Linkage Newsletter

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(this and all previous newsletters are available on our ftp site/Web page)

EDITORIAL

After ten years with Columbia University, the 'genetic linkage' group will be moving to Rockefeller University, New York, where a new *Laboratory of Statistical Genetics* is being formed. The move will take place throughout this summer and will be completed in November of this year. A new ftp site and Web page will be set up at Rockefeller but addresses are not known yet (note Dr. Ott's new email address above). They will be posted on our current ftp site/Web page, which will continue to exist for some time (at least one year).

LINKAGE COURSES

The next courses in genetic linkage analysis have been scheduled as follows, and interested researchers are urged to **apply early** as our courses tend to fill up quickly:

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). The second course will be held only with a sufficient number of applications (which we expect). Deadline for applications has been extended to April 8.

October 7-11, 1996, at University of Zurich, Switzerland (advanced course, maximum of 12 participants). Deadline for applications is August 30, 1996.

October 14-18, 1996, at Rockefeller University (advanced course, maximum of 20 participants, with preference to participants at U.S. institutions and companies). Deadline for applications is August 30, 1996.

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

Fortran and Windows 95

The only Fortran program currently distributed by us is LIPED. If compiled with Microsoft (MS) Fortran version 5.10, various compiler switches allow it to run under DOS, OS/2 and Windows 3.1. Under Windows 95, programs compiled for DOS still run in a DOS window; however, programs compiled for Windows 3.1 will not run in Windows 95. Presumably, for Windows 95 an updated Fortran compiler must be obtained from Microsoft. If anyone has experience in this matter, suggestions would be appreciated.

OS/2 and Windows 95

Even though I was an early fan of OS/2 ever since its version 1.1 came out, "market forces" made me decide that we no longer want to support OS/2 versions of our programs; these versions are still available on our ftp site but they will not be updated. Users with a need for running large programs may find it convenient to turn to our programs compiled with NDP Pascal for DOS. This compiler does not impose any limitations on array sizes, code or data segments, etc.

FASTLINK 3.0P

(submitted by A. Schäffer)

I am pleased to announce that FASTLINK 3.0P is now available. FASTLINK is a faster version of the main programs in LINKAGE. As of version 2.3P, FASTLINK runs in parallel on either UNIX multiprocessors or networks of UNIX workstations.

As with previous versions, the code is available by ftp from:

softlib.cs.rice.edu

Login as anonymous, leave full e-mail address as password.

cd pub/fastlink

If you are a UNIX user:

get fastlink.tar.Z

If you are a DOS user:

cd dos

<retrieve everything in that directory>

If you are a VMS user:

get README

get README.VMS

and follow the instructions there for what you need

Retrievers in Europe may find it more convenient to retrieve from the mirror site at:

ftp.ebi.ac.uk

The instructions are similar, but instead of:

cd pub/fastlink (for softlib)

do

cd pub/software/linkage_and_mapping/FASTLINK/fastlink (for ebi)

Among the improvements in FASTLINK 3.0P (compared to 2.3P) are:

--The code runs faster on data sets that have loops or unused alleles. If you used FASTLINK 2.3P, you may have noticed that it printed diagnostics when a data set had unused alleles, but it did not take advantage of the situation.

--UNKNOWN now detects violations of Mendelian rules of inheritance in looped pedigrees. It never did this before.

--maxhap and maxfem are no longer in the code as constants. If you were resetting maxhap each time and recompiling, you won't have to do that any more. If you were setting maxhap unnecessarily high to avoid recompiling, you may perceive some speedup.

See the file README.updates for more details on recent code changes in FASTLINK.

Some algorithmic aspects of the most recent improvements can be found in:

A. A. Schaffer, Faster Linkage Analysis Computations for Pedigrees with Loops or Unused Alleles, *Human Heredity*, to appear.

This paper can be found as paper5.ps at the ftp sites.

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Two problems in LINKAGE programs

(submitted by A. Schäffer)

Two LINKAGE problems have arisen recently in FASTLINK bug reports that users should be aware of. I call them “problems” and not “bugs” because one has to abuse LINKAGE to get them to happen.

Problem 1. If a loop involves someone who is multiply married, and it is unbroken, then LINKAGE might not go into an infinite loop. If it doesn't, plausible but wrong results are printed. I have now seen 3 pedigrees with this problem. This is not a “bug” because if one uses MAKEPED with LOOPS embedded as one should, the loop will be caught there.

Problem 2. If an allele frequency is specified as 0.0 various problems can arise. The one I saw is:

--user specified frequency of first allele is 0
--data set had a pedigree in which nobody was typed at that locus
--unknown converted everyone to homozygous 1 1 at that locus
--because the allele frequency was 0.0, the likelihood also came back as 0.0, making the log likelihood -infinity.

Both problems are also present in all versions of FASTLINK until the most recent (3.0P). I fixed problem 1 with a new diagnostic in UNKNOWN in the initial 3.0P release. I addressed problem 2 with a new warning in the main programs.

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