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# FINEX, FAMILIAS: two different approaches for the analysis of defective paternity cases

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**Abstract.** We provide an overview of the main features of two computer programs enabling to calculate Bayesian probabilities in defective paternity cases: FINEX and FAMILIAS. These packages turn out very useful when computation complexities exceed the ordinary pencil-and-paper approach powers. FAMILIAS is especially suited for all cases in which there is a basic uncertainty on the most likely pedigree. FINEX is an Expert System-based program enabling to tackle very complex cases with plenty of data. © 2003 Published by Elsevier B.V.

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Paternity tests can be carried out even in the absence of the putative father, by the analysis of some of his relatives [1]. The evaluation of such cases (that are often defined as 'defective paternity cases') is one of the most interesting topics of today's genetic identification.

In more general terms, these cases are part of a larger category of defective identification cases, whose most universal example can be synthesized in the following questions: 'Are two individuals relatives? And what is their most plausible relationship, if there is any?'

The production of probabilistic evidence in these cases will depend on genetic data available and on its combination with all prior information that is actually known to the analyst.

Some very basic prior information—for example, the age and sex of persons involved—will usually help to limit the ways in which two people can exchange family ties.

In the same way, more detailed information on other individuals and their relation to either propositus (or both) (axiomatically regarded as true) can be extremely useful to restrict the parental hypotheses to just one or very few.

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The Bayesian analysis will always focus on the frequencies of the genetic data available and on the segregational probabilities to be assigned according to the a priory assumptions. Also, the inherent computations may range from plain simplicity to the highest complexity, depending on how big the genealogic tree is.

Two classical computer packages have been devised to tackle these cases: FINEX [2] and FAMILIAS) [3]. Both programs rely on the Bayesian theory but they address the problem from different viewpoints.

FINEX was originally written to automate the process of constructing Bayesian networks (or probabilistic expert systems, PES) and give them a friendly interface (by reproducing the usual genetic tree in the computer screen). In turn, the basic idea underlying Bayesian networks is restructuring a very define genetic problem (in our case, a disputed relationship) in terms of a graphical model (with elementary deterministic relations, probabilistic computational nodes and a query node). What is of interest for our purposes is the fact that FINEX ends up to address the problem as a 'one query problem', according to the prior evidence.

In contrast, FAMILIAS is an open-frame program that, in spite of all prior evidence, tends to examine all possible pedigrees according to the available data and can tell us which is the most plausible.

Our recent casework experience with defective cases showed that these cases tend to be worked out according to a definite a priori opinion on the most plausible family relationship. However, more often that is currently thought, the prior opinion does not exactly comply with the genetic evidence available. Therefore, some of these cases are dismissed under the assumption that the family tie under scrutiny does not sufficiently fit with the genetic evidence proven, whereas the hypothesis of just another family relation would fit much better with this latter. In a recent case, we happen to observe, a judge asked us to verify whether two persons were or not first cousin—a hypothesis that did not actually comply with the genetic data. At a closer scrutiny, the half brother case would fit much better than the judicial query.

The combined use of the two computer programs offers different perspectives of insight into a typical defective case and it will ensure coverage of a broad pattern of hypotheses along with computational counter-check.

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