Linkage Newsletter

LINKAGE COURSES

The next four linkage courses have been scheduled as follows:

January 8-12, 1996, at Columbia University, New York (advanced course, maximum of 20 participants, deadline for application is Nov. 20;   course announced in previous Newsletter).

February 26 - March 1, 1996, at the University of Zurich, Irchel Campus Computer Center, Switzerland (basic course, maximum of 18 participants).

June 10-14, 1996, at Columbia University, New York (basic course, maximum of 30 participants).

June 24-28, 1996, at Columbia University, New York (basic course, maximum of 30 participants).

To obtain information on these courses, please write to Katherine Montague, course coordinator, by email (preferred) or fax.

We will use our book (Terwilliger and Ott, *Handbook of Human Genetic Linkage,* Johns Hopkins University Press, 1994), with supplemental handouts for advanced courses.   Participants are expected to buy the book and bring it to the course;   in case of problems please contact Katherine Montague in advance of the course.   A list of corrections for the book may be downloaded from our anonymous ftp site, linkage.cpmc.columbia.edu (file *corr_ter.txt* in directory *book*).

SOFTWARE NEWS

Bug in FastLINK

Rita Kruse, Bonn Germany, made me aware of the following problem in FastLINK: For a pedigree with seven loops, the lod score was different depending on the order in which "loop individuals" were defined.   For one order, a maximum lod score of 6.50 was obtained while under another order, with the same data, the maximum lod score was only 0.66.   This difference occurred only with FASTLINK while the LINKAGE programs consistently furnished a lod score of 6.50.   Dr. Alejandro Schaffer confirmed this bug and has already corrected it in version 2.3P of FASTLINK.

SIMLINK and RHMAP on the Web

The following announcement was contributed by Dr. Michael Boehnke, Ann Arbor:

For some time, I have been distributing two programs for genetic analysis: RHMAP and SIMLINK. RHMAP is a program package for the statistical analysis of radiation hybrid mapping data. SIMLINK is a program for evaluating the statistical power of a proposed linkage study. Both RHMAP and SIMLINK are written in FORTRAN 77, and both previously were distributed free of charge on floppy diskettes after completion of a user agreement.

Beginning October 31, 1995, the primary method of distribution for RHMAP and SIMLINK will be via the World Wide Web (WWW). To access the current versions of RHMAP and SIMLINK (2.01 and 4.11, respectively), you will need a WWW browser such as Mosaic or Netscape. Using a browser, you can download the software packages from http://www.sph.umich.edu/group/statgen/software.

Both analysis packages, containing source code and manuals, are available as archives for Unix and DOS systems. Once you download the program package archives, you will need to dearchive the files. On Unix computers the "tar" utility should be used, e.g., "tar -xvf filename". (For other computer systems, e.g., VMS, etc., one can usually obtain public-domain utilities which can read "tar" files. Links to several such utilities are provided on the web page.) Simply compile the FORTRAN 77 code on your computer to obtain an executable. For DOS computers the archives are self-extracting and contain DOS executables of the programs. Simply issue the name of the archive as a DOS command, e.g., rhmapzip.exe, and all the files in the package, including the executable(s), will be extracted.

Also beginning October 31, the primary method for notification of software updates for RHMAP and SIMLINK will be via e-mail. If you already have or do in the future obtain one or both of the programs, I urge you to add yourself to the appropriate mailing list by sending a short e-mail note to me at boehnke@umich.edu indicating which package(s) you use and your preferred e-mail address for notification. This will insure that you continue to get program updates, and will be helpful for me at grant renewal time.

For those who lack Internet access, I will continue to distribute RHMAP and SIMLINK by floppy diskette. However, I ask you to make use of this option only if it truly is necessary. In this case, you will need to request a user agreement which you will need to fill out and send back.

Please feel free to contact me if you have any questions.

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Department of Biostatistics  FAX:        313-763-2215
University of Michigan       E-Mail:     boehnke@umich.edu
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Announcement of GenoCheck program

The following announcement was contributed by Dr. Margaret Gelder Ehm, Houston:

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                        GenoCheck, version 1.0

                            Meg Gelder Ehm
                            Rice University
                        Department of Statistics
                          Houston, Texas  USA
                         gelder@stat.rice.edu
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New error detection capabilities are available for genetic linkage data!

GenoCheck, 1.0 is an error checking program designed to identify individuals and
loci that are likely to contain errors. The statistical method was designed to
identify typing error, but is general enough to pinpoint any unlikely genotype
still consistent with Mendelian inheritance.

GenoCheck was developed using FASTLINK 2.2 (modified version of LINKAGE 5.1) and
uses a similar file configuration and installation procedure. The code contains
checkpointing facilities that allow users to recover from crashes without having
to rerun the program and comes with documentation.

The instructions for retrieving the code are given below:

ftp softlib.cs.rice.edu

Login as anonymous and leave your full e-mail address as the password.

cd pub/GenoCheck

In that directory you will find various files. You can get everything at once
by retrieving:

genocheck.tar.Z

and then (outside of ftp) doing the commands:

uncompress genocheck.tar.Z
tar xvf genocheck.tar

If you prefer to get the files piecemeal, instead of getting genocheck.tar.Z start
by getting README*. The file README (with no extension) will describe all of
the documentation.

The statistical algorithm implemented in GenoCheck, version 1.0 is described in
the papers:

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M. G. Ehm, R. W. Cottingham Jr., and M. Kimmel.  Error Detection in Genetic Linkage
Data Using Likelihood Based Methods.  Journal of Biological Systems, Vol. 3, No.
1 (1995) 13-25.

M. G. Ehm, R. W. Cottingham Jr., and M. Kimmel.  Error Detection in Genetic Linkage
Data Using Likelihood Based Methods.  American Journal of Human Genetics, Vol.
58, No. 1 (1996) (to appear).

Please e-mail any questions or suggestions about GenoCheck to gelder@stat.rice.edu.
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INFOBIOGEN server on the Web

Dr. Lucien Bachner (bachner@infobiogen.fr) requested that information about his server be included in this newsletter. Here is a brief description: The server may be accessed at URL http://www.infobiogen.fr/vjf/server_vjf.html. Academic users may obtain an account at Infobiogen (after returning a form) which enables them to access a large number of programs and databases useful for gene mapping and DNA analysis. Interaction with the server is in French.

Dr. Bachner is also organizing linkage training courses at the beginners level. The first was held October 24-25, he is planning the second for end of May 96 or June. Language is French. The same course is also scheduled at Institut Pasteur, December 19-20.

New version of ANALYZE package

A new version of the ANALYZE program package has been released. It simplifies the performance of a large array of parametric and nonparametric tests for linkage and association on data entered in LINKAGE format pedigree and parameter files. The programs are distributed at two different sites. You can obtain them either from

ftp.well.ox.ac.uk   in directory software/analyze

or from

linkage.cpmc.columbia.edu   in directory software/analyze.

Users are advised to download and study the README files. A DOS version of the whole package is in preparation and should be available on the latter ftp site by the end of November.

SURVEY

We occasionally hear from people that they are having problems obtaining our books through book stores. Typically these books are not stocked in regular book stores but those outlets designated by the Johns Hopkins University Press should always have books on stock. Readers who had problems obtaining our books (either through a book store or directly from the publisher) are invited to let us know; please also indicate the date when you had problems. We would like to have customer service improved in this area.

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Introductory Linkage Course

Feb. 26-
March 1, 1996

University of Zürich, Switzerland (Irchel Campus Computer Center 12 IBM PS/2s, Proff. Eric Kubli (Zürich) and Jürg Ott (New York). Course fee: $600 (US) Maximum number of participants: 18 The course will be taught in English. Application deadline: December 20, 1995

Course Descriptions and Prerequisites

This course is for researchers with little or no experience in using linkage programs. A basic knowledge of linkage analysis is, however, required. *Topics:* Introduction to linkage analysis; practical aspects of data collection; strategies and methods of linkage analysis; incomplete penetrance (narrow and wide definition); inbreeding loops; simple risk calculations: introduction to computer simulation. The major part of the course will consist of carrying out exercises using the LINKAGE programs.

People should plan an arriving in Zürich no latter than Sunday evening prior to the course (February 25). For additional information, please fax a request to +1 (212) 568-2750 or call Katherine Monataque at (212) 960-2507.

Course Fee

The fee for the 5-day-course is *$600* for researchers at an academic institution, and *$700* for individuals from private (for profit) companies. For applicants from Switzerland: course fee -700 Fr.or Fr.560 for people affiliated with ETH or University of Zürich. <u>Send no money now</u> --applicants will receive a bill and information regarding cancellation policy. As there is presently no support for this course from sources other than course fee, no reduction of the cost to applicants if possible. This fee covers tuition and course related expenses (diskettes, etc.) but not room, board or meals. Course participants will receive a list of good and moderately priced hotels in Zürich and will not have to make their own arrangements.

Participants are expected to purchase the textbook which will be used in the course (Terwilliger and Ott, "Handbook for Human Genetic Linkage," John Hopkins Univ. Press). Our office can give you the address of representatives of John Hopkins University Press for your country upon request.

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Introductory Linkage Course

Course #1 - Monday through Friday, June 10-14, 1996

Course #2 - Monday through Friday, June 24-28, 1996

Course Description and Prerequisites

This course is for researchers with little or no experience in using linkage programs. A basic knowledge of linkage analysis is, however, required. *Topics:* Introduction to linkage analysis; practical aspects of data collection; strategies and methods of linkage analysis; incomplete penetrance (narrow and wide definition); inbreeding loops; simple risk calculations; introduction to computer simulation. The major part of the course will consist of carrying out exercises using the LINKAGE programs.

The course will be held in the microcomputer classroom of the Health Sciences Library (Columbia-Presbyterian Medical Center, 701 West 168th Street) which is equipped with 20 IBM PS/2 machines. The number of participants is *limited to 30*. People should plan on arriving in New York no later than in the evening of Sunday, June 9 or June 23, 1996. For additional information, please fax a request to +1 (212) 568-2750 or call Katherine Montague at (212) 960-2507.

Application deadline: March 11, 1996. Participants are accepted on a "first come, first served" basis for the beginning course, so applications should be sent in as soon as possible.

Course Fee

The fee for the 5-day-course is *$600* for researchers at an academic institution, and *$700* for individuals from private (for profit) companies. It may be paid by check made payable to Columbia University Dept. of Psychiatry, or by Government pay order, but send no money now -- applicants will receive a bill and information regarding cancellation policy. As there is presently no support for this course from sources other than the course fee, no reduction of the cost to applicants is possible. This fee covers tuition and course related expenses (handouts, diskettes, etc.) but not room, board or meals. Course participants will receive a list of good and moderately priced hotels ($65+) in New York and will have to make their own arrangements (except foreign participants).

Participants are expected to purchase the textbook which will be used in the course (Terwilliger and Ott, "Handbook for Human Genetic Linkage," Johns Hopkins Univ. Press). Our office can give you the address of representatives of Johns Hopkins University Press.