2/26/82

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TELECON MINUTES
JANUARY 25 1982

The meeting was called to order with participants as follows: AIM Executive Committee members Drs. Saul Amarel, William Baker, Edward Feigenbaum, Joshua Lederberg, Roy Maffly and Ted Shortliffe. Dr. Harry Pople and Tom Rindfleisch also attended the meeting; Drs. Jack Myers and Donald Lindberg were not present.

See meeting agenda (attached).

ITEM I: AIM WORKSHOP PLANNING

Dr. Pople proposed a change in focus for the workshop, from that of a specialized scientific conference (where various project groups present papers) to a "critical questions" conference where future directions for the field of artificial intelligence are discussed. Dr. Pople cited several reasons for this emphasis : 1. Long-term funding for AIM is shaky and strategies for improving this situation must be developed, 2. We need to re-examine and re-emphasize shared objectives and joint ventures in the AIM community with the field of AI generally.

Dr. Feigenbaum agreed, noting that there is much publicity for AI now and if we make our vision clear and show the industrial people where this might lead, then we might be able to generate some industrial research funds for the field which have not been forthcoming from the federal government.

The Japanese "Fifth Generation" effort and the cooperative approach between Japanese government and industry in supporting research were cited as one model for how this works outside of the United States.

Dr. Pople commented that some U.S. industries have begun to express an interest in AI programs. TELENET, for example, has approached him about selling access to CADUCEUS. They really want to put something interesting on the wire. It is not clear how much basic research they could justify supporting, though.

Dr. Feigenbaum said there has not been much evidence of even the computer manufacturers becoming very interested until this year. It was mentioned that IBM has now mounted their effort in CAI. Dr. Pople raised the possibility that underdeveloped countries might represent a market for AIM programs and we might find some interested industrial partners.

Dr. Feigenbaum noted that the knowledge engineering group at Hewlett-Packard also is exploring possible medical AI applications.

It was suggested that we include experts from the biomedical community who are not AI advocates to help with the review/planning effort. Mention was made of Octo Barnett, Homer Warner and Gene Robbins as the kind of people

who could help us. Time would be a critical factor in that these people would have to do quite a bit of homework and may not be able to make the committment.

Dr.Amarel asked whether there are any people in the medical community not necessarily close to computers who are involved in planning and the use of technology? Dr. Baker replied that when he discussed this with Jack Myers, he had had some suggestions that he was going to mull over.

Dr. Myers and Dr. Shortliffe had just been together at a conference on the issue of Technology and Medical Education. There were several people who expressed the kind of interest that would suggest that they might participate in an AIM meeting such as this. Dr. Shortliffe said he thought Dr. Myers and he could suggest a list of candidate names. Generally, they would be clinicians involved in education and not specifically involved in technology or AI.

Regarding the numbers of people to be invited, Dr. Shortliffe said that since we are looking for interactions between people who are leaders in AIM and leaders from other fields who are interested in what AIM is about, this means a very different list from the list we have used in prior years. He added that we can probably come in under the numbers we felt obligated to invite in previous workshops.

Dr. Baker agreed that we need a few participants who represent areas in medicine outside of AIM who can help project what is going to take place 15 years from now. He indicated that it would be difficult to attract such key medical people without an honorarium in addition to covering expenses. Some support can probably be made available for these specially invited people. But he needs a tentative plan and an agenda that he can bring to the council meeting the second week in February.

ACTION: Comments and suggestions are to be sent to Dr. Pople by the end of the week of January 25th.

AIM WORKSHOP - TIME AND LENGTH OF WORKSHOP

The proper length of time for the workshop was discussed. Dr. Amarel felt that 1 to 1 1/2 days would be best; Dr. Baker suggested 2 1/2 days. Dr. Shortliffe felt that it was a little hard without seeing the actual agenda, but thought that the workshop could easily last 2 full days.

Dr. Feigenbaum suggested that the workshop have a flexible end time, with the body of the meeting on Saturday and Sunday prior to AAAI, and that Monday be flexible so that people can optionally attend the AAAI tutorials or extended discussions about AIM plans. Some industrial people who may attend the AIM workshop might want to attend the tutorials, for example. Others felt that the overlap problem would not be unworkable.

The scheduling was left for Dr. Pople to resolve.

ITEM II: Genet Advisory Committee Status

Dr. Baker reported on the formation of the Genet Advisory Committee. Dr. Alan Maxam has agreed to serve as chairman of a committee which will be modeled after AIM-EXEC.

Inputs have yet to received about candidate committee members from Kedes, Brutlag or Friedland.

Currently Genet committee candidates include Dr. Abelson (GMS steering committee), Dr. Newburg of NSF, Dr. Lederberg (AIM Exec representative) and Mr. Rindfleisch.

ACTION: Dr. Baker will collect names of people suggested to be on the committee and send them on to Dr. Maxam.

ACTION: Dr. Baker will organize the charge for the committee and the first meeting.

ACTION: A list of Genet users should be sent to Dr. Lederberg by Dr. Friedland.

ITEM: Rutgers Dolphin

Dr. Amarel reported that ARPA has approved the funding for the Dolphin and a letter of intent was sent to Xerox. He will advise Mr. Rindfleisch when it is definite.

ACTION: Mr. Rindfleisch will send out Dolphin failure experience.

ITEM: INTERLISP

Dr. Feigenbaum announced that a new Interlisp will be released soon which will increase the speed of Dolphins by a factor of 2. Xerox EOS has approval for a second generation machine, based on the Star. The Interlisp/VAX system runs full function but slow.

ITEM: AAAS Meeting (in conjunction with SCIENCE Magazine)

Dennis Smith and Peter Friedland are planning a program for an AAAS meeting on advanced computer technology for scientists. Dr. Feigenbaum reports that the meeting will be announced in the 2/21 issue of SCIENCE.

Randy Gellerman, Ph.D.
2/26/82

AGENDA
AIM Executive Committee Telecon
January 25, 1982
1:00-2:00 PST

1) AIM Workshop Planning

2) Genet Advisory Committee Status

3) General Discussion

AGENDA

AIM EXECUTIVE COMMITTEE TELECON

MARCH 11, 1982

11:00 - 12:00 PST

1) GENET Advisory Committee

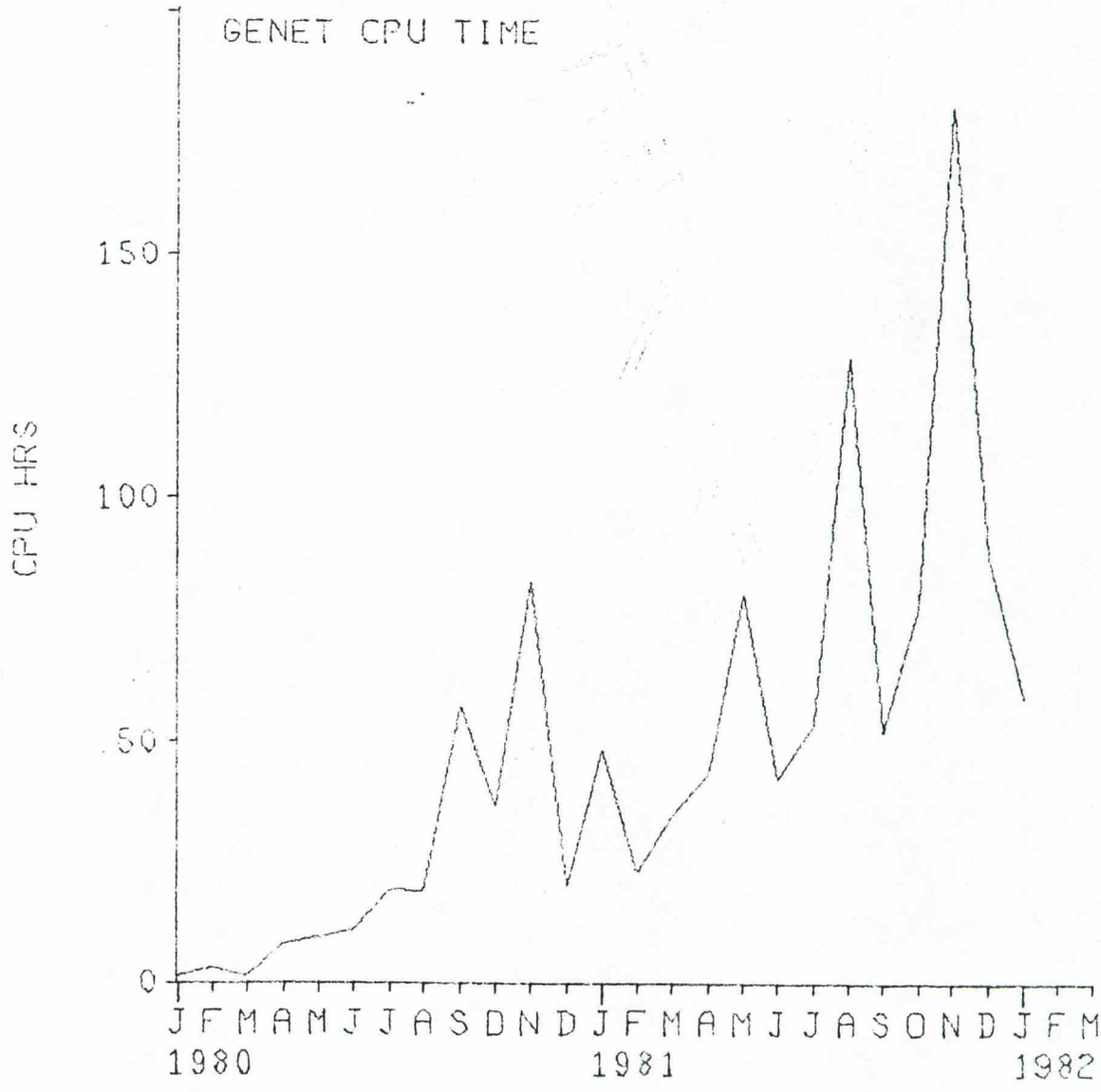
2) AIM Workshop

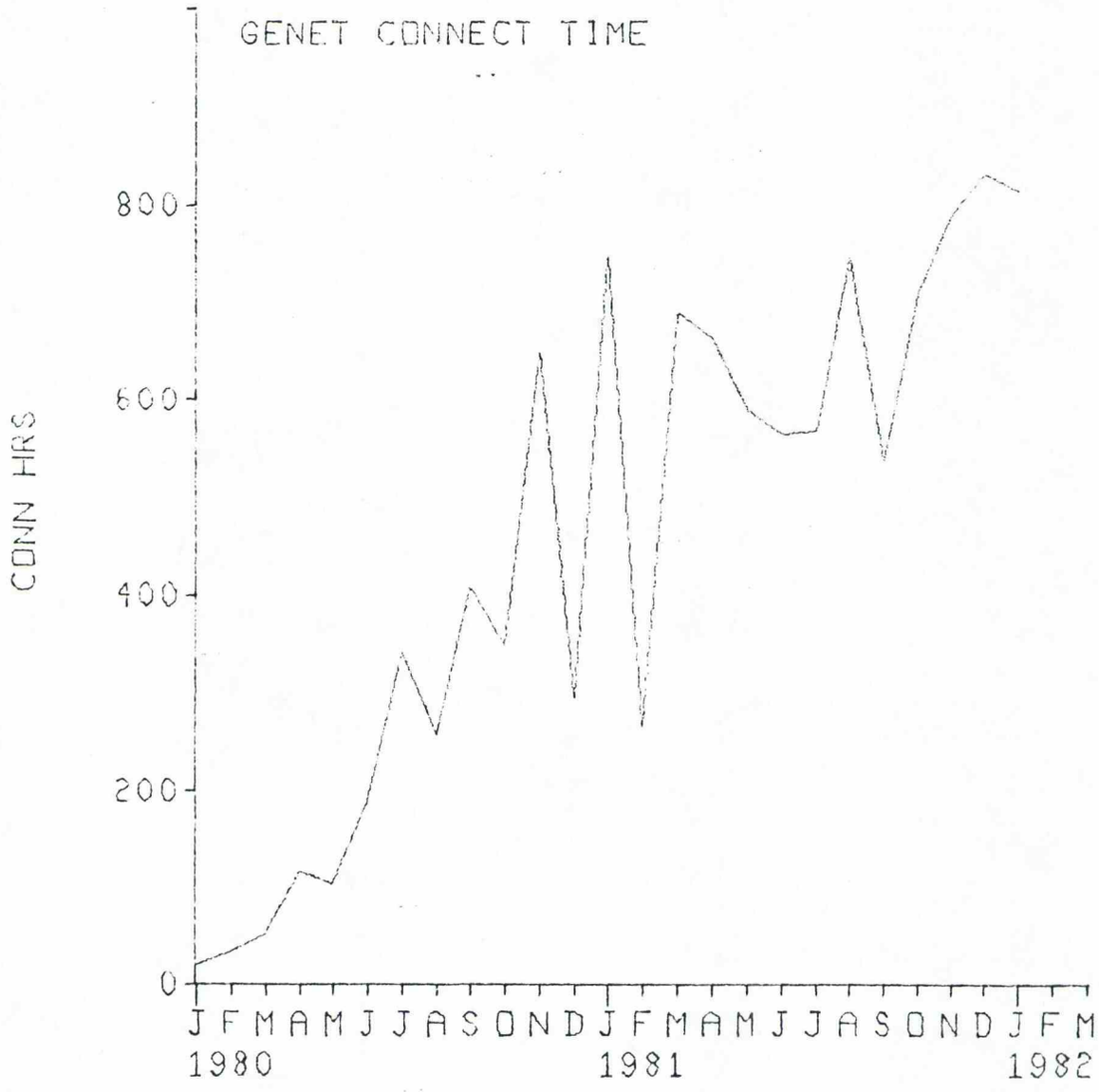
3) BRP "Funding Arrangements" Policy

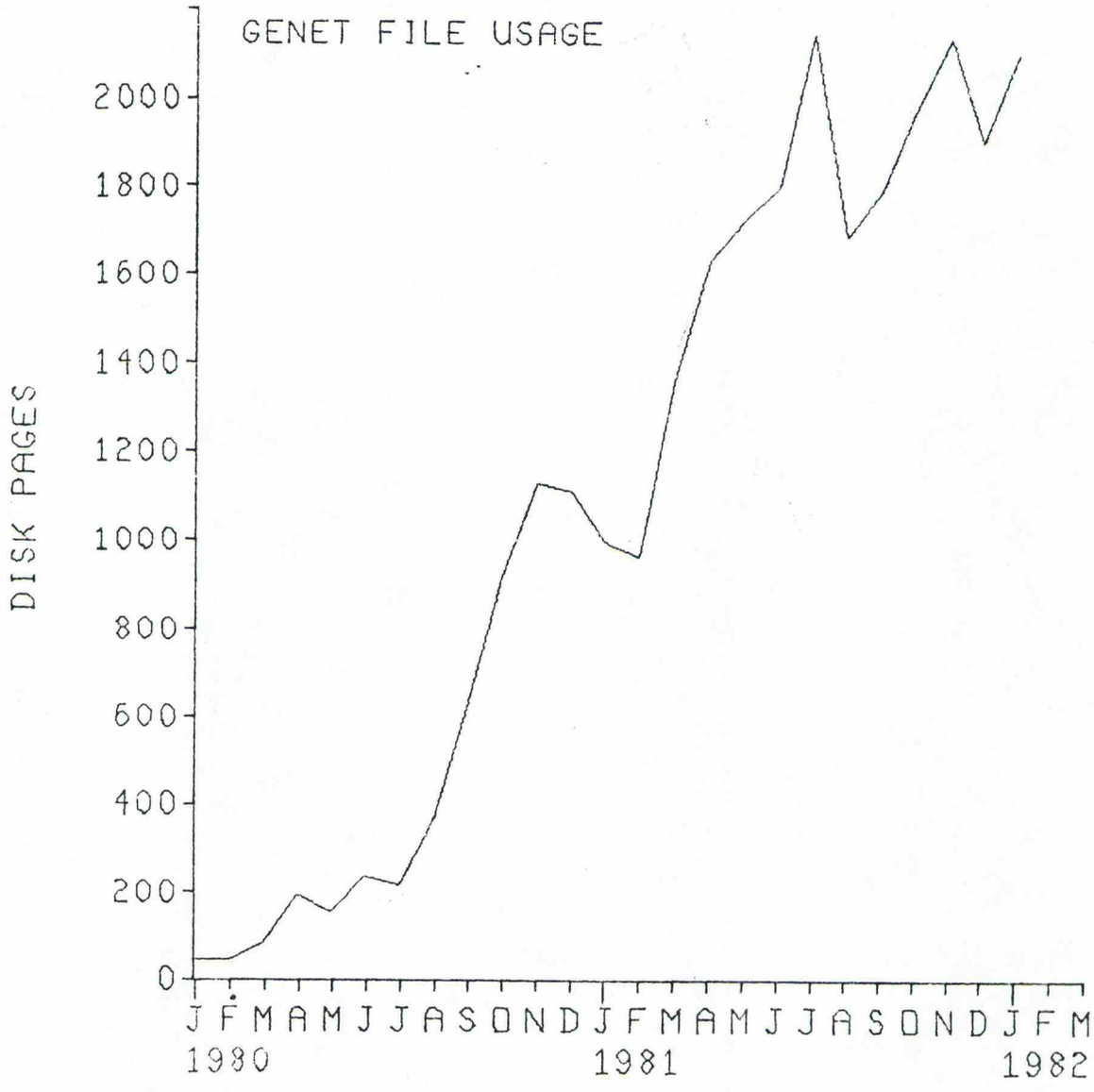
4) General Discussion

3/2/82
T. Rindfleisch

HISTORICAL DATA ON GENET USAGE OF THE SUMEX-AIM SYSTEM


GENET CPU TIME
CPU HRS
150
100
50
0
J F M A M J J A S O N D J F M A M J J A S O N D J F M
1980
1981
1982


GENET CONNECT TIME
CONN HRS
800
600
400
200
0
J F M A M J J A S O N D J F M A M J J A S O N D J F M
1980
1981
1982


GENET FILE USAGE
DISK PAGES
2000
1800
1600
1400
1200
1000
800
600
400
200
0
J F M A M J J A S O N D J F M A M J J A S O N D J F M
1980
1981
1982

HISTORICAL DATA ON GENET USAGE OF THE SUMEX-AIM SYSTEM

May 1, 1981
T. Rindfleisch
P. Friedland
J. Clayton

THE GENET GUEST SERVICE ON SUMEX

The MOLGEN project at Stanford has focused on applications of artificial intelligence and symbolic computation to the field of molecular biology. The research began in 1975 and is currently in the first year of a three year grant renewal. In early 1980 it was realized that some of the systems developed by MOLGEN were of direct utility to many scientists in the domain. Accordingly, with the cooperation of the SUMEX-AIM staff and close coordination with the AIM Executive Committee, it was decided in February 1980 to provide a carefully limited guest service for the community use of such systems.

There were two major reasons for the establishment of this guest service, which took the form of the GENET account on SUMEX. The first was to broaden MOLGEN's base of scientist collaborators, to find molecular biologists at institutions other than Stanford who could contribute actively to our knowledge-based approach to problem solving. The second was to introduce a generally computer-naive community to the benefits of resource sharing provided by a system like SUMEX, with the hope of serving as a model for an eventual resource for molecular biology.

We believe that we have succeeded in these two goals. Many of our GENET guests have become active collaborators in core MOLGEN research. These collaborators include Professor Allan Maxam at Harvard Medical School, Dr. Walter Goad at Los Alamos, Dr. Richard Roberts at Cold Spring Harbor, Dr. William Pearson at Johns Hopkins, Drs. Walter Bodmer, Julia Bodmer, and Robert Kamen at the Imperial Cancer Research Fund, Professor Fred Blattner at Wisconsin, Dr. Andrew Taylor at University of Oregon, and Dr. Dan Davison of SUNY-Stonybrook. We are also pleased by the numerous comments SUMEX has received from GENET users praising the user-sensitive nature of the resource, especially in comparison to typical university computer centers.

GENET has been important both for MOLGEN and for the national community of molecular biology. It has ensured a steady flow of ideas for the artificial intelligence research that is core to both the MOLGEN grant and the SUMEX-AIM mission. It has also provided a useful service to an international community that is not readily available elsewhere.

GENET GUEST COMMUNITY MANAGEMENT

Our decision to support the GENET guest experiment and our approach to doing so within the SUMEX-AIM resource has been reviewed and approved both by the AIM Executive Committee and by the Initial Review Group/National Advisory Research Resources Council in the course of the peer review of our pending SUMEX renewal application. We have tried to manage the GENET guest experiment in such a way that we maintain the "friendly" interface of the SUMEX-AIM resource for molecular biologists unfamiliar with computers while taking appropriate steps so that GENET usage does not detract from on-going AI research and so that we assure prudent administration SUMEX as an NIH-BRP resource. The key elements in our management approach include:

1) Controlled announcement of the GENET opportunity -- Beginning in February 1980, the availability of GENET services was announced, primarily by talks at professional conferences with accompanying program demonstrations. We decided against publishing "blanket" announcements in professional journals in order to maintain a very high standard of collaborator interest and scientific expertise within the limited group we could serve with available SUMEX resources.

2) Close coordination with the AIM Executive Committee -- We kept the AIM Executive Committee apprised of plans for the GENET experiment and of progress and growth of the community. At the August 1980 AIM Workshop meeting of the Executive Committee, Professor L. Kedes of the MOLGEN project made a presentation on the status of GENET. The Executive Committee approved continuation of the GENET service but because of the significant growth in the number of GENET users and their consumption of CPU resources, a limit of two simultaneous GENET jobs was placed on the community. The Executive Committee also approved the concept of a proposed Molecular Biology Computing Resource related to but separate from the existing SUMEX resource.

3) Careful control of GENET usage -- We have closely monitored the very rapid growth in GENET usage of SUMEX (see data below). With Executive Committee advice and in cooperation with the MOLGEN project personnel managing the GENET community, we have instituted several successively stringent controls on GENET users:

   a) All GENET users run out of the same directory so scheduler control limits are enforced to hold GENET usage as a whole down relative to that of AI research projects during heavy loads.

   b) The GENET directory has been intentionally limited in disk space allocation so that large numbers of files cannot be retained.

   c) Starting in October 1980, a limit of two simultaneous logged-in GENET jobs was placed on the community.

d) Starting in December 1980, a policy statement was issued restricting GENET use to academic collaborators. MOLGEN project management informed industrial collaborators that they could no longer use the GENET facility and actively monitored adherence to this policy. Previously, valuable feedback had been obtained from a small group of industrial collaborators for MOLGEN AI program development. However, with the rapid growth of the highly competitive molecular genetics industry, there was no way we could adequately control industrial users consistent with SUMEX's status as a federally funded national resource. Thus, we decided to exclude them. In April 1981, we instituted a GENET user password checking system to further control community access, particularly in regard to industrial users.

4) Limited commitment of SUMEX staff resources -- The day to day management of the GENET community has been the responsibility of MOLGEN project personnel. SUMEX personnel have only contributed to developing system facilities to help manage GENET (guest and GENET password capabilities), assisted with technical communications problems, and advised in establishing GENET management policies consistent with AIM Executive Committee and SUMEX Principal Investigator resource policies. The total commitment of staff time has been on the order of 1-2 man-months.

GENET USER COMMUNITY

The GENET community consists of approximately 200 users from 63 research institutions. Of these 200 users, approximately 35 are consistently active users. That is, they log in, run programs, and interact with the MOLGEN members on an almost daily basis. Many of these users have made valuable contributions to our work. About 100 others are frequent, but not regular users. They log in only when they have a major analysis task to perform, which seems to be on the order of once a month.

The remaining users rarely use the system. They have logged in a few times, but for one reason or another they never become regular users of the system. Quite often this is because a lab group will settle on having one or two graduate students or post-doctoral associates become the "computer experts" of the group, and as a result, the computer use by the other people in the lab drops to an almost non-existent level. Unfortunately, an equally prevalent reason for users to stop using the GENET account is a lack of resource time. Probably the major complaint that we get from GENET users is concerning the lack of compute time and availability of the system. One account just is not enough for 200 people to share, especially when it is

ACCOUNT: GENET (February 1980 - March 1981)

MONTH/ YEAR	CPU HOURS	TOTAL CONNECT HOURS	TYMNET CONNECT HOURS	GENET % OF SUMEX TYMNET USE	FILE PAGES
Feb/80	3.23	32.72	18.88	2.0%	57
Mar/80	1.28	51.57	12.80	1.4	95
Apr/80	8.37	117.87	51.73	5.4	209
May/80	9.20	104.46	66.65	8.0	166
Jun/80	11.08	188.35	118.03	11.7	253
Jul/80	19.21	342.87	189.00	18.2	231
Aug/80	18.71	257.23	188.53	18.2	367
Sep/80	57.32	409.83	254.53	28.5	626
Oct/80	36.47	348.66	211.95	23.3	920
Nov/80	82.90	648.56	308.40	31.1	1133
Dec/80	19.86	295.85	188.67	22.8	1110
Jan/81	48.00	747.91	277.30	27.2	996
Feb/81	22.58	265.39	163.55	16.1	962
Mar/81	29.73	613.74	313.57	25.0	982

GENET USERS BY RESEARCH INSTITUTION

The following is list of GENET users by affiliation. The accompanying texts are excerpts from messages sent to MOLGEN project members concerning how the particular user plans to use or has used the GENET facility. For some universities we have complete lists of all professors, post-doctoral candidates, and graduate students using GENET. However, for many we have just a list of the most active users from the institution.

ALBERT EINSTEIN COLLEGE OF MEDICINE

Perry Nisen - Mol. Biol.
E. Benz - DBC
D. Brown - DBC
B. Birshtein - Cell Biol.
S. Tilley - Cell Biol.
G. Childs - Genetics
John Sninsky (EXO-MOLGEN user)
Bob Wydro
(3 additional graduate students)

I have been using the sequence analysis programs to identify sequence homologies between prokaryotic transposable DNA elements (i.e. Insertion Sequences and Transposable antibiotic resistance elements) and with E.coli RNA sequences. I have also been comparing some eukaryotic transposable sequences with the prokaryotic elements.

BAYLOR COLLEGE OF MEDICINE

Thomas Caskey, M.D. - Medicine
Savio Woo, Ph.D. - Cell Biol.
Burt O'Malley, M.D. - Cell Biol.
Wayne Wray - Cell Biol.
Albert Ting - Cell Biol.

Dr. Wray received the information about this system from Dr. Kedes at the recent Gordon Conference. Dr. Wray's research deals with the isolation and the characterization of mammalian chromosomes. Albert Ting is interested in searching for seq homologies between the various genes being sequenced in our department and published sequences such as IVS consensus sequences and the U-RNA's. We have not run the programs yet, but they look mighty interesting. Thank you much for providing us access to your powerful programs. - Ting

BETHESDA RESEARCH LABORATORY (BRL)

Carolyn Tolstoshev
Dr. Bob Blakesley

{No description of usage available}

BRANDEIS UNIVERSITY

Dr. Pieter Wensink - RMSRC
Mien-Chie Hung - RMSRC
Garabedian - RMSRC

Michael Rosbash, Ph. D. - Biology
John Teem - Biology

Candice Stoner - BioChem
Sharon Ogden - BioChem
Robert Schleif - BioChem

The Schleif group members at Brandeis using Genet will be R. Schleif, B. Kosiba, C. Stoner and possibly others. We will use the GENET programs in sequencing and comparing completed sequences of the Arabinose promoters and structural genes. - Schleif

I will use this program to study DNA sequence of yolk protein gene. We are very appreciate your providing this program for us.
Thank you. - Mien Chie Hung

We are studying yolk-protein and tubulin genes from Drosophila Melanogaster and have been using DNA sequence program of the sumex system. With this system, we have been storing and analyzing our DNA sequence for the last few months. We find it is very convenient to have such a good system, which not only saves time but also pulls out information which would be very difficult to get if analyzed manually. - Wensink

CAL TECH

Roy Britten

{No description of usage available}

CARNEGIE INSTITUTE OF WASHINGTON

Dr. Gerry Rubin - Embryology

{No description of usage available}

CASE WESTERN RESERVE UNIVERSITY

David Samols - Biochem.

{No description of usage available}

CHILDREN'S HOSPITAL MEDICAL CENTER

Alice Huang, Ph.D. - Infectious Dis.

{No description of usage available}

COLD SPRING HARBOR LABORATORY

Dr. Rich Roberts
Dr. Tom Gingeras
Dr. Tom Broker

{No description of usage available}

COLLEGE OF MEDICINE AND DENTISTRY OF NEW JERSEY

Dr. Zari Humayun (Microbiology)
Dr. Rod Rothstein (Microbiology)
Stefan Karfopoulos (Microbiology)
(4 additional graduate students)

Thank you for permitting our use of your DNA sequences and programs on behalf of the Microbiology Department of the College of Medicine and Dentistry of New Jersey. It all goes well when we create our own files and then use the "SEQ" program.

I will be comparing repeated DNA sequences from yeast. These sequences are called DELTA. - Rod Rothstein

Having recently sequenced clones of small circular DNA of monkey, we are studying sequence homology to other sequences (i.e. repeats and origins). - Stefan Karfopoulos

CORNELL UNIVERSITY

Dr. John Lis - Biochem.
Brian Fristensky - Biochem.

Our lab is studying the expression of heat-shock genes in Drosophila. We are interested in using MAP to aid us in restriction mapping of the heat-shock genes and the sequences preceding them. - Lis

DUKE UNIVERSITY MEDICAL CENTER

Dr. Paul Modrich - BioChem.

{No description of usage available}

EUROPAISCHES LABORATORIUM FUR MOLEKULARBIOLOGIE

Dr. Hans Lehrach

{No description of usage available}

We are studying yolk-protein and tubulin genes from Drosophila Melanogaster and have been using DNA sequence program of the sumex system. With this system, we have been storing and analyzing our DNA sequence for the last few months. We find it is very convenient to have such a good system, which not only saves time but also pulls out information which would be very difficult to get if analyzed manually.
- Wensink

CAL TECH

Roy Britten

{No description of usage available}

CARNEGIE INSTITUTE OF WASHINGTON

Dr. Gerry Rubin - Embryology

{No description of usage available}

CASE WESTERN RESERVE UNIVERSITY

David Samols - Biochem.

{No description of usage available}

CHILDREN'S HOSPITAL MEDICAL CENTER

Alice Huang, Ph.D. - Infectious Dis.

{No description of usage available}

COLD SPRING HARBOR LABORATORY

Dr. Rich Roberts
Dr. Tom Gingeras
Dr. Tom Broker

{No description of usage available}

FREDERICK CANCER RESEARCH CENTER

Gray F. Crouse - Cancer Biology Program
Dr. Cheeptip Benyajati - Cancer Biology Program
Michael Berman - Cancer Biology Program

We are doing DNA sequencing, restriction mapping, and other standard procedures of molecular biology for which the facilities of SUMEX are very useful.

FLORIDA STATE UNIVERSITY

Don Sittman - Chemistry

I am interested in doing sequence analysis of the mouse histone genes. I was referred to the SUMEX project by Larry Kedes. - Don

FOX CHASE - CANCER RESEARCH INSTITUTE

Shirley Tilghman, Ph.D.
Peter Young
Fern Eiferman

Looking at internal homologies in mouse alphafeto protein (AFP). Want to use SEQ to determine significance of these homologies in particular using Doug Brutlag's probability calculations. - Peter and Fern

GEORGETOWN UNIVERSITY

Dr. Fredrickson

{No description of usage available}

restriction/modification system. This work was done by Brigitte Hausler working in Hamilton Smith's lab in the Department of Microbiology. I would still like to compare restriction mapping programs but have not had a chance yet. - Pearson

KENT STATE

Bruce Roe, Ph.D.

{No description of usage available}

LABORATOIRE DE GENETIQUE MOLECULAIRE - FRANCE

Dr. Giorgio Bernardi
Dr. Jacques Ninio
Jean-Pierre Dumas
S. D. Ehrlich

{No description of usage available}

LOS ALAMOS SCIENTIFIC LABORATORY

Walter Goad
Minoru Kanonisa

I'm engaged in the interim effort to bring up a nucleic acid sequence library, with your (molgen) group.

MASSACHUSETTS INSTITUTE OF TECHNOLOGY

Sam Yin - Biol.

Philip Auron (Alex Rich's laboratory)
Geoff Hendy
Hank Kronenberg
Alfred Nordheim
Gary Quigley
Paul Schimmel
Jon Friedman
Mark Rose
David Nelson (Cancer Center)

Our research includes studying TRNA genes in N. Crassa mitochondria. - YIN

PUBLIC HEALTH RESEARCH INSTITUTE

Saleem Khan - Plasmid Biology
Dave Dubnau - Plasmid Biology
Dr. Richard Novik
Loren A. Day
Debra G. Putterman

We will be using the DNA sequencing program and files. I have preliminary information regarding the SUMEX system from Stefan Karfopoulos at the College of Medicine and Dentistry of New Jersey. My primary purpose will be to analyze plasmid DNA sequences of small size. I appreciate the convenience of your facility and would like to thank you if there are any forms or administrative details please send them to. - Khan

We will be using MOLGEN for the analysis of sequences from the plasmid PEI94. At present our data consists of about 1500 base pairs. We would like to thank you for use of your facility. - Dubnau

PURDUE UNIVERSITY

Irwin Tessman - Biological Sciences

Research: Bacteriophage gene regulation.

RICE UNIVERSITY

Dr. Kathy Beckingham - Biochem.

{No description of usage available}

ROCKEFELLER UNIVERSITY

James Darnell, M.D.
Zinder

{No description of usage available}

STANFORD UNIVERSITY

Michael Deeley - Biol.
Howard Gershenfeld - Pathology
Mark Walberg - Pathology
Rick Van Etten - Pathology
Maureen Bibb - Pathology
H. Blanc
Richard Cassin - BioSci.
Stephen M. Beverley
Petter Gustaffson
Annie Chang - Genetics
Frank Kunst
Alex Gabain
Chris Miller
Peter Meacock
Michael Schechtman
T. Chappell
Glenn T. Horn - Struc. Biol.

I am a postdoc with Roger Kornberg working on the mechanism of splicing of mouse beta-globin mRNAs. - Horn

SUNY at ALBANY

David Holmes - Biol.

I am currently using the SEQ program to look for sequence homology within and between histone and histone-like genes.

SUNY at STONY BROOK

Dan Davison - MicroBiology
Bill Wishart - MicroBiology
Paul G. Rothberg - Microbiology
Glenn Larson - MicroBiology
Candace Swimmer - Micro (Tom Shenk's Lab)
Dr. Ann Jacobson - Microbiology
Dr. Ken Marcu - Biochemistry
Michael Kuehn - Biochemistry (Norman Arnhiem's Lab)
Alan Diamond - Biochemistry

Using program to do sequence analysis of ribosomal DNA spacer from mouse. - Kuehn

I was referred to you by Tom Gingeris at Cold Spring Harbor, and will be using the system to analyze various published and unpublished insertion sequences. This system is very impressive, and I thank you for permitting this laboratory (Dr. Eiichi Ohtsubo) to use it. We will acknowledge NIH-AIM-SUMEX, as requested. - Dan Davison

Ken and company will primarily be using the MAP programs.
- Marcu

I am using GENET to help me analyze polio DNA sequences.
- Larson

Dan Davison, John Milazzo and Ann Jacobson are giving a course on computer science for Molecular biology at SUNY. John is presenting the programs at Cold Spring Harbor (he works with Rich Roberts), Dan is presenting SEQ and Ann is presenting Tinoco, Studnicka programs for RNA secondary structure.

Sorry about the delay in replying to your note. The demo is for a DNA sequencing course which had sequenced an IS, IS102 (October J. Bact.) The course instructor asked me if I could arrange an analysis for today. This is not the DNA sequence analysis course, which starts in a month here, although some of the same people will be in that course.

The program is an automatic Kimura evolutionary calculation--- completely trivial at this point--- it return the estimated nucleo- tide substitution rate, and if a time estimate is supplied, a substitution rate per site per year. I eventually want the whole process to be handled by the machine--the two sequences to be compared are inputs, and the substitution rate is the output. - dan davison

SYRACUSE UNIVERSITY

Dr. John N. Vournakis - Biol.
Michael Lane - Biol. Res. Lab.
William Curtis - Biol.
Calvin Vary - Biol.
Anthony Troutt - Biol.
Jim Celetano - Biol.
Margaret van den Berg - Biol.
Thomas Savin - Biol.

{No description of usage available}

TEXAS A & M

Tom Chiang - Medical Biol.

{No description of usage available}

TUFTS UNIVERSITY

Dr. Michael Malamy - Mol. Biol.

{No description of usage available}

UNIVERSITY OF ARIZONA

David W. Mount - Microbiology
Martinez J. Hewlett - Cell. and Dev. Bio

We are studying the regulation of DNA repair functions in E. COLI. The major functions are normally repressed by a simple repressor, much like the phage Lambda repressor. In cells damaged with UV light or treated to inhibit their DNA synthesis the repressor (the LEXA gene product) is destroyed by the RECA protease. We are interested in the sequences which regulate the genes under LEXA control. One of the functions we are studying is inducible mutagenesis and we have devised a way to sequence rapidly a large number of mutants using phage M13MP from messing. Finally, we have a very large strain collection for these studies and wish to utilize X-SEARCH.SAI to catalogue these strains. John Roth has done this with Salmonella, and found X-SEARCH to provide the necessary flexibility. Eventually, I wish to establish X-SEARCH at our own institution but for now would appreciate initiating the cataloguing at Stanford. Please let me know if this use is compatible with your own intended uses of GENET.

UNIVERSITY OF CALIFORNIA - BERKELEY

Gail Christie - Mol. Biol.

{No description of usage available}

UNIVERSITY OF CALIFORNIA - LOS ANGELES

Michael Grunstein, Ph.D. - Molecular Biology
David Kolodrubetz - Molecular Biol.
Dr. Larry Simpson - Biology

I would like to use the GENET programs to help in the analysis for the sequences of the yeast histone genes being carried out in the lab of Dr. Michael Grunstein. - Kolodrubetz

UNIVERSITY OF CALIFORNIA - SAN DIEGO

Dr. Rick Firtel - Biol.
Bret Marquis - Biol.
Dr. John Abelson - Chem.
Mercer
S. Poole
J. Brandis
Nayak

I do sequence analysis for Dr. Melvin Simon and Dr. John Abelson. I would like to use GENET for this purpose. Your programs have been very useful to me. With the exception of Queen and Korn's program and two substantially smaller routines I have written myself in C. I am very limited in what I can do. - Bret

UNIVERSITY OF CALIFORNIA - SAN FRANCISCO

Y.W.Kan, M.D. - Medicine
David Martin, M.D. - Medicine
Dr. Howard Goodman - Biochemistry and Biophysics
Dr. Hugo Martinez - Biochemistry and Biophysics

{No description of usage available}

UNIVERSITY OF CALIFORNIA - SANTA BIOLOGY

Molly Fitzgerald-Hayes

{No description of usage available}

UNIVERSITY OF GEORGIA

Richard Meagher
Tom McKnight
Dilip Shah

{No description of usage available}

UNIVERSITY OF ILLINOIS - CHICAGO

Scott Kellogg, Ph.D. - Micro.
Robert Storti, Ph.D. - Biochem.

{No description of usage available}

UNIVERSITY OF KANSAS

Lyn Yarbrough - Biochem.

{No description of usage available}

UNIVERSITY OF MICHIGAN

Ron Hart - Biological Chemistry
Dr. Margaret Lomax - Biol.
Wesley M. Brown - Biol.

I work with Bill Folk on the cloning and sequencing of hamster tRNA genes. I will also be using the system for Dale Oxender, who has some Coli transport genes sequenced, and Larry Grossman, who sequences mouse mitochondrial genes. - Hart

UNIVERSITY OF MINNESOTA

Dr. Irwin Rubenstein - Genetics & Cell Biol.
Mark Peifer - Genetics & Cell Biol.

{No description of usage available}

UNIVERSITY OF NORTH CAROLINA - MEDICAL SCHOOL

Dr. Jack Griffith - Cancer Research Center
Marshall Hall Edgell - Bacteriology

My research interests which prompt this interaction are the mouse beta globins; DNA sequencing, DNA sequence analysis and programming. I would like to know whether you have "up" programs for sequence alignment of several sequences or tree generation? - EDGELL

UNIVERSITY OF OREGON

Andrew Taylor - Molecular Biology
Bob Jensen - Mol. Bio.
Dr. Charles Faust, Jr. - Health Sciences Center

I am interested in regulating sequences. - Jensen

We (Gerry Smith's Lab) have recently determined the sequence of the CHI recombinational hotspot in E.COLI. We want to examine the sequences in your files for the CHI sequence.

Subject: REPORT FROM ANDY TAYLOR ON WHAT HE'S BEEN DOING

Let me first remind you that we (in Gerry Smith's lab at Oregon) have been sequencing "Chi sites", which are sequences which increase the frequency of genetic recombination in their vicinity. They were first discovered in, and are easiest scored in, bacteriophage lambda. When we first started using the computer we had sequenced two chi sites and had found extensive (19 bases out of 25) sequence homology between them.

The first use we made of a computer was to search the sequence of PBR322 for sequences one base removed from our best guess for chi (the 8 bases our two chi's had in perfect register). We found that Pbr didn't have the 8'mer but there were several places at which it could arise. We isolated mutants of Pbr322 containing chi: thanks to knowing their position it was easy to get sequencing strategies for them. The program was also used to find restriction sites for enzymes isolated since the Pbr sequence was published.

We were also trying to sequence a Chi in the LAC-Z gene of E.coli. The protein sequence of LAC-Z, but not its complete DNA sequence, is available. By using the "reverse translation" procedure of Korn and Queen we were able to identify the only position where the chi octamer could occur, and were also able to plan a sequencing strategy, based on computer restriction analysis of DNA and protein sequences.

Thus, by sequence analysis of 3 Chi's in lambda, 3 in PBR322 and one in LAC-Z, we were able to identify, by eye, the Chi octamer as the only region common to all sequences. Our sequence analysis of chi+ mutants, their chi- parents and of chi-revertants of a chi+ mutant allowed positive identification of 6 of the 8 bases in the chi octamer as essential for activity. Sumex provided the evidence for the other two by identifying (in sequences known to be chi-), 8'mers differing from the chi octamer by either of the two remaining bases.

Extensive sequence analysis of 6 of the chi sequences failed to reveal any very significant homologies between the sequences, or any special features (such as dyads) present in all 6. We can therefore state that the only sequence necessary for Chi's action is the octamer GCTGGTGG, with the possible exception of a very wooly match of 4 bases out of 7 which occurs, at a varying distance from the octamer, in all 6 sequences.

We then searched the SUMEX DNA bank for the occurrence of chi's. As you will recall from my pesterings, I found a chi in all 4 single-stranded phages I examined. With a lot of computation, and some hand work, I have shown a) that there are 138 octamers common to PHI-X,G4 and fd. b) there are 110 of those also present on m13 and c) that there are only 13 octamers which are common to all 4 sequences and which are present on each of the two pairs of related sequences (PHI-X and G4; fd and m13) in non-homologous places. We can therefore conclude that chi is important for the phages, and can further conclude (as fd and m13 only differ by 200 bases of 6400, yet have their chi's in different places) that the need for chi is a recent one.

I have found Sumex to be a great help in the planning and interpretation of our sequencing experiments, and also in the comparison of chi with other sequences. In fact the program keeps suggesting new things to look at. The whole sumex set-up seems designed to impress the new user: the interactive nature of the SEQ program, and it's self-documentation, make it very easy for the novice to use. When I got bolder and started running my own programs, found the HELP files on things I needed to be wonderfully explicit. And I am most impressed with the message-sending facilities!! Thanks for all your efforts in getting the system running: I hope it matures into a national facility.

UNIVERSITY OF PENNSYLVANIA

Joel Flax

{No description of usage available}

UNIVERSITY OF ROCHESTER

Brad Kosiba - Radiation Biol.

{No description of usage available}

UNIVERSITY OF TEXAS - DALLAS

Dr. Ray MacDonald - Biochemistry

{No description of usage available}

UNIVERSITY OF TEXAS SCHOOL OF MEDICINE - HOUSTON

Terry Landers - Biochem.

{No description of usage available}

UNIVERSITY OF UTAH

Dr. John Roth - Howard Hughes Medical Research Institute

{No description of usage available}

UNIVERSITY OF WISCONSIN

Dr. Fred Blattner - Genetics
Dr. Bernard Weisblum - Pharmacology
Dr. Howard Temin - Oncology

{No description of usage available}

WASHINGTON UNIVERSITY MEDICAL SCHOOL

Wayne M. Barnes - Biochemistry
Dr. Mark Boguski - Biochemistry
Barry Honda
Heintz

I work on the DNA sequence and genetic control of the histidine operon of Salmonella typhimurium. I usually use my own extensions and modifications to Stadens first package of programs, on our own VAX computer. I mostly require your system to run a program like the Korn program to determine RNA structures.

WEIZMANN INSTITUTE OF SCIENCE

Dr. Joel Sussman - Structural Chemistry

{No description of usage available}

WESLEYAN UNIVERSITY

Dr. Barry Kiefer - Biology

{No description of usage available}

WORCESTER FOUNDATION FOR EXPERIMENTAL RESEARCH

Dr. William Crain
David Durica

We are examining the genomic organization of actin coding sequences in the seq urchin, S. purpuratus. - Durica

YALE UNIVERSITY SCHOOL OF MEDICINE

Sherman Weissman, M.D. - Human Genetics

{No description of usage available}

Two things concern us regarding this format. Will the panel be too large? Will the time allotted to each part of the program be sufficient? This program is attractive because it allows the views of students, administrators, and faculty to be presented simultaneously.

Our second event focuses on patent, copyright, and licensing policies. On Wednesday, April 28th from 4:00 to 6:00, Neils Reimers, Clive Liston, and Earl Cilley of the Office of Technology and Licensing will describe and comment on the University's patent, copyright and licensing procedures.

On Monday, May 3rd from 4:00 to 6:00, Bill Smith, John Halamka and Tom Dietterich will conduct a student workshop on patents, copyrights, and student consulting policies.

A number of different programs are currently being considered for Monday, May 10th. They range from a faculty panel presentation to a lecture on the moral, ethical and philosophical aspects of close academic/industrial relations.

Thank you for your interest in this issue. We look forward to working with you as the symposium is planned. Be sure to contact us if you have any questions or suggestions.

cc: Dick Gillam
Bart Bernstein
Charles Drekmeier
Carl Djerassi
Jon Claerbout
Brian Mariscal
Clive Liston
Neils Reimers
Kathy Ku
Earl Cilley
Eric Berg