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Drawing Medical Pedigree Trees with TEX and PSTricks

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Abstract Medical pedigrees look like genealogical trees, but also have certain interesting features. Usually they are drawn by hand by medical geneticists. This is a cumbersome and time-consuming process. Freely available programs for drawing genealogies are not fully suitable for this task because of the special format of medical pedigrees.

We discuss a package for drawing pedigrees based on PSTricks. The information is input by geneticists in a spreadsheet; a Perl program extracts it and calls TEX to produce the final output.

1 Introduction

Medical pedigree is a very important tool for clinicians, genetic researchers and medical educators. As noted by Bennett et al. [1995], "The construction of an accurate family pedigree is a fundamental component of a clinical genetic evaluation and of human genetic research." Unfortunately, up to now most geneticist make the pedigrees manually. There are several programs for making pedigrees (see a list at http://www.kumc.edu/gec/prof/genecomp.html#pedigree), but they are rather expensive, lack multi-language support and the quality of typesetting is wanting. Maybe this is why they are not in wide use.

We tried to write a program suitable for constructing complex pedigrees from genetics data in English, Russian and possibly other languages. TEX and PSTricks [Van Zandt, 1993] seemed to be a natural choice. First, the quality of TEX typesetting is unsurpassed. Pedigrees combine graphical and textual data, therefore a

package like PSTricks is handy to produce them. There are good facilities for multi-language support in TEX, therefore we could easily deploy them. TEX code can be easily generated by other programs, which is another advantage of implementing the drawing as a TEX file.

The idea to draw genealogical trees with TEX and PSTricks is by no means new. One can enjoy the beautiful trees at `http://www.tug.org/PSTricks/main.cgi?file=Examples/Genealogy/genealogy`.

The problem is, medical pedigrees differ from genealogical trees. They even might not be trees from the mathematical point of view: any marriage between relatives add a cycle to the graph of relationships. Even if there are no such marriages, pedigrees are not layered rooted trees in the terminology of graph theory [Di Battista et al., 1999]. The difference is the following. Layered rooted trees have the "oldest" node (global ancestor). This node has no ancestors. It has descendants, and each of them is an ancestor for its own layered rooted tree. On the other hand, a geneticist drawing a pedigree is interested both in the male and female ancestors of the patient, as well as in the male and female ancestors of them, etc. Therefore a pedigree might have several "local ancestors": nodes, that do not have ancestors. This makes the problem of drawing pedigrees so interesting.

We divided the general problem of drawing pedigrees into two parts. First, we developed a set of PSTricks macros [Veytsman and Akhmadeeva, 2006b] to draw (almost) any pedigree. They can be used "manually", i.e. the user can put nodes at any place on the canvas and make any connections between them, using `\rput`, `\psmatrix` or even `\pstree` (if the pedigree is in fact a layered tree). Second, we developed a Perl program [Veytsman and Akhmadeeva, 2006a] that can process relationship data in the CSV (comma separated values format) and output TEX code for an important subset of pedigrees: when there are no inbreeding, and only the people having common genes with the primary patient (proband) are shown. Both these parts are discussed below.

2 PSTricks Macros

From the point of view of graph theory a pedigree is a collection of nodes and connections. There are three main kinds of nodes in our set of macros: `\PstPerson` to

show persons, `\PstAbortion` to show terminated pregnancies, and marriage node[1], which is implemented as a simple `\pnode`[2]. Each node but `\PstAbortion` may have descendants: children of this person or of this marriage. Each node but marriage node has exactly one ancestor node: a person or a marriage. Additionally a marriage node has male and female spouses.

The nodes may have a number of properties: they might be affected by a disease or no, they might be deceased, they are male or female. These properties are shown by optional arguments to the corresponding command. Each node drawing command has one obligatory argument: the name of the node, which is used to draw node connections.

The simplest connection command `\PstDescent` shows the relationship between an ancestor (person or marriage node) and descendant. It is implemented internally as `\ncangle` command. There are special commands to show relationships between twins and their parents, between spouses, infertility of a union or a person, etc.

A very complex pedigree is used as an example in the paper [Bennett et al., 1995]. On Figure 1 we reproduce this pedigree. The corresponding code is shown on Figures 2, 3 and 4.

A version of node-drawing commands makes tree nodes. They are useful if the pedigree is a tree or can be constructed from a tree by adding several connections. An example of such pedigree is shown on Figure 5, and the corresponding code on Figure 6. Note that the pedigree on this figure is not a tree from the mathematical point of view due to the marriage between Peter and Joan.

The full user manual [Veytsman and Akhmadeeva, 2006b] is distributed with the macros. Since PSTricks contributed code by tradition works both with LaTeX and plain TeX, our code is written to work in both these modes too. However, most of testing was done in the LaTeX mode only.

3 Perl Program

The TeX code in the examples above is straightforward. Nevertheless, it might be too much to expect from geneticists to write it themselves. Therefore if we want the code to work not only for the authors, but also for medical and science professionals,

1. For our purposes both official marriages and unofficial unions are loosely referred to as marriages
2. There are also special nodes for special circumstances: twin node is used to show the relation between twins, a special node is used to show infertility of person or a marriage, etc.

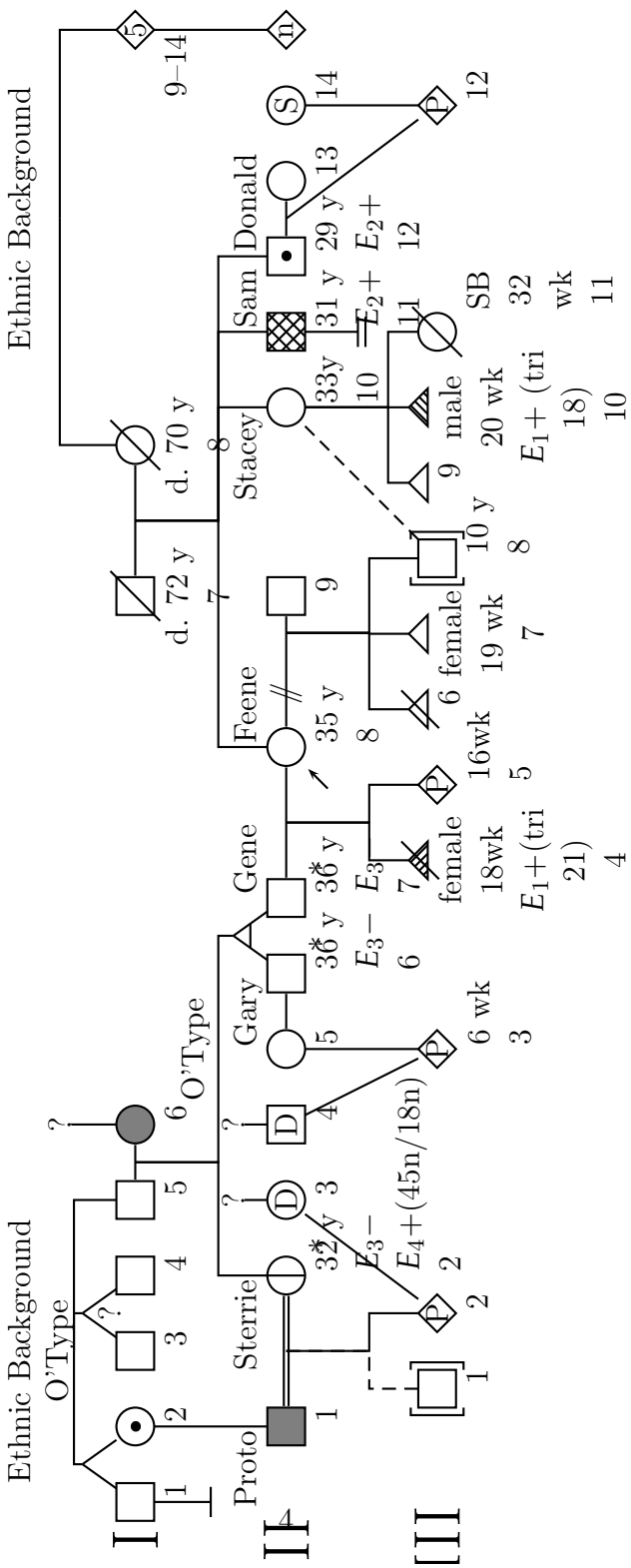


Figure 1: A Complex Pedigree From [Bennett et al., 1995]

```
\psset{armB=1.1, hatchsep=1.5pt}
\rput(3.5,8){Ethnic Background}
\rput(18.5,8){Ethnic Background}
\rput(3.5,7.5){\rnode{OType1}{O'Type}}
\rput(18.5,7.5){\pnode{Origin2}}
\rput(6.5,7.5){\rnode{Quest1}{?}}
\rput(1,6.5){\Huge I}
\rput(1.5,6.5){\pstPerson[male, belowtext=1]{I1}}
\rput(2.5,6.5){\pstPerson[female, obligatory, belowtext=2]{I2}}
\rput(3.5,6.5){\pstPerson[male, belowtext=3]{I3}}
\rput(4.5,6.5){\pstPerson[male, belowtext=4]{I4}}
\rput(5.5,6.5){\pstPerson[male, belowtext=5]{I5}}
\rput(6.5,6.5){\pstPerson[female, affected,
    belowtext=6]{I6}}
\rput(2,7.2){\pnode{Twins1}}
\rput(4,7.2){\pnode{Twins2}}
\pstTwins[armB=0]{OType1}{Twins1}{I1}{I2}
\pstTwins[qzygotic, armB=0, mzlinepos=0.8]{OType1}{Twins2}{I3}{I4}
\pstDescent[armB=0]{OType1}{I5}
\pstDescent[armB=0]{Quest1}{I6}
\pstRelationship[descentnode=I5I6]{I5}{I6}
\rput(1.5,5.5){\pstChildless{CI1}}
\ncline{I1}{CI1}
\rput(13.5,6.5){\pstPerson[male, deceased, belowtextrp=t,
     belowtext=\parbox{2cm}{\centering d. 72 y\\7}]{I7}}
\rput(15.5,6.5){\pstPerson[female, deceased, belowtextrp=t,
     belowtext=\parbox{2cm}{\centering d. 70 y\\8}]{I8}}
\pstRelationship[descentnode=I7I8]{I7}{I8}
\rput(21,6.5){\pstPerson[insidetext=5, belowtext=9--14,
   belowtextrp=rt]{I9}}
\pstDescent[armB=0]{Origin2}{I8}
\pstDescent[armB=0]{Origin2}{I9}
```

Figure 2: Code for Figure 1: Generation I

```
\rput(1,4.5){\Huge II}
\rput(2.5,4.5){\pstPerson[male, affected, belowtext=1,
     abovetext=Proto, abovetextrp=rB]{II1}}
\rput(4.5,4.5){\pstPerson[female, asymptomatic,
    belowtext=\parbox{3cm}{32 y\\ $E_3-$\\$E_4+$(45n/18n)\\2},
    abovetext={Sterrie}, abovetextrp=rB, evaluated]{II2}}
\pstDescent{I2}{II1}\pstDescent{I5I6}{II2}
\pstRelationship[consanguinic, descentnode=II1II2]{II1}{II2}
\rput(5.5,5.2){\rnode{Quest2}{?}}
\rput(5.5,4.5){\pstPerson[female, insidetext=D, belowtext=3]{II3}}
\rput(6.5,5.2){\rnode{Quest3}{?}}
\rput(6.5,4.5){\pstPerson[male, insidetext=D, belowtext=4]{II4}}
\ncline{Quest2}{II3}\ncline{Quest3}{II4}
\rput(7.5,4.5){\pstPerson[female, belowtext=5]{II5}}
\rput(8.5,4.5){\pstPerson[male, abovetext=Gary, abovetextrp=rB,
   belowtext=\parbox{2cm}{36 y\\$E_3-$\\6}, evaluated]{II6}}
\rput(9.5,4.5){\pstPerson[male, abovetext={Gene},
   belowtext=\parbox{2cm}{36 y\\$E_3-$\\7}, evaluated]{II7}}
\rput(9,5.2){\pnode{Twins3}}
\pstTwins[monozygotic]{I5I6}{Twins3}{II6}{II7}
\pstRelationship{II5}{II6}
\rput(7.5,5.7){O'Type}
\rput(11.5,4.5){\pstPerson[female, proband,
    belowtext=\parbox{1cm}{35 y\\8}, abovetext=Feene]{II8}}
\pstRelationship[descentnode=II7II8]{II7}{II8}
\rput(13.5,4.5){\pstPerson[male, belowtext=9]{II9}}
\pstRelationship[broken, descentnode=II8II9,
    descentnodepos=0.85]{II8}{II9}
\rput(16,4.5){\pstPerson[abovetext=Stacey, female,
    abovetextrp=rB, belowtext=\parbox{1cm}{33y\\ 10}]{II10}}
\def\affectedstyle{fillstyle=crosshatch}
\rput(17,4.5){\pstPerson[male, affected, abovetext=Sam,
    belowtext=\parbox{3cm}{31 y\\ $E_2+$\\ 11}, hatchsep=3pt]{II11}}
\rput(17,3.5){\pstChildless[infertile]{C2}}
\ncline{II11}{C2}
\rput(18,4.5){\pstPerson[male, obligatory, abovetext=Donald,
    belowtext=\parbox{3cm}{29 y\\ $E_2+$ \\ 12}]{II12}}
\pstDescent{I7I8}{II8}\pstDescent{I7I8}{II10}
\pstDescent{I7I8}{II11}\pstDescent{I7I8}{II12}
\rput(19,4.5){\pstPerson[female, belowtext=13]{II13}}
\pstRelationship[descentnode=II12II13]{II12}{II13}
\rput(20,4.5){\pstPerson[female, insidetext=S, belowtext=14]{II14}}
\rput(21,4.5){\pstPerson[insidetext=n]{II15}}
\pstDescent{I9}{II15}
```

Figure 3: Code for Figure 1: Generation II

```
\rput(1,2.5){\Huge III}
\rput(3,2.5){\pstPerson[male, adopted, belowtext=1]{III1}}
\rput(4,2.5){\pstPerson[insidetext=P, belowtext=2]{III2}}
\pstDescent[linestyle=dashed]{II1II2}{III1}
\pstDescent{II1II2}{III2}
\ncline{II3}{III2}
\rput(7.5,2.5){\pstPerson[insidetext=P,
     belowtext=\parbox{2cm}{6 wk\\3}]{III3}}
\pstDescent{II5}{III3}
\ncline{II4}{III3}
\def\affectedstyle{fillstyle=vlines}
\rput(10,2.5){\pstAbortion[affected,
    belowtext=\parbox{2cm}{\centering
        female\\18wk\\$E_1+$(tri 21)\\4}, belowtextrp=t]{III4}}
\rput(11,2.5){\pstPerson[insidetext=P,
    belowtext=\parbox{1cm}{16wk\\5}]{III5}}
\pstDescent{II7II8}{III4}
\pstDescent{II7II8}{III5}
\rput(12,2.5){\pstAbortion[belowtext=6]{III6}}
\rput(13,2.5){\pstAbortion[sab, belowtextrp=t,
      belowtext=\parbox{2cm}{\centering female\\19 wk\\ 7}]{III7}}
\rput(14,2.5){\pstPerson[adopted, male,
      belowtext=\parbox{1cm}{10 y\\ 8}]{III8}}
\pstDescent{II8II9}{III6}
\pstDescent{II8II9}{III7}
\pstDescent{II8II9}{III8}
\ncline[linestyle=dashed]{II10}{III8}
\rput(15,2.5){\pstAbortion[sab, belowtext=9]{III9}}
\def\affectedstyle{fillstyle=hlines}
\rput(16,2.5){\pstAbortion[sab, belowtextrp=t, affected,
    belowtext=\parbox{2cm}{\centering male\\ 20 wk\\ $E_1+$
    (tri 18)\\ 10}]{III10}}
\rput(17,2.5){\pstPerson[deceased, female,
    belowtext=\parbox{1cm}{\centering SB\\32 wk\\ 11}]{III11}}
\pstDescent{II10}{III9}
\pstDescent{II10}{III10}
\pstDescent{II10}{III11}
\rput(20,2.5){\pstPerson[insidetext=P,
    belowtext=12]{III12}}
\pstDescent{II14}{III12}
\ncline{II12II13}{III12}
```

Figure 4: Code for Figure 1: Generation III

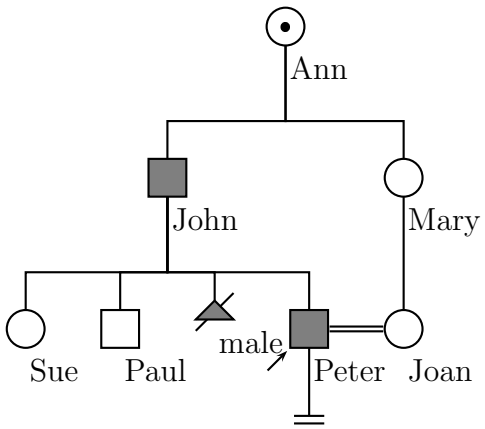


Figure 5: Example of Pedigree with Tree-Making Commands

```
\begin{pspicture}(0,1)(7,7)
   \rput(3,4){%
     \pstree{\TpstPerson[female, obligatory, belowtext=Ann]{Ann}}{%
       \def\psedge{\pstDescent}\psset{armB=1}
       \pstree{\TpstPerson[male, affected, belowtext=John]{John}}{%
         \TpstPerson[female, belowtext=Sue]{Sue}
         \TpstPerson[male, belowtext=Paul]{Paul}
         \TpstAbortion[affected, belowtext=male]{A1}
         \pstree[thislevelsep=1.2]{\TpstPerson[male,
           belowtext=Peter, affected, proband]{Peter}}{%
           \def\psedge{\ncline}
           \TpstChildless[infertile]{C1}
           }
       }
       \pstree{\TpstPerson[female, belowtext=Mary]{Mary}}{
       \TpstPerson[female, belowtext=Joan]{Joan}
       }
     }
   }
   \pstRelationship[consanguinic]{Peter}{Joan}
\end{pspicture}
```

Figure 6: Code Producing Figure 5

we must find a way to generate this code from the relationship data automatically. This is the aim of the second part of our project [Veytsman and Akhmadeeva, 2006a].

The idea of the program is to take the data in a simple format, easy for the users to understand (and easy to generate in it turn from databases or other sources) and convert them into TEX code above. The input format was chosen to be a plain text CSV format (originally the acronym meant Comma Separated Values, but it is often used now for any plain text separated data). In this format each person record is a line separated into fields by the symbol "|". The fields show the name of the person, the dates of birth and death, the genetic condition, etc. An important field is Id, a unique identifier of the person. The relations between the persons are set by the fields "Mother" and "Father", which contain Ids of the parents of the given person. In this way we do not need to specifically show the relations between spouses, siblings, etc.: spouses in our system are the persons who have common children, and siblings are the persons with common parent(s). An example of an input file is shown on Figure 7. Such files are easy to generate by common spreadsheet programs and from databases.

The code generated from the input file on Figure 7 is shown on Figure 8, and the typeset pedigree on Figure 9.

Our program works with a subset of all possible pedigrees. Still, this subset covers most pedigrees used by geneticists. First, we do not include inbreeding unions in the pedigrees, so our graphs are in fact trees. Second, we show only the persons that have common genes with the proband[3]. Note that a pedigree that violates these rules may not allow two-dimensional drawing without self-intersections at all.

The biggest problem is that even with these rules the pedigree tree is in the general case not a layered tree, and the algorithm by Reingold and Tilford [Di Battista et al., 1999, § 3.1] would not work. We therefore describe a generalization of Reingold-Tilford algorithm.

Let us remind the main idea of Reingold-Tilford algorithm. We draw a tree down in the y direction. The algorithm is recursive. We start from the root of the tree. If it has no descendants, it is easy to draw it. If it has descendants, each descendant is a rooted layered tree. We draw them, recursively applying the algorithm. Then we move them in the horizontal direction as close as possible, and put the root one layer above with x coordinate in the middle of the descendants.

3. Proband is the first person among the relatives who came to a geneticist; he is the primary patient.

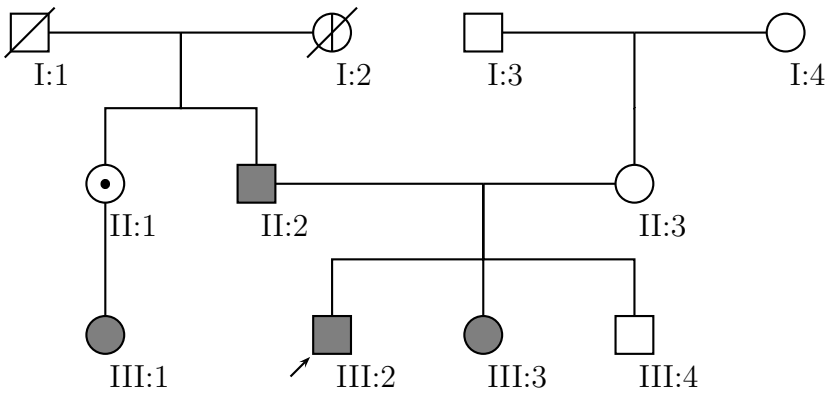
Id	Name	Sex	DoB	DoD	Mother	Father	Proband	Condition	Comment
P	John Smith	male	1970/02/05		M1	F1	yes	affected	Evaluated 2005/12/01
M1	Mary Smith (Brown)	female	1940/02/05		GM2	GF2		normal	
F1	Bill Smith	male	1938/04/03		GM1	GF1		affected	
GM1	Joan Smith	female	1902/07/01	1975/12/13				asymptomatic	
GF1	Joseph Smith	male	unknown	unknown				normal	
GF2	Jim Brown	male	1905/11/01					normal	
GM2	Lisa Brown	female	1910/03/03					normal	
S1	Rebecca Smith	female	1972/12/25		M1	F1		affected	
S2	Alexander Smith	male	1975/11/12		M1	F1		normal	
A1	Ann Gold (Smith)	female	1941/09/02		GM1	GF1		obligatory	Aunt of the proband
C1	Jenny Smith	female	1969/12/03		A1			affected	Cousin of the proband

Figure 7: Example Of Data File

```
\begin{pspicture}(-8,-4)(6,4)
\rput(-6, 2){\pstPerson[male, normal, belowtext=I:1, deceased]{GF1}}
\rput(-4, 2){\pnode{GF1_m_GM1}}
\rput(-2, 2){\pstPerson[female, asymptomatic, belowtext=I:2, deceased]{GM1}}
\rput(0, 2){\pstPerson[male, normal, belowtext=I:3]{GF2}}
\rput(2, 2){\pnode{GF2_m_GM2}}
\rput(4, 2){\pstPerson[female, normal, belowtext=I:4]{GM2}}
\rput(-5, 0){\pstPerson[female, obligatory, belowtext=II:1]{A1}}
\rput(-3, 0){\pstPerson[male, affected, belowtext=II:2]{F1}}
\rput(0, 0){\pnode{F1_m_M1}}
\rput(2, 0){\pstPerson[female, normal, belowtext=II:3]{M1}}
\rput(-5, -2){\pstPerson[female, affected, belowtext=III:1]{C1}}
\rput(-2, -2){\pstPerson[male, affected, belowtext=III:2, proband]{P}}
\rput(0, -2){\pstPerson[female, affected, belowtext=III:3]{S1}}
\rput(2, -2){\pstPerson[male, normal, belowtext=III:4]{S2}}
\pstDescent{GF1_m_GM1}{A1}
\pstDescent{GF1_m_GM1}{F1}
\ncline{GF1_m_GM1}{GM1}
\ncline{GF1_m_GM1}{GF1}
\pstDescent{GF2_m_GM2}{M1}
\ncline{GF2_m_GM2}{GM2}
\ncline{GF2_m_GM2}{GF2}
\pstDescent{A1}{C1}
\pstDescent{F1_m_M1}{P}
\pstDescent{F1_m_M1}{S1}
\pstDescent{F1_m_M1}{S2}
\ncline{F1_m_M1}{M1}
\ncline{F1_m_M1}{F1}
\end{pspicture}

\begin{description}
\item[I:1] Joseph Smith; born: unknown; died: unknown.
\item[I:2] Joan Smith; born: 1902/07/01; died: 1975/12/13.
\item[I:3] Jim Brown; born: 1905/11/01.
\item[I:4] Lisa Brown; born: 1910/03/03.
\item[II:1] Ann Gold (Smith); born: 1941/09/02; Aunt of the proband.
\item[II:2] Bill Smith; born: 1938/04/03.
\item[II:3] Mary Smith (Brown); born: 1940/02/05.
\item[III:1] Jenny Smith; born: 1969/12/03; Cousin of the proband.
\item[III:2] John Smith; born: 1970/02/05; Evaluated 2005/12/01.
\item[III:3] Rebecca Smith; born: 1972/12/25.
\item[III:4] Alexander Smith; born: 1975/11/12.
\end{description}
```

Figure 8: Example of Program Output (Data From Figure 7)



I:1 Joseph Smith; born: unknown; died: unknown.

I:2 Joan Smith; born: 1902/07/01; died: 1975/12/13.

I:3 Jim Brown; born: 1905/11/01.

I:4 Lisa Brown; born: 1910/03/03.

II:1 Ann Gold (Smith); born: 1941/09/02; Aunt of the proband.

II:2 Bill Smith; born: 1938/04/03.

II:3 Mary Smith (Brown); born: 1940/02/05.

III:1 Jenny Smith; born: 1969/12/03; Cousin of the proband.

III:2 John Smith; born: 1970/02/05; Evaluated 2005/12/01.

III:3 Rebecca Smith; born: 1972/12/25.

III:4 Alexander Smith; born: 1975/11/12.

Figure 9: Example of the Typeset Pedigree (Code From Figure 8)

Now we can generalize this algorithm for our case.

There are two kinds of nodes in the pedigree graph: person nodes and marriage nodes. A node has a precedessor and children. A marriage node does not have a precedessor, but has male spouse and female spouse (usually male spouses are on the left and female spouses are on the right on pedigrees). Any node has a downward tree of its children, grandchildren etc. The downward tree may be empty.

Any node in an acyclic graph can be a root. However, in layered trees there is a special root: the one that has no precedessor. Similarly we will call a local root a node that has no predecessor. All marriage nodes are local roots. Some person nodes can be local roots as well.

Our algorithm is recursive and starts from a local root. Strictly speaking, it can start from any local root, but medical pedigrees have a special person: proband, the person who was the first to be examined by genetic specialists. Therefore it makes sense to start from the local root which has proband in its downward tree.

If this local root is a person node, the pedigree is the layered tree, and Reingold-Tilford algorithm is sufficient. Therefore we should consider only the case when the local root is a marriage node. In this case we can typeset the downward tree using Reingold-Tilford algorithm. The male and female spouses do not belong to this tree. However, each of them belongs to each own subpedigree. We will call them left subpedigree and right subpedigree. We recursively apply our algorithm to typeset left and right subpedigrees. Then we move the left subpedigree to the right and right subpedigree to the left as far as we can without intersection between them and the downward tree.

This process is shown on Figure 10. Obviously this algorithm converges and leads to typesetting the pedigree without intersections between the subtrees and subpedigrees.

The program is implemented in Perl and can process input in English or Russian, creating pedigree legend in any of these languages (the Russian examples can be found in the manual [Veytsman and Akhmadeeva, 2006a]). It is quite straightforward to add language modules for any other language or script that TEX can typeset.

4 Installation Notes

A couple of words about the installation of the packages.

The installation of the TEX part follows the guidelines `http://www.tex.ac.`

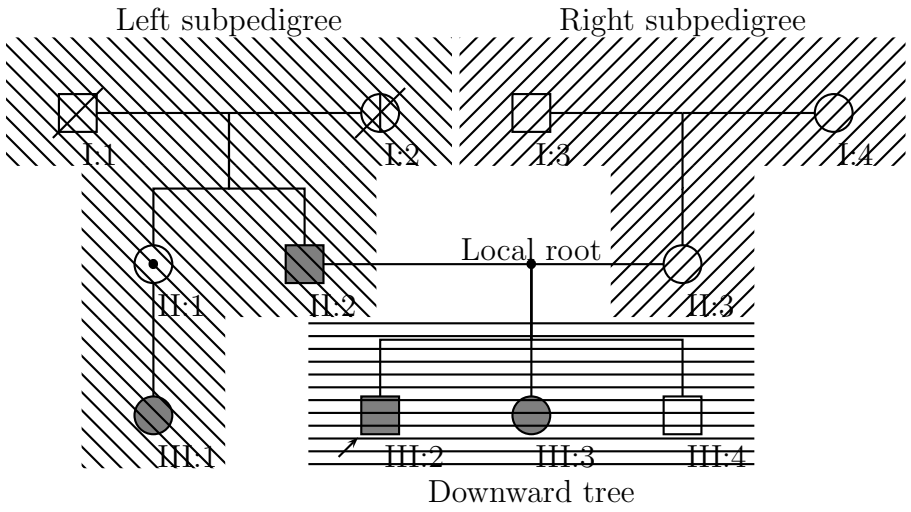


Figure 10: Subpedigrees and Downward Tree

`uk/cgi-bin/texfaq2html?label=instpackages`. Just run `latex` on `pst-pdgr.ins` and move the files `pst-pdgr.sty` and `pst-pdgr.tex` to the place 'where LaTeX can find them' (see `http://www.tex.ac.uk/cgi-bin/texfaq2html?label=wherefiles`). Do not forget to refresh the filenames database.

The TEX package depends on a number of other packages, which should be installed on your system. You need fresh versions of `pstricks`, `pst-xkey`. If you want typeset the documentation you also need `pstricks-add`, but if you are satisfied with the PDF manual provided with the package, you might skip this step.

The Perl part includes the executable, library and manual pages. There is a `Makefile`, and in most cases the command `make install` would work for you.

5 Conclusions and Future Work

Our programs were written mostly as a proof of concept. Surprisingly (or unsurprisingly if we recall the properties of TEX) the typesetting quality of the output is rather high. The next logical step is to make them user-friendly, so any genetic specialist can use them without reading manual.

Since we cannot count on the medical and genetic personnel to have TEX and Perl on their computers, we envision a "Pedigree Live" disk akin to the TEXlive one: a CD with Perl and subset of TEX on it, which "just works" after inserting in the computer. This requires creating a cross-platform user interface and the selection of programs and tools to be included on a CD.

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