

Linkage Newsletter

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(this and all previous newsletters are available at our web site, <http://linkage.rockefeller.edu/newsletter/>)

EDITORIAL

For various reasons, no newsletter was written last year. The last published newsletter is dated December 1996 and was mailed just a little over one year ago. New issues of the newsletter will be published depending on need and how much material we receive for inclusion.

LINKAGE COURSES

The next basic linkage courses will be held as indicated below. Interested researchers are urged to **apply early** as our courses tend to fill up quickly. To obtain information on these courses, please write to Katherine Montague, course coordinator, by email (preferred) or fax.

March 16-20, 1998, at University of Zürich, Switzerland (maximum of 18 participants).
Deadline for applications was January 15, 1998, but we still have one or two open slots.

June 15-19, 1997, at Rockefeller University (maximum of 30 participants). Deadline for applications is May 1, 1998.

We will use our book (Terwilliger and Ott, *Handbook of Human Genetic Linkage*, Johns Hopkins University Press, 1994). 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. For a list of corrections see <http://linkage.rockefeller.edu/ott/corr-ter.htm>.

The date for this year's advanced course (summer/fall of 1998) is not yet known. Please watch our web page at <http://linkage.rockefeller.edu/course/here.html> for dates. Advanced courses are reserved for individuals with a very good background in linkage analysis). Our advanced courses have been greatly modernized and now include presentations by outside scientists who are experts in areas such as genomic databases or particular computer programs. Therefore, we can no longer offer advanced courses outside of New York. Depending on demand, we will offer more than one advanced course per year. This will be particularly important for foreign participants since for the advanced course supported by the NIHGRR, the number of participants from outside the U.S. is very limited.

SOFTWARE

New program

(submitted by Dr. Alejandro Schaffer)

We announce the availability of CASPAR (Computerized Affected Sibling Pair Analyzer and Reporter), a software package for studying the genetics polygenic diseases. CASPAR's main novel feature is conditional linkage analyses, in which the population can be subdivided according to criteria at some loci and analyzed for linkage at other loci. CASPAR uses simulation to overcome the problems inherent in such multiple testing.

```
To retrieve CASPAR:
ftp fastlink.nih.gov
cd pub/caspar
binary
get caspar.tar.Z
```

```
Then on your computer:
uncompress caspar.tar.Z
tar xvf caspar.tar
```

Please send comments, questions, complaints, and problem reports to:
Richa Agarwala (richa@helix.nih.gov) and
Alejandro Schaffer (schaffer@helix.nih.gov)

Other participants in CASPAR development are:
Jeremy Buhler, Kenneth Gabbay, Marek Kimmel, David Owerbach

FastLINK

(submitted by Dr. Alejandro Schaffer)

FASTLINK version 4.0P is now available. The principal improvement over version 3.0P is a method to automatically select loop breakers that addresses a problem posed in 1975 by Ken Lange and Robert Elston. The new code was developed in collaboration with Ann Becker and Dan Geiger of Technion. A description of what we did can be found in:

A. Becker, D. Geiger, A. A. Schaffer (1998) Automatic Selection of Loop Breakers for Genetic Linkage Analysis. *Hum Hered* 48:49-60

This paper comes as paper6.ps with the code distribution.

To retrieve for other than DOS:

```
ftp fastlink.nih.gov
binary
cd pub/fastlink
get fastlink.tar.Z
```

For DOS replace the last two lines with:

```
cd pub/fastlink/dos
mget *
```

Thanks to Jim Tomlin (NIH) and John Powell (NIH) for vigorous beta testing. Thanks to Marilyn Raymond (NIH) for a great challenge data set. Thanks to Don Plugge for assistance with the port to VMS.

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