

## CoPE: a collaborative pedigree drawing environment

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### Abstract

**Summary:** We developed a collaborative pedigree environment called CoPE. This environment includes a Java program for drawing pedigrees and a standardized system for pedigree storage. Unlike other existing pedigree programs, this software is particularly intended for epidemiologists in the sense that it allows customized automatic drawing of large numbers of pedigrees and remote and distributed consultation of pedigrees.

**Availability:** At <http://www.infobiogen.fr/services/CoPE>

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The genetic dissection of human diseases is often undertaken by collaborative programs that involve several distant research groups. Therefore, we developed a collaborative environment that allows collaborators to share familial data. This environment includes a program for drawing pedigrees and their related information: CoPE (present version 0.4).

CoPE is written in the Java programming language. When used as an applet, CoPE allows collaborators to interact remotely with the family data. With just your WWW browser, you can run COPE and access remote pedigree data via the standard protocol HTTP. CoPE can also be used as a Java application. This mode requires the installation of CoPE and the Java runtime environment. It allows each user to store his own files and creates PostScript files for printing. When used as an application, CoPE can also produce PostScript files from many different families without user interaction.

CoPE has a highly configurable and very expressive interface. CoPE fetches the family information from a data file with LINKAGE format (Lathrop and Ott, 1990). Each line in this file describes an individual and includes the pedigree ID, the individual's ID, his father's and mother's IDs, his sex, the status for the disease, and any other data related to the individual that the user may wish to see on the output drawing, such as clinical characteristics or epidemiological data (age, risk factors, etc.). The nature and representation of this

additional information are explained in a description file and a mapping file.

The description file contains the name, font, colour and comments for each piece of additional information, the place where it should appear on the drawing, and the name of the protocol (if any) used to map the data onto a symbol on the drawing. The additional information can be represented on the display as text or haplotypes underneath the representation of an individual, or as a graphical symbol superposed upon this representation. In haplotypes, colours may be used to pinpoint recombinations.

The representation used in the drawing follows the recommendations from Bennett *et al.* (1995). Individuals are represented as circles for women, squares for men, and diamonds when the sex is unknown. The graphical symbols used to represent the additional information are defined in the mapping file (typical example: a filled circle or square for an affected woman or man in simple diseases). A large list of symbols is proposed, including arrows, handles and quarters. The colour of the symbol can also be specified. This mapping file allows the user to define specific representation styles for each study.

A fourth file, the parameter file, contains the general parameters of the drawing, e.g. the title font, the space between siblings or conjoints, and the type of individual ordering in a sibship.

All the values of these files (except for the data file) can be edited and modified interactively. The results of the modification can be saved into a file when CoPE is run as an application. When CoPE is run as an applet, this is not possible because the browsers impose the restriction that an applet can only communicate with the server from which it was downloaded. The user can also pop-up a window containing information on a family or an individual. The current version of CoPE is limited in that it cannot handle inter-generation matings or multiple matings ( $\geq 3$ ). Twins are represented as brothers and sisters.

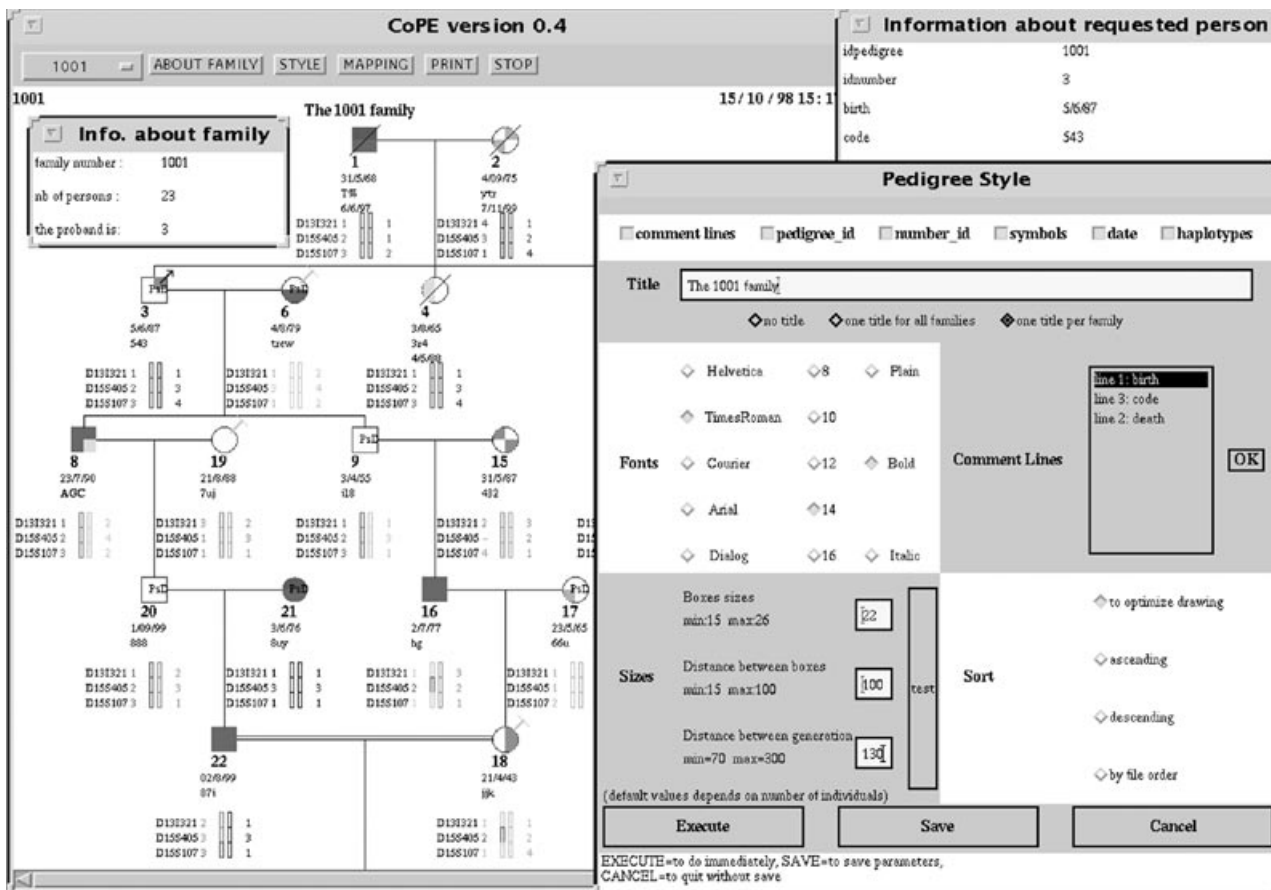


Fig. 1. CoPE: typical output.

Other programs for pedigree drawing include PedDraw, GAP Pedigree Drawing, Kindred, Cyrillic, FTREE, Progeny (J.D.Terwilliger and J.Ott, *Handbook of Human Genetic Linkage*, The John Hopkins University Press, London, 1994, p. 292). GAP: <http://icarus2.hsc.usc.edu/epicenter/gap.html>. Kindred: <http://icarus2.hsc.usc.edu/epicenter/kindred.html>. Cyrillic: <http://www.cherwell.com/cyrillic/>, <http://mantis.dcrn.nih.gov/Publications/Pedigree/Comment.html>. Progeny: <http://www.progeny2000.com>). A comparison between these programs can be found in [http://www.mdacc.tmc.edu/~hcc/10\\_4Pedigree.html](http://www.mdacc.tmc.edu/~hcc/10_4Pedigree.html) and [http://mantis.dcrn.nih.gov/Publications/Pedigree/Ped\\_three.html](http://mantis.dcrn.nih.gov/Publications/Pedigree/Ped_three.html). They are generally interactive programs useful for clinicians manipulating a few pedigrees. Contrary to most pedigree drawing software, our program is intended for epidemiologists and statisticians, rather than clinicians. It allows automatic drawing of large pedigrees and the inclusion of any type of data. Figure 1.

As a first step, we developed a software to draw pedigrees. We are now designing a system for storage of familial data

based on a distributed object-oriented technology. It will be connected to the drawing pedigree software. CoPE will be then a complete environment to share familial data, offering a standard storage format and available through the Internet.

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### References

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