, Coles LS, Attema J, Diamond P. The role of architectural transcription factors in cytokine gene expression. *J. Leuk. Biol.* 69: 21, 2001.

Shuai K. Modulation of STAT signaling by STAT-interacting proteins. *Oncogene* 19: 2638, 2000.

Quote to Ponder:

*Life is short
Eat dessert first*

Study ID Numbers 199/12531; MDA-DM-96296; NCI-G97-1206 **Interferon alfa** in Treating Patients With Recurrent Unresectable Meningiomas and Malignant Meningiomas
Contact: Wai-Kwan Alfred Yung
University of Texas - MD Anderson Cancer Center, Houston, TX. Tel: 713-794-1285

Study ID Numbers 98-N-0160
Recombinant Human Interferon Beta-1a (Avonex) for the Treatment of Patients with HTLV-1-Associated Myelopathy (HAM)
Contact: National Institute of Neurological Disorders and Stroke (NINDS), Bethesda, MD. Tel: 1-800-411-1222

Study ID Number: NIAID AIEDRP A1-01-001 A Single Center, Randomized Open Label Study of Initial **Interleukin-2** Compared to Delayed Interleukin-2 When Added to Zidovudine, 3TC and Nelfinavir In Order to Modulate Immune Function and to Sustain Suppression of HIV-1 Replication Among Those Persons with Primary or Early HIV Infection. Contact: Rick Hecht, San Francisco AIDS Clinic / San Francisco Gen Hosp., San Francisco CA. Tel: 415-476-4071

Study ID Numbers 99-I-0089
Interferon Gamma Administration in Leukocyte Adhesion Deficiency Type I.
Contact: National Institute of Allergy and Infectious Diseases (NIAID), Bethesda, MD. Tel: 1-800-411-1222

Study ID Numbers 94-I-0149
Treatment of Multiply Drug Resistant Tuberculosis with **Interferon Gamma**: A Phase I/II Dose Escalation Trial. Contact: National Institute of Allergy and Infectious Diseases (NIAID), Bethesda, MD. Tel: 1-800-411-1222

Study ID Numbers B013; GIMY-001 Safety and Antifungal Activity of Recombinant **Interferon-gamma 1b** (rIFN-gamma 1b) Given with Standard Therapy in Patients with Cryptococcal Meningitis. Contact: Dr Peter Pappas, Univ of Alabama at Birmingham, Birmingham, AL. Tel: 205-934-5191

Study ID Numbers 199/15374; FHCRC-1461.00; NCI-G00-1845
Melphalan, Peripheral Stem Cell Transplantation, and **Interleukin-2** Followed by **Interferon alfa** in Treating Patients With Advanced Multiple Myeloma. Contact: Leona Holmberg Fred Hutchinson Cancer Research Center, Seattle, WA. 206-667-6447

Study ID Numbers 199/15732; MAYO-MC998C; NCI-312
Monoclonal Antibody Therapy Plus Sargramostim and **Interleukin-11** in Treating Patients With Relapsed or Refractory Non-Hodgkin's Lymphoma. Contact: Thomas E. Witzig, Mayo Clinic Cancer Center, Rochester, MN. Tel: 507-284-2176

Study ID Numbers 199/14592; FHCRC-1365.00; NCI-G99-1622
Interleukin-11 Plus Filgrastim Prior to Peripheral Stem Cell

Transplantation in Patients With Non-Hodgkin's Lymphoma, Hodgkin's Disease, Breast Cancer, or Other Solid Tumors. Contact: Leona Holmberg, Fred Hutchinson Cancer Research Center, Seattle, WA. Tel: 206-667-6447

Study ID Numbers 99-I-0147
Interleukin-12 in the Treatment of Severe Nontuberculous Mycobacterial Contact: National Institute of Allergy and Infectious Diseases (NIAID), Bethesda, MD. Tel: 1-800-411-1222

Study ID Numbers 199/15819; STLHC-IMM-0001; NCI-V01-1656. Phase I Study of Fluorouracil and **Interleukin-12-Primed** Activated T Cells With Sargramostim (**GM-CSF**) and **Interferon alfa** in Patients With Metastatic Renal Cell or Colorectal Cancer. Contact: John P. Hanson, Jr., St. Luke's Medical Center, Milwaukee, WI. Tel: 414-385-3086

Study ID Number: NIAID ACTG A5049A. Phase I, Limited-Center, Sequential Cohort Trial of HIV Vaccine (Polyvalent Peptide Vaccine C4-V3) in Conjunction with **Interleukin-12** in Subjects with Maximal Suppression of HIV Replication and CD4 Count > 400 Cells/mm³. Contact: Jan Fritsche, Rush Presbyterian - Saint Luke's Med Ctr Chicago IL (312)942-5865; Paulette MacDougall, Duke Univ Med Ctr Durham NC; Karen Waterman, Univ of Texas Galveston, Galveston TX. Tel: (409)772-0361

Study ID Numbers 199/15418; JHOC-NABTT-9903; NABTT-9903; NEOPHARM-TS-G1-TI4 Phase I/II Study of Interstitial **Interleukin-13 PE38QQR** Recombinant Cytotoxin in Patients With Malignant Glioma. Contact: Stuart A. Grossman, Johns Hopkins Oncology Center, Baltimore, MD. Tel: 410-955-8837

Study ID Numbers NIAMS-043; N01-AR-9-2244 **Tumor Necrosis Factor** in Ankylosing Spondylitis. Contact: Maureen Fitzpatrick, UCSF-Clinical Trials Center, San Francisco, CA. Tel: 1-415-502-5108

Study ID Numbers 99-I-0040 Phase I/II Trial of **TNFR:Fc (Etanercept)** in Patients with **Wegener's Granulomatosis**. **Contact:** National Institute of Allergy and Infectious Diseases (NIAID), Bethesda, MD. Tel: 1-800-411-1222

WWW

Animal Genome Databases

<http://www.thearkdb.org>

The Roslin Institute Bioinformatics Group (<http://bioinformatics.roslin.ac.uk>) are pleased to announce that the ARKdb database system has moved to a new, easy-to-remember domain. The main site can now be found at <http://www.thearkdb.org>. The Roslin site is also accessible as <http://roslin.thearkdb.org>, while the mirror sites at Texas A&M and

Iowa State can be accessed as <http://texas.thearkdb.org> and <http://iowa.thearkdb.org>. We would like to take the opportunity to thank the administrators at those two sites for their help in getting the new URLs set up.

The full set of ArkDB genome databases covering pigs, chickens, sheep, cattle, horses, deer, cats, tilapia, salmonids and turkey can be found on the Roslin site. The Iowa mirror site carries chicken and pig databases whilst Texas houses cattle, horses and sheep.

There are bound to be glitches in the system that we have missed. Please let us know about them, no matter how trivial, and we will try to fix them as soon as possible. You can now contact us with ARKdb-related issues at <mailto:info@thearkdb.org> or <mailto:feedback@thearkdb.org>. If you need to cite data held within the ARKdb databases, please cite ARKdb-<species name> genome database, with URL <http://www.thearkdb.org> and refer to the published paper Hu et al., (2001). Nucleic Acids Research 29(1), 106-110 also noting the date on which the data was retrieved /accessed.

Watch out for more ARKdb announcements over the next few weeks as we seek your views on re-developing these genome databases.

Dr Alan Archibald
Dr Andy Law
Head of Department of
Head of Bioinformatics
Genomics and Bioinformatics
Roslin Institute, Scotland, UK

BioBanner

<http://biobanner.czweb.org/>

I just started the project called BioBanner. The idea was to join BioScience community web sites through banner advertising. Banner ads are efficient tool for increasing web site traffic, but only if its well targeted. Unfortunately, non-commercial web sites (such as my lab pages) don't have funds to pay advertising service. Hence I decided to create my own, for free, and only for BioScience web sites. If you want to advertise your achievements, papers, conferences..., I will be happy if you register.

What is BioBanner about?

BioBanner is a free banner exchange advertising system for promoting non-commercial Life Sciences web sites.

What does BioBanner offer?

If you have a web site, which fulfils our criteria, you can advertise by exchanging banners with our members. As they have the sites of similar orientation, and visitors with similar interests, your advertising will be well targeted.

Who can advertise with BioBanner?

Any non-commercial site, with content in English language that deals with Life Sciences research or education. Fill out simple form and you can immediately put BioBanner on your site and upload your ad.

Sincerely,
Martin Kucej
BioBanner admin

"Never go to a doctor whose office plants have died."

Erma Bombeck

Biovisa

www.biovisa.net

This is a fully customizable community site built by and for bio researchers. We have a collection of 1171 online journals, 866 online protocols and 52 forums by 3/8/2001.

The website is database-driven, so that you can mark any protocols, journals, forums, or threads in forums, of your interest and organize them in a convenient way. And you can write your own or read others' comments on a protocol that interests you. Our collection of 52 forums helps you reach more people.

The website is growing daily and new features are added based on feedbacks from our colleagues. So if you have time, please take a look at it. Any feedbacks would be highly appreciated.

GeneX Gene Expression Database

<http://genex.ncgr.org>

The GeneX team is happy (well, relieved anyway ;)) to announce a public release of NCGR's GeneX Gene Expression Database system.

The GeneX project is an Open Source endeavor to provide the gene expression community a way of designing a system that best meets their needs. The system can be downloaded from Sourceforge (<http://genex.sourceforge.net>) or from NCGR's GeneX web site (<http://genex.ncgr.org>) and is licensed under the GNU LGPL.

We hope this provides a partial outlet for those labs that have experience with expression analysis, some coding ability, and the desire to contribute to project that can, with a little effort, add the features that they want but doesn't require a build-from-scratch effort.

It provides a basic working system including:

- installation scripts
- a small amount of example data
- the Genex.pm Perl wrapper API to the database
- utilities to manipulate the XML transport format
- analytical tools which can be used with data from the database or with data uploaded directly. They include apps for significance & permutation testing as well as several kinds of clustering.
 - * CyberT - a significance testing tool which uses repeated t-tests (with Bonferonni correction) and an optional Bayesian estimation of variance. CyberT also uses xgobi (an XWindows app) to perform 3D visualizations of the results, Principle Component Analysis, and linked maps.
 - * Rcluster - an interface to the R cluster libs (several clustering approaches, using several metrics)
 - * xcluster - Gavin Sherlock's speedy and memory-efficient clustering app which also includes KMeans clustering and Self-Organizing Maps (we provide the interface - you have to license the xcluster code directly from Stanford: <http://genome-www.stanford.edu/~sherlock/cluster.html>)
- an interactive tool to load & annotate data (& a scriptable one is under development to load multiple experiments in bulk, albeit with less annotation).

Its advantages are that it:

- is freely available in source code (tarball and anonymous CVS).
- has relatively small hardware requirements.
- requires no proprietary software to run.
- is relatively simple to install .. operative word 'relatively' ;) .
- supports multiple kinds of array data (Affy, Cy3,Cy5, radiolabeled blot).
- can incorporate commandline analytical routines very easily as CGIs.
- can share data via an XML for which there are free tools available.
- it has been developed using a number of R (aka GNU S) libs: (<http://cran.r-project.org/>) and will continue to add more support for this Open Source Software approach.
- can export data in a variety of formats for use with other tools.
 - * J-Express (<http://www.ii.uib.no/~bjarted/jexpress>) can directly import one std format.
 - * with a local installation, you can export the data in xgobi format and with minimal scripting in R, you could export in a number of other formats as well. Use the source, Luke!
- it has a fairly active development community.

Its disadvantages (hey! it's free; there ARE disadvantages!) are:

- the user interface is crude.
- the query interface is crude and simple (but pretty easy to customize).
- we do not yet provide for easy normalization, altho such an interface is under development (contributed by an external user) and more input would be most welcome.
- it uses a heterogeneous (albeit standard) mix of software components.
- it requires some knowledge of

Linux and Postgres (or whatever RDBMS in which you want to implement it) to make it work. It is definitely *NOT* Plug and Play.

- it is a relatively young project and therefore will probably not support some critical operations.
- the current data loader is functional, but sub-optimal (and is being re-written from scratch with the input of several labs).
- there are some known security issues (and certainly more unknown ones)
- its scalability is largely untested.

We're hoping that with enough interested, engaged users, each contributing what they can (suggestions, bug descriptions, & especially code), useful features can be suggested and implemented, bugs can be killed quickly, ports to additional RDBMS can be completed, useful applications can be added, the Data Model and XML feature set improved and contributed back to make the MGED MAML XML as robust as it needs to be.

We welcome your feedback (really!) [genex@ncgr.org]

The GeneX Team

- * Bill Beavis > William Anderson
- * Greg Colello > Andrew Dalke
- * Harry Mangalam > Carol Harger
- * Lonny Montoya > Peter Hraber
- * Michael Pear > Karen Schlauch (honorary)
- * Todd Peterson > Mark Waugh
- * Jason Stewart > Jennifer Weller
- * Jiaye Zhou

Mill Hill Essays

<http://www.nimr.mrc.ac.uk/millhillessays/2000/>

May 5th 2000 was the fiftieth anniversary of the opening of the new Institute at Mill Hill by their majesties King George VIth and Queen Elizabeth. Rather than follow our usual aim in this essay series, of considering medical science topics in the news, we decided to include this small volume as part of our anniversary celebrations. For this purpose we have selected areas of our own work at the Institute which have been continuous important strands of medical research for the last half century. Many other aspects of our research are of course not included, but we hope you will get a flavour of the range of our interests from this small selection.

Contents:

- From microbes to cancer (Don Williamson and Lee Johnston)
- Of frogs and men (Tim Mohun and Jim Smith)
- The immune system in health and disease (Victor Tybulewicz)
- Unravelling the workings of the brain (Geoff Raisman)
- Distemper and influenza at Mill Hill (Rick Carver and John Skehel)
- The red road [Malaria] (Tony Holder)

The Mill Hill Essays are published annually to promote the public understanding of Science. They were inspired by a series of BBC Radio lectures given by eminent scientists in the 1950's, and subsequently published as a book. They are written by members of staff of the National Institute

for Medical Research and guest authors, and are designed to be accessible to anyone with an interest in science and the natural world. Five volumes of essays have been published and are available in print or online:

Printed copies are available on request.
Frank Norman
National Institute for Medical Research Librarian
The Ridgeway, Mill Hill
London NW7 1AA, UK
Tel: 020 8 913 8629
Email: fnorman@nimr.mrc.ac.uk
Fax: 020 8 913 8534

Peakmatcher

<http://www.agro.agri.umn.edu/~peak/peakmatcher.htm>

Peakmatcher utilizes text-based output from programs such as ABI PRISM Genotyper software to create a binary (1/0) table. It operates as a Microsoft Excel macro. It is particularly useful for very large genetic diversity studies using fluorescent AFLPs.

Protoeme Analysis Database

<http://www.ebi.ac.uk/proteome/>

Now available ... analysis of 45 proteomes including Arabidopsis thaliana and Arabidopsis thaliana. A recent addition is the chromosome tables for most of the organisms. They provide an alphabetically ordered list of genes, together with chromosome position, information about the protein it encodes, and useful links to other databases.

"Nothing is interesting if you're not interested."

Helen MacInness

PubGene

<http://www.pubgene.org>

PubGene is a collection of tools, including modules for supervised analysis of gene expression data based on the information contained in MEDLINE (<http://www.nlm.nih.gov>).

For documentation and reference, please see <http://genetics.nature.com/> (Jenssen, T.-K., Laegreid, A., Komorowski, J., Hovig, E.: A literature network of human genes for high-throughput gene-expression analysis. p.21-28. Nature Genetics. May 2001).

The complete MEDLINE titles and abstracts are indexed for the occurrence of all instances of human gene names and literature aliases, and mapped to their correct primary gene symbols, as defined by the HUGO nomenclature committee. All pairs of primary gene symbols are indexed to create a network of genes based on their literature associations. This approach opens the path for a whole new range of tools for the biologist, and for gene expression analysis in particular. The web site is a work in progress, and content may increase with time.

Among the more prominent features at present are:

- * Gene network browsing: view the literature neighbors of any human gene having MEDLINE recorded publications
- * Gene subnet viewing: identify and view the literature interactions between your own selection of genes
- * Explore relevant MeSH terms for your gene(s) of interest
- * Explore gene ontology terms for

your gene(s) of interest

- * Find the MEDLINE references most relevant for your selected set of genes (without boolean searches)
- * Do complete gene expression analysis on your own data. The result will indicate which literature gene clusters are most significantly affected.

For further information or questions regarding this web site please contact: ehovig@radium.uio.no or tkj@idi.ntnu.no

ROSE - Random-model Of Sequence Evolution

<http://bibiserv.TechFak.Uni-Bielefeld.DE/rose/>

We are pleased to announce that release 1.2 of Rose is now available on the Bielefeld Bioinformatics Server. Rose implements probabilistic models of RNA, DNA, and protein sequence evolution via insertions, deletions and substitutions. The source code is published under the GPL.

New Features:

- Standard DNA evolution models (JC, HKY, F81, F84, K2P)
 - multiple runs, single invocation
 - FASTA or PHYLIP output formats
- Rose Copyright (c) 1997-2001
University of Bielefeld, Germany
and Deutsches
Krebsforschungszentrum (DKFZ)
Heidelberg, Germany.

Rose 1.2 Download
http://BiBiServ.TechFak.Uni-Bielefeld.DE/cgi-bin/bibi_download?tool=rose&version=1.2

Authors: Jens Stoye (1), Dirk Evers (2), Folker Meyer (3)
(1) Max Planck Institute (MPI) for Molecular Genetics, Computational Molecular Biology, Berlin, Germany; (2) Faculty of Technology, University of Bielefeld, Germany; (3) Center for Genome Research, University of Bielefeld, Germany

About Rose:

Guided by an evolutionary tree, a family of related sequences is created from a common ancestor sequence by insertion, deletion and substitution of characters. During this artificial evolutionary process, the 'true' history is logged and the 'correct' multiple sequence alignment is created simultaneously. The model also allows for varying rates of mutation within the sequences, making it possible to establish so-called sequence motifs. The data created by Rose are suitable for the evaluation of methods in multiple sequence alignment computation and the prediction of phylogenetic relationships. It can also be useful when teaching courses in or developing models of sequence evolution and in the study of evolutionary processes.

Jens Stoye
Max Planck Institute for Molecular Genetics
Computational Molecular Biology
Ihnestr. 73 14195 Berlin, Germany
stoye@molgen.mpg.de
<http://www.dkfz.de/tbi/people/stoye/>
Tel: +49-30-8413-1352
Fax: +49-30-8413-1152

*The world's termites
outweigh the world's humans
10 to 1.*

Specialized Programs of Research Excellence

<http://spores.nci.nih.gov>

In 1992, the NCI established the Specialized Programs of Research Excellence (SPOREs) to promote interdisciplinary research and to speed the bidirectional exchange between basic and clinical science to move basic research finding from the laboratory to applied settings involving patients and populations. The goal of the SPOREs program is to bring to clinical care settings novel ideas that have the potential to reduce cancer incidence and mortality, improve survival, and to improve the quality of life. Current SPORE organ systems include Breast, Prostate, Lung, Gastrointestinal, and Ovary.

StackPACK v2.1 Transcript Reconstruction and Variation Analysis Tools

http://www.sanbi.ac.za/CODES/STACKPACK_REQUEST/

The South African National Bioinformatics Institute, in collaboration with Electric Genetics (South Africa), is happy to announce the academic availability of the ****significantly enhanced**** stackPACK v2.1 clustering toolset. The new system has been tested so far on datasets of up to 450 000 sequences at SANBI. StackPACK v2.1 is now available for Linux, SGI, Irix, Sun Solaris and Compaq for both Academic and Commercial users.

The primary goal of stackPACK v2.1 is to significantly improve the ability to handle large data sets and large clusters. StackPACK is the most widely used transcript reconstruction and variation analysis system available and is employed by over a hundred key research sites worldwide. The stackPACK system processes EST and mRNA data through a pipeline consisting of a series of steps including optional masking, loose clustering, assembly and alignment, alignment analysis for variation (alternate splicing) in clusters/transcripts and linking of non-overlapping clusters by clone ID. The system is unique due to its visualization tools and efficient data management, using a relational database. StackPACK can be run either through command line or through an rapid web-based interface.

What's New

****The primary goal of stackPACK v2.1 is to significantly improve the ability to handle large data sets and large clusters.****

- Single-cluster functions are now 'distributed' so the user may run simultaneous multiple assemble or masking jobs, even on a single cpu system.
- the d2_cluster sequence clustering algorithm is 10 times faster and has reduced memory requirements.
- User interface speed is significantly increased.
- Both web-based and command line data extraction reports are faster and have and reduced memory requirements.
- **New viewing and reporting functions highlight potential areas of interest****
- Export options now enable smoother data exchange with third-party programs, reducing the time spent reformatting or parsing output.
- Four new display options allow

rapid assessment of the assembly and assembly analysis alignment views.

- Alignments may be output directly to MSF and CLUSTAL formats.
 - Two additional data extraction reports, listing all constituent EST or mRNA sequences of all clusters and outputting the Alignment Analysis CRAW logs for all clusters.
 - **Enhancements in terms of user flexibility and control of the pipeline processes and applications****
 - Undo option for most of the steps in the pipeline, allowing the reversal of all steps subsequent to and including the step being undone.
 - Ability to mask sequences using either cross_match or RepeatMasker, or to cluster unmasked or externally masked data.
 - Configuration file expansion allows significantly enhanced parameter flexibility.
 - Many new parameters are added to the configuration file including the number of cpus for multi-processor steps, additional program flags and specific program locations.
- stackPack can be provided on a server to your community, contact liza@egenetics.com for information on server setup.
- Interested in transcript reconstruction?
STACKers mail list is for information on EST clustering and transcript reconstruction. Please point your browser to the following URL in order to subscribe to STACKers: <http://fling.sanbi.ac.za/mailman/listinfo/stackers>
- Scientific Publications
StackPACK has been described in several peer-reviewed publications.
- The method employed and assessment of quality of the resource is fully described in: STACK: sequence tag

alignment and consensus
knowledgebase.
Christoffels A, Gelder Av, Greyling
G, Miller R, Hide T, Hide W.
Nucleic Acids Res. 2001 Jan
1;29(1):234-8.

A Comprehensive Approach to
Clustering of Expressed Human
Gene Sequence:
The Sequence Tag Alignment and
Consensus Knowledge Base Robert
T. Miller, Alan G. Christoffels,
Chella Gopalakrishnan, John Burke,
Andrey A. Ptitsyn, Tania R.
Broveak, and Winston A. Hide.
November 1999: Genome Research:
9:1143-1155

· The clustering algorithm employed
in stackPACK is described in:
d2_cluster: A Validated Method for
Clustering EST and Full-Length
cDNA Sequences. John Burke, Dan
Davison, and Winston Hide. No-
vember 1999: Genome Research:
9:1135-1142

Additionally, stackPACK has been
instrumental in several discoveries.
A listing of scientific publications
and posters involving stackPACK
can be found at:

[http://www.egenetics.com/
?Section=publications&Parent=science](http://www.egenetics.com/?Section=publications&Parent=science)

Contact Details

StackPACK, originally developed at
the South African National
Bioinformatics Institute, is further
developed and maintained by
Electric Genetics who also provides
free support for academic users. For
queries about stackPACK v2.1 or
assistance with download and
installation, email:
support@egenetics.com For further
information on stackPACK, refer to
the Electric Genetics website at:
<http://www.egenetics.com/>

?Section=Stackpack&Parent=products.
For further information on research
at the South African National
Bioinformatics Institute, please
visit: [http://www.sanbi.ac.za/
Research.html](http://www.sanbi.ac.za/Research.html)

ALL THE VIROLOGY ON THE WWW

<http://www.virology.net>

All the Virology on the WWW
(ATV) is pleased to announce
several new developments of
interest to our visitors:

* Scientific Meeting Calendar at
ATV — All the Virology meetings
in one site, sorted by date. [http://
www.virology.net/
garryfavwebmeet.html](http://www.virology.net/garryfavwebmeet.html)
* Job Listings and Job Sites for
Virologists — Looking for a job or
a postdoc? We've the resources you
need. [http://www.virology.net/
garryfavwebjobs.html](http://www.virology.net/garryfavwebjobs.html)
* Free! Space for your
Article in ATV's new
Virology and Microbiology
Article Repository. [http://
www.virology.net/
ATVarticles.html](http://www.virology.net/ATVarticles.html)
* Big Picture Book of Viruses -
submit your images or tell us about
your favorites! [http://
www.virology.net/Big_Virology/
BVHomePage.html](http://www.virology.net/Big_Virology/BVHomePage.html)
* More About All the
Virology on the WWW.
<http://www.virology.net>

This site is maintained and updated
often. Any submissions, additions
or corrections that you might have
would be very much appreciated,
and can be made using the
following form: [http://
www.virology.net/
garryfavwebadd.html](http://www.virology.net/garryfavwebadd.html)

With your assistance, this Web Site
will continue to be the best resource
of its kind on the web. For those of
you who maintain your own web
pages, please send me your address
or use our site submission form and
I will gladly add it to the list.

(Please note that netiquette forbids
us from sending out information
releases to those individuals who do
not wish to receive them. Our
distribution list is small, and hand
selected. All recipients of our
releases were added to this seldom
used (last message in March 1999)
list after a visit to our Internet site
or from a request to be included.
On rare occasions we make a
mistake and inadvertently send out
material which you may not wish to
receive. Please send us a nice note
and we will remove you from our
list immediately).

David M. Sander, Ph.D
E-Mail: dmsander@ix.netcom.com
Sander & Associates, Consultants
2561 East Tiffany Lane
Fax: (916) 361-7281
Sacramento, CA 95827-1403
Phone: (916) 366-9663

**For Government
employees
everywhere**

It is the year 2000 and Noah lives in
the United States. The Lord
speaks to Noah and says, "In one
year, I am going to make it rain and
cover the whole earth with water
until all is destroyed. But I want
you to save the righteous people and
two of every kind of living thing on
the earth.

Therefore, I am commanding you to
build an Ark." In a flash of

lightning, God delivered the specifications for an Ark.

Fearful and trembling, Noah took the plans and agreed to build the Ark.

"Remember", said the Lord, "You must complete the Ark and bring everything aboard in one year."

Exactly one year later, a fierce storm cloud covered the earth and all the seas of the earth went into a tumult. The Lord saw Noah sitting in his front yard weeping. "Noah," He shouted, "Where is the Ark?"

"Lord, please forgive me!" cried Noah. "I did my best, but there were big problems. First, I had to get a permit for construction and your plans did not comply with the codes. I had to hire an engineering firm and redraw the plans.

Then I got into a fight with OSHA over whether or not the Ark needed a fire sprinkler system and floatation devices.

Then my neighbor objected, claiming I was violating zoning ordinances by building the Ark in my front yard, so I had to get a variance from the city planning commission.

I had problems getting enough wood for the Ark, because there was a ban on cutting trees to protect the Spotted Owl. I finally convinced the U.S. Forest Service that I needed the wood to save the owls. However, the Fish and Wildlife Service won't let me catch any owls. So, no owls.

The carpenters formed a union and went out on strike. I had to negotiate a settlement with the National Labor Union. Now I have

16 carpenters on the Ark, but still no owls. When I started rounding up the other animals, I got sued by an animal rights group. They objected to me only taking two of each kind aboard.

Just when I got the suit dismissed, the EPA notified me that I could not complete the Ark without filing an environmental impact statement on your proposed flood. They didn't take very kindly to the idea that they had no jurisdiction over the conduct of the Creator of the universe.

Then the Army Corps of Engineers demanded a map of the proposed new flood plan. I sent them a globe.

Right now, I am trying to resolve a complaint filed with the Equal Employment Opportunity Commission that I am practicing discrimination by not taking godless, unbelieving people aboard!

The IRS has seized my assets, claiming that I'm building the Ark in preparation to flee the country to avoid paying taxes. I just got a notice from the state that I owe them some kind of user tax and failed to register the Ark as a "recreational water craft."

Finally, the ACLU got the courts to issue an injunction against further construction of the Ark, saying that since God is flooding the earth, it is a religious event and therefore, unconstitutional. I really don't think I can finish the Ark for another 5 or 6 years!" Noah wailed.

The sky began to clear, the sun began to shine and the seas began to calm. A rainbow arched across the sky.

Noah looked up hopefully. "You mean you are not going to destroy the earth, Lord?"

"No," said the Lord sadly. "I don't have to. The government already has."

<p style="text-align: center;">ISICR 2001 PLENARY SESSIONS/ CHAIRS/SPEAKERS</p>

8:00-11:30 A.M. - MONDAY,
OCTOBER 8

P1. Regulation of cytokine signaling pathways
Chairs: Ian M. Kerr, Ph.D. and Andrew C. Larner, M.D., Ph.D.

Ian M. Kerr
Robert D. Schreiber
Michael David
Sarah Courtneidge
Nicos Anthony Nicola

3:00-6:00 P.M. - MONDAY,
OCTOBER 8

P2. Interferons, cytokines and immunoregulation
Chairs: Richard A. Flavell, Ph.D. and Richard M. Ransohoff, M.D.

Richard A. Flavell
John O'Shea
Jenny Ting
Barrett Rollins
Keiko Ozato
Paul Lehmann

8:00-11:30 A.M. - TUESDAY,
OCTOBER 9

P3. Interferons, cytokines and cancer
Chairs: John M. Kirkwood, M.D. and Ronald M. Bukowski, M.D.

Bernard Escudier
Moshe Talpaz
John Kirkwood
James Mier

James Talmadge
Tadatsugu Taniguchi

8:00-11:30 A.M. - WEDNESDAY,
OCTOBER 10

P4. Interferons, cytokines and
virus-host interactions

Chairs: Christine A. Biron, Ph.D.
and Ganes C. Sen, Ph.D.

Christine Biron
Ganes Sen
John Hiscott
Otto Haller
Grant McFadden

3:00-6:00 P.M. - WEDNESDAY,
OCTOBER 10

P5. Cytokines and apoptosis

Chairs: Theresa L. Whiteside,
Ph.D. and Ernest C. Borden, M.D.

Avi Ashkenazi
Pascal Schneider
David Lynch
Theresa Whiteside
Michael Shurin
James Finke

8:00-11:30 A.M. - THURSDAY,
OCTOBER 11

P6. Interferons, multiple sclerosis
and other neurological diseases

Chairs: Timothy Vartanian, M.D.
and Richard A. Rudick, M.D.

Doug Golenboch
Tim Vartanian
Richard Rudick
Samia Khoury
Vincent Tuohy

Facts to ponder

- In Cleveland, Ohio, it's illegal to catch mice without a hunting license
- Hang On Snoopy is the official rock song of Ohio.



October 7-11, 2001

VENUE:

Sheraton Cleveland City Centre
Hotel
777 St. Clair Avenue
Cleveland, Ohio 44114, USA
Phone: 216-771-7600
Fax: 216-771-5129

Exciting and sophisticated, the Sheraton Cleveland City Centre Hotel is located in the heart of downtown Cleveland—very close to the world-renowned Rock and Roll Hall of Fame and Museum and the Great Lakes Science Center. You'll find delightful shopping right outside Sheraton's doors in the Galleria at Erieview, as well as nearby at The Avenue at Tower City. All within a few blocks of the hotel you'll find Cleveland's famed Flats, the Warehouse District and the Theater District offering diverse downtown nightlife and entertainment options. At the Sheraton you'll enjoy the best that this sophisticated and exciting city offers, and the hospitality of our elegant, yet friendly hotel.

MEETING SECRETARIAT:

ADPRO/Meeting Coordinators, Inc.
4400 Renaissance Parkway
Cleveland, OH 44128, USA
Phone: 216-646-2055
Fax: 216-464-3884
Inquiries: Ask for Jane Bacha
E-mail: jbacha@adpro.net

Internet Website:

www.isicr2001.org
Visit our website for regularly updated information regarding the meeting and its program. On-line Registration submission is available. Links to exciting Cleveland sites and major corporate sponsors of ISICR 2001 are included.

Important Deadlines:

June 29, 2001 Notification of acceptance of papers
August 15, 2001 Hotel reservation

Letter of invitation:

The Organizing Committee will issue a letter of invitation for those who need help with necessary procedures for attendance. No financial commitment is implied in a letter of invitation.

Sponsors:

Aeterna Laboratories Inc. ,
Affymetrix, Amarillo Biosciences,
Biogen , Chugai Pharmaceuticals,
Cleveland Clinic Foundation
Taussig Cancer Center, Continental
Airlines, Immunex, Novartis,
Schering AG, Serono Foundation
for the Advancement of Medical
Sciences

