
I first encountered the Cylindrical program when its author, Cyril Chapman, spent some time in Cambridge in 1989; it was running on an old Amstrad 1640 under the QEM operating system but even then was obviously a useful tool. So it was with pleasure that I accepted the offer of reviewing the most current release of Cyril's program. The program has come a long way from those early days, but has managed to retain the feeling of a package designed by a user to do the job that it was intended for on a day to day basis, rather than by a programmer who includes anything that might be useful. As a result it is relatively small for a Windows based program (Cylindrical itself is about 2.3 MB, and complete installation, including example files, takes up less than 4 MB of hard disk space) and is shipped on a single high density disk. Installation on my computer (a Viglen Genie 486-25 Mz, with 4 MB of RAM, running Windows 3.11) took very little time and was achieved without problems.

For those who have used Cylindrical 1 this is where the first differences from the new release become apparent; the new version allows the user to establish directories for individual projects, each with its own Windows icon and separate data files. This is an improvement that could be of particular value in larger centres to group together families belonging to different research projects or suffering from different diseases. There are several other changes from the first commercial release, and most are improvements that make the program more powerful, yet also simpler and faster.

The program itself remains much as before and can be thought of in two ways; on the one hand it is a functional database that stores information about patients grouped into families, while on the other it is a pedigree drawing program that generates pictures of the relationships among patients. In my opinion, this duality centred on a physical picture of the pedigree is what makes Cylindrical such a useful, and probably unique, program. The program stores each family in a separate file consisting of a picture of the pedigree built up in stages. Initially, a single person is created by clicking the left mouse button anywhere within the computer screen. This generates a symbol at the position of the mouse click, selecting this with the right mouse button then brings up a dialogue box that allows the creation of symbols representing one or more first degree relatives. For example, one could add the patient's partner, parents, siblings, or children to the pedigree. From then on additional new members of the pedigree are added by clicking on any of their first degree relatives already on the screen. One vast improvement over earlier versions is that the program now allows the rapid generation of a complete pedigree by automatically creating full sibships, including parents, without each person having to be created separately. Pedigrees are "drawn" on an imaginary "virtual" piece of paper that can be much larger than the visible screen. The visible screen can then be "moved" from one part of the virtual screen to another to create and visualise larger pedigrees than could possibly be viewed at once (the program is said to permit pedigrees containing 10 000 people). Personal information, such as birth date, address, DNA storage information, genetic marker results, disease status, etc., can then be entered into the picture or group of people by selecting them from the skeleton pedigree at any time after its creation. The families, diseases, and set of genetic markers, which have biochemical risk factors and VNTR probes, can then be chosen from lists created by the user. These disease and marker data are stored separately from the main program in DAT files. The program itself is extremely simple and treats each locus as if it were segregating independently. However, because the program can be forced to accept extended parental haplotypes as "true", using the algorithm in conjunction with human intuition allows the user to generate complete chromosomal haplotypes quickly with minimal effort, even in large pedigrees with many markers.

Printing information from the program is also relatively flexible. A direct print of the pedigree on screen is easily obtained using the print option, and this output can contain a wealth of additional information, such as markers used in the family, date of printing, and name of the laboratory, determined by default values entered by the user. However, a more flexible print can be obtained using the export option (this even gets around the persistently annoying tendency for the program to print a family over two physical pages, even when it would easily fit on one), which allows any pedigree to be drawn on a single page, either as a horizontal drawing or in a circular format, and permits the added information to be moved around to enhance the legibility of the final output. Sub-parts of a pedigree can be displayed and printed separately, e.g. on each page of a word processor documents using the Windows Clipboard. In addition to the production of graphical output, Cylindrical can also produce tabulated lists of patient demographic and marker details for a family, arranged alphabetically or by pedigree number. However, the usefulness of this part of the program is severely hampered by the fact...
that you can only generate demographic OR marker lists unless you go through a complex process of transferring the information to a word processor, and this in itself proved to be a process fraught with errors. However, one particularly useful output option is the production of files that can be directly read and acted upon by linkage analysis programs such as Linkage (including the formats necessary for calculation of genetic risk), a functionality that can save hours of typing if large families are being analysed.

On the down side, the manual that comes with the program, although well laid out, with a clear Tutorial section followed by a detailed Reference section, is surprisingly poorly produced. The copy I have is marred on about one in 20 pages by a dark vertical line running from the top of the page to the bottom. It also has some annoying, if trivial, errors, including the mention on p 11, under the heading “Files needed to run Cyrillic”, that “Only four files are essential to run the program” followed by a list containing three names! However, the on-line Help facility is considerably expanded in this version so perhaps one can excuse such annoyances. As a database the program is severely limited by its own structure since it is impossible to “look” for a patient by name except by inspecting the pedigree picture visually. This means that the program could not be a stand alone database but would still be a useful adjunct to any more conventional patient record system, and indeed using the inbuilt DLL function it would be possible to swap information between Cyrillic and some Windows based systems.

On the whole, this is a well thought out program for the storage and presentation of genetic information that does exactly what it claims to, and is a significant improvement on the previous version. It would be a useful tool in any clinical genetics centre or diagnostic laboratory, and would also, in my opinion, be a welcome addition to any research programme that groups patients and their results into families, where its flexibility and interaction with programs such as Linkage would be particularly useful.

R McMahon

NOTICES

International Standing Committee on Human Cytogenetic Nomenclature

New members of the International Standing Committee on Human Cytogenetic Nomenclature (ISCN) will be elected at an open meeting of cytogeneticists on Wednesday 21 August 1996, during the 9th International Congress of Human Genetics in Rio de Janeiro, Brazil (see programme for venue). The Committee is elected for five years and consists of five members from Europe, Canada, and the USA, and two from other geographical areas. Nominations of candidates interested in serving on the Committee should be submitted before 1 July 1996. Only candidates duly nominated before 1 July 1996 will be put on the ballot. Those who are interested in voting but are unable to attend the International Congress in Rio de Janeiro can request ballot papers before 15 July 1996. Felix Mitelman, Chairman, International Standing Committee on Human Cytogenetic Nomenclature, Department of Clinical Genetics, University Hospital, S-221 85 Lund, Sweden. Fax: +46 46 131061. E-mail: Felix.Mitelman@klingen.lu.se.

International Genetic Epidemiology Society (IGES) Conference

This conference will be held on 17 and 18 August 1996 at the Gloria Hotel, Rio de Janeiro, Brazil, immediately preceding the International Congress of Human Genetics conference which is meeting in Rio on 18-23 August 1996. For further details contact: Dr Ruth Otman, G H Sergievskiy Center, Columbia University, 630 West 168th Street, Unit 16, New York, New York 10032, USA. Tel: (212) 305–9188. Fax: (212) 305–2426. Email: ro6@columbia.edu.

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