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2003
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ISICR Board of Directors:
Congratulations to the following members who are newly elected to the ISICR Board of Directors:
Ara Hovanessian
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W. Robert Fleischmann
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ISICR COMMITTEES

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

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"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 (Shuichito 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 Wemoski, 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. Gaffney .................. 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, Cleveland 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.

• 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


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

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 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 199/15374; 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; STLMC-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

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

"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 bioresearchers. 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 flourescent 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).


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

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.

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The world’s termites outweigh the world’s humans 10 to 1.
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

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 un-masked 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.


The clustering algorithm employed in stackPACK is described in:

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

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/

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).

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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
* 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
* Free! Space for your Article in ATV’s new Virology and Microbiology Article Repository. 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
* 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

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.”
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

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**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.

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**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

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**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