

# Linkage Newsletter

Vol. 9 No. 2 July 1995

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## World Wide Web server

Dr. Wentian Li has installed a WWW server for our group. It may be reached at <http://linkage.cpmc.columbia.edu>. Our anonymous ftp site ([linkage.cpmc.columbia.edu](ftp://linkage.cpmc.columbia.edu)) is now fully functional and readers are encouraged to download programs and other files.

## LINKAGE COURSES

The next two linkage courses are advanced courses and will take place as follows:

October 2-6, 1995, at the University of Zurich, Irchel Campus Computer Center, Switzerland (maximum number of participants is 14).

January 8-12, 1996, at Columbia University, New York (maximum of 20 participants).

To obtain information on these courses, please write to Katherine Montague, course coordinator, by email or fax. These courses are for researchers with experience in using the LINKAGE programs, or who have an otherwise excellent understanding of genetic linkage analysis.

Also, course participants must be familiar with PCs. *Topics:* Working with age at disease onset; models for genetic heterogeneity; genetic linkage and allelic association; complex traits; etc. Course work will be divided between theoretical introductions to topics, practical exercises carried out on IBM PC's using the LINKAGE and other programs, and informal discussions. We will use our book (Terwilliger and Ott, *Handbook of Human Genetic Linkage*, Johns Hopkins University Press, 1994) and some handouts for topics not covered in the book. 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. Participants are encouraged to bring their own data.

The next introductory courses will be held in the spring or early summer of 1996, one or two at Columbia University New York and one at the University of Zurich (dates not yet set).

# SOFTWARE NEWS

## PC versions of LINKAGE

In an earlier issue of this newsletter, we reported problems with version 5.2 of LINKAGE for DOS. This is to point out to users that similar problems may also occur on other platforms. For example, on our Sparcstation IPC, when version 5.2 is compiled without optimization, it yields the same results as version 5.1 and FastLINK. However, it tends to yield different results when compiled with optimization. Since a completely new version of LINKAGE (written in C) will be available soon, there would be no point in trying to fix these problems.

## Haplotyping programs

The following announcement was contributed by Dr. Daniel Weeks:

We are pleased to announce that our haplotyping programs SIMCROSS and SIMWALK are now available in the pub directory by anonymous ftp to [watson.hgen.pitt.edu](ftp://watson.hgen.pitt.edu/pub) (url: <ftp://watson.hgen.pitt.edu/pub>). These are programs for generating optimal haplotype configurations on general pedigrees using a likelihood-based approach to correctly take intermarker recombination fractions into account.

These two programs are described briefly in our Letter to the Editor which just appeared in the June issue of the American Journal of Human Genetics:

Weeks DE, Sobel E, O'Connell JR, Lange K (1995) Computer programs for multilocus haplotyping of general pedigrees. American Journal of Human Genetics 56:1506-1507.

and are described in depth in the forthcoming article:

Sobel E, Lange K, O'Connell JR, Weeks DE (1995) Haplotyping algorithms. In: Speed TP, Waterman MS (eds) Genetic mapping and DNA sequencing. Springer-Verlag, New York, in press.

If you have any questions or comments regarding these two programs, please feel free to contact me.

-- Dan Weeks --

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