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## DNA·VIEW Version 28.35 notes

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## I. Installation

Here's a new software CD. It can be used to upgrade an existing installation.

The installation procedure is

### I.A. Insert the CD.

### I.B. It should autostart.

If it doesn't, you can click on the `SetupDNAVIEW...EXE` file on the CD to make it start.

### I.C. Answer the prompts.

Some of the prompts below may not occur.

### I.C.1. The password if requested is .....

### I.C.2. Select destination location

I.C.2.a. If updating, choose the directory where DNA·VIEW already is.

I.C.2.b. For a **new installation**, anywhere you like. Examples:

I.C.2.b.i.) Traditionally DNA·VIEW was installed to `C:\dnaview`.

I.C.2.b.ii.) Typical Windows style would be `C:\Programs and Files\dnaview`.

I.C.2.c. For installation to a **network server**, note that there must be a mapped drive letter. See the DNA·VIEW manual §XVI.D

### I.C.3. Select components

I.C.3.a. Update DNAVIEW program files to version 28.35

Use this option to leave your data unchanged, but to perform either or both of

I.C.3.a.i.) change the program version to a different version (probably newer)

I.C.3.a.ii.) install or re-install a startup file or **desktop startup icon**

I.C.3.b. Install DNAVIEW version 28.35 programs and empty data files

For initial installation or installation of a second copy (in a different folder) or to destroy all case data.

### I.C.4. Select start menu folder

This refers to where DNAVIEW will be found when you click START, All Programs.

### I.C.5. Select additional tasks

I.C.5.a. Create DNAVIEW desktop icon. Very handy – an icon on your desktop to click to start DNA·VIEW.

I.C.5.b. Create DNAVIEW start menu entry. Less handy but some prefer it.

Click the obvious buttons to complete installation.

## I.D. Install Pater

If installing PATER as well as DNA·VIEW, running the PATER installer – `SetupPATER...EXE` on the same CD – is a separate operation. Use My Computer to double-click on the installer to run it.

## I.E. Icons

The installation produces a folder called DNAVIEW on the desktop with a collection of icons.

### I.E.1. Icon functions

Their functions are as follows –

I.E.1.a. **DNAVIEW** – starts DNA·VIEW

I.E.1.b. **PATER** – starts PATER

I.E.1.c. **DNAVIEW** – starts DNA·VIEW and allows the few graphics commands, i.e. drawing of allele frequency histograms.

I.E.1.d. **DNAVIEW Report Viewer** – Utility program to open DNA·VIEW Kinship or Paternity reports (the "formatted" version) cleanly in Excel.

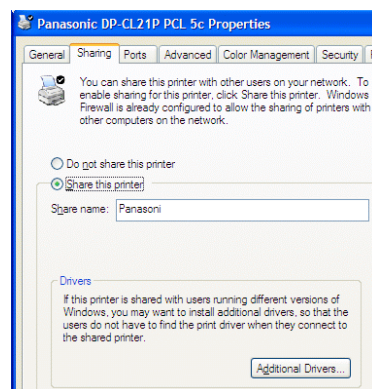
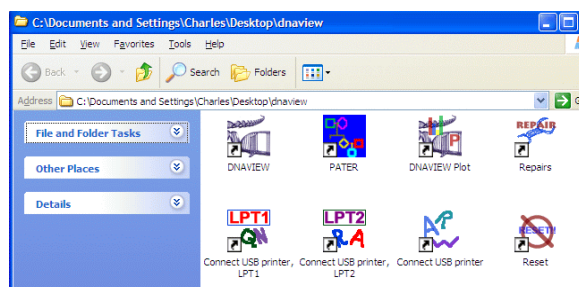
### I.E.1.e. Connect USB printer

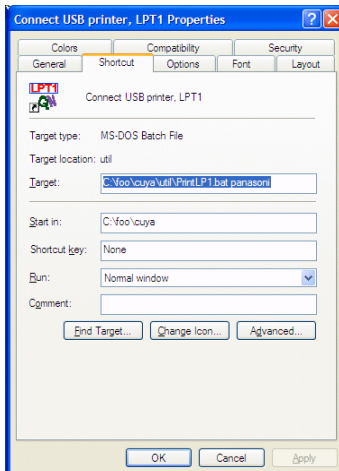
These several icons create the connection that is necessary for DNA·VIEW or PATER, which nominally print to an old-fashioned "parallel" port – LPT1 or LPT2 – to print to a USB or network printer. You will probably only need one of them; which one is a matter of convenience.

Customization of the icon is necessary. If you double click on one of them and it is not yet customized, it will give instructions for customization.

I.E.1.e.i.) Print icon customization

» Choose the network or USB printer you wish to print to.





- » Determine its "Share name". The easiest situation is if the printer can be shared through your own computer. Open "Printers and Faxes" from or near the Control Panel, right click on the printer you want to use, and choose Properties. Choose the Sharing tab. Choose the option "Share this printer" if possible. Note the Share name. If there is none, add one of your choosing, preferably without spaces.

Click ok to close the printer properties window.

- » Right click on the icon "Connect USB printer, LPT1". Choose Properties. Select the Shortcut tab. Click in the Target window, hit **End**, and type *space* followed by the printer's share name. Click Apply.
- » While the Properties are open is a good time to complete customization of the print icon per §I.E.2.

#### I.E.1.e.ii.) Establish printer connection

Now you can double-click on the icon itself to invoke it in order to establish a connection with the printer. The connection is suppose to be permanent but if it happens to disappear you can invoke it again.

I.E.1.f. **Repair** – may rarely be necessary to repair e.g. a problem caused by unceremonious shutdown of DNA·VIEW or PATER such as by a power failure.

I.E.1.g. **Reset** – has the potential to discard all DNA·VIEW data files and reinstall empty ones. Clicking on the icon is harmless though; it will not do anything except to tell you what you have to do to actually reset.

### I.E.2. Customizing the icons

There are a few detailed icon option settings that it was not possible to incorporate into the installer. Therefore for best performance and appearance I suggest the following steps, for each icon that you will use:

I.E.2.a. Right-click on the icon. On the fly-open menu, click on Properties.

I.E.2.b. Enable the mouse in DNA·VIEW and PATER

Choose the Options tab. Be sure that Quick Edit Mode is *NOT* checked.

I.E.2.c. Choose a convenient window size.

- » On the Options tab under Display Options, choose Window (rather than Full Screen).
- » Choose the Fonts tab and choose a good-sized font. If you choose Lucida, then size 18 or 20 is about right.
- » Choose the Layout tab and ensure that Window Size is 80 (width) × 25 (height).

## II. Running DNA·VIEW

### II.A. Startup

**II.A.1. Click the icon or choose DNA·VIEW from the start menu.**

**II.A.2. Annoying message**

If, when trying to start DNA·VIEW/Toolbox, Windows complains about COM1 and asks "**Close or Ignore?**", click "Ignore" and everything will work fine.

**II.A.3. Printing from DNA·VIEW**

**II.A.4. Computer seem slower? (DNA·VIEW PLOT only)**

If DNA·VIEW – when started with the **DNAVIEW Plot** icon – plays badly with others (hogs all the CPU cycles, even **printing from DNA·VIEW takes one minute**), the problem is *process priority* between DOS and Windows XP.

This problem won't happen if you start the program with the (simple) DNAVIEW or PATER icon described above (§I.E). It's only an issue if you use the DNAVIEW PLOT icon.

A basic fix – **Lowering priority of DNA·VIEW in Windows**

II.A.4.a. Start Windows' Task Manager (While holding *Ctrl-Alt*, hit *Del*)

II.A.4.b. Start DNA-VIEW

II.A.4.c. At the Task Manager:

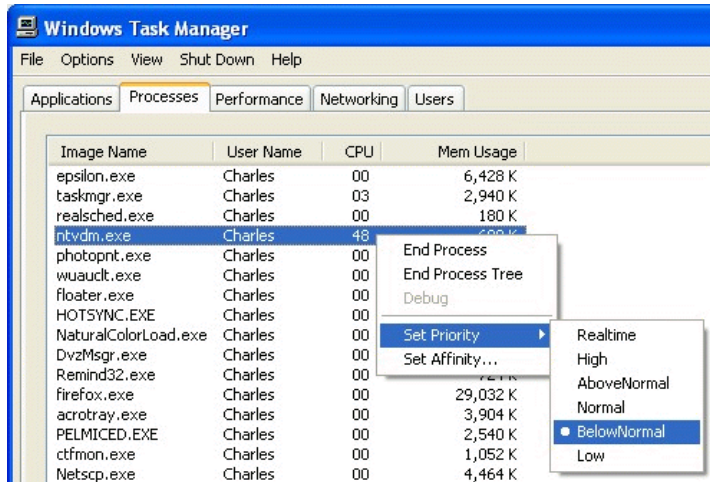
II.A.4.c.i.) Click the "Processes" tab.

II.A.4.c.ii.) Find the DOS process, which is called *ntvdm.exe* by typing *n* a sufficient number of times. Right click on it.

II.A.4.c.iii.) From the fly-out, choose *Set Priority*

II.A.4.c.iv.) From the next fly-out, click on *Below Normal*

II.A.4.c.v.) Close the Task Manager with the *X*



II.A.4.d. This change is temporary, lasting only until you close DNA-VIEW.

### II.A.5. Menu selection – **Very important!**

Please note §XV.A.1.d.i about the **context menu selection method!**

## III. Miscellaneous

### III.A. Population databases

A variety of population allele databases are included as part of a new install. They are also available to import into an existing installation from the \freqs directory of the CD via the first Import/Export option. Additional databases are on the CD in the Freq folder.

### III.B. Sample data files

The installed system has some sample data files. For example, to quickly see a casework computation, try §IV.C in the manual.

### III.C. Option for choosing locus name format

The *Options* command (in **Housekeeping**) includes an option *Locus name style like ...*. It offers four possibilities for locus name display viz:

- The bare locus name, such as *D16S539*
- Include the chromosomal information,
- Include the category such as *STR*.

### III.D. Questions

Please feel free to ask if you have any questions, or any difficulty at all.

## IV. New features

### IV.A. Convenience features for type-in responses

Use the help key *F1* for a popup that documents the special keystrokes described below. This help is available whenever you are supplying a type-in response, whether one-line (e.g. when typing a comment or inventing a file name), or when entering a kinship scenario.

```

Left-Dbl-Click  Exit -- accept window contents
Left-Click      Move cursor
Ctrl-C          Break -- abort to main menu
Ctrl-Z          Restore window to initial contents
Ctrl-Insert    Insert empty line above cursor
Ctrl-Delete    Delete line at cursor
Ctrl-a         Cut rectangle corner-to-cursor
Ctrl-v         Paste the cut rectangle
PageUp         Recall previous response
Ctrl-Up-Arrow  MENU of previous responses
PageDown      Recall next response
Ctrl-Dn-Arrow Recall next response
Right-Click   Clear window
Rgt-Dbl-Click Clear window
Ctrl-Shift-Del Delete current response from history menu
Alt-F6       HELP screens for program
F1           HELP editing keystrokes (this screen)
  
```

#### IV.A.1. Editing keystrokes

*Ctrl-Del* deletes a line (if multiple line input) or the line. *Ctrl-Insert* inserts a blank line (useful if editing a Kinship scenario). *Ctrl-z* restores the text as it was before you began editing.

#### IV.A.2. Memory

IV.A.2.a. Scrolling to previous responses

*PageUp* and *PageDown* (sometimes also *Up-arrow* and *Down-arrow*) scroll through previous type-in responses. *Ctrl-Shift-Delete* deletes an item from the memory list.

IV.A.2.b. Menu of previous responses

*Ctrl-Up-Arrow* pops up a menu of previous responses.

*DEL* deletes an item from the list of previous responses.

### IV.B. Paternity computation mutation calculation

*Case option*: Include mutation possibilities if effect > x% (e.g. 1-10%)

A new choice in *Case Options* (in the *Paternity Case* command) lets the user control to what extent mutation possibilities are considered. Consider an example such as

```

Mother 12 14
Child  12      15
Man    12      16.
  
```

```

compute
modify genotypes
compute
race: Caucasian
language is: Paternity
D8S1179 data
D21S11 data
D7S820 data
CSF1PO data
D3S1358 data
  
```

compute one locus

Obviously we must consider the possibility of a 16→15 (paternal) mutation as part of the computation of X=Pr(given DNA types|paternity). Another possible explanation, not far-fetched, would be a maternal 14→15 mutation with the man contributing the 12. A computation of X should probably include both of these possibilities.

There are further theoretically possible explanations as well, such as with two mutations and mutation by more than one step. Including all of these in the computation would introduce complexity – difficulty in verifying the computation – with no worthwhile gain in accuracy. It seems better to leave trivial terms off.

The mechanism implemented is to give the user the choice of omitting any terms that would affect the answer by less than a user-chosen percentage.

### IV.C. Paternity analysis detail: compute one locus

This *Paternity Case* option allows convenient analysis of a specified pattern. It uses data from the presently selected case as a starting point, but permits arbitrary modification.

```

*** D8S1179 STR
Paternity      Mother 12 14
race=Caucasian Child 12 14
                Tested Man 14 15
  
```

#### IV.C.1. Typical operation

IV.C.1.a. Select a locus – e.g. D8S1179 data from the menu

```

*** D8S1179 STR frequencies from 392 observations JFS 44(6) Caucasian
Paternity      Mother 12 14      0.1476 0.2036
race=c         Child 12 14      0.1476 0.2036
                Tested Man 14 15 0.2036 0.112
PI = X/Y = 0.25 / 0.1755725 = 1.428913
  
```

IV.C.1.b. select *compute*

IV.C.1.c. select *modify genotypes* from the menu and type in different genotypes; *compute*. Try a different *race* if you like.

With this tool you can examine step-by-step the effect on the calculation of examples involving possible mutation and/or null alleles.

IV.C.1.d. Switching between `language is: Paternity/Maternity` makes a difference when the analysis involves possible mutation.

IV.C.1.e. The `locus:` menu choice lets you select and enter data for an arbitrary locus, including one for which the case has no actual data.

#### IV.D. Case option: Omit names in kinship cases

#### IV.E. Kinship analysis detail: calculate one locus, showing parsing

This option from the `Immigration/Kinship` menu allows you to select any locus.

##### IV.E.1. Operation

The screen displays detailed information about the kinship calculation for that locus, including



##### IV.E.1.a. Parsing

The “parsing” (blue on white background) shows the child-mother-father trios that the program perceives the scenario to mean, for each of the hypotheses. This is debugging/training information.

##### IV.E.1.b. Alleles and frequencies

##### IV.E.1.c. Genotypes

The actual genotypes are shown, but you may enter different ones if you wish. Hit `Esc` to proceed to the computation.

##### IV.E.2. Uses

The primary intended use for this tool is to let the computer make various trial calculations to help you make a mutation analysis. When there is an inconsistency somewhere in a presumptive family, sometimes it is possible to reason that the likelihood in view of the inconsistency can be written as an expression involving one or more likelihoods of related problems in which one or another allele is changed (mutated).

#### IV.F. Kinship – pairwise relationship charts

Two of the menu options under `immigration/kinship` display a quick calculation of pair-wise comparisons between all the personae in the case.

**Experimental feature/Caveat!** – the LR's calculated are intended to include Y-haplotype matching odds. However, as of Version 28.35 the Y-haplotype calculation is incorrect when the Y-haplotypes match partially but not exactly. The `id` (identity) and `pi` (parentage) calculations are about right, but the remaining pairwise kinship LR's are too generous.

##### IV.F.1. Test all relations

The triangular relationship “distance” matrix shows pairwise relationship indices (LR) between each role in the case. Six relationships are computed:

`id`=identity/identical twin

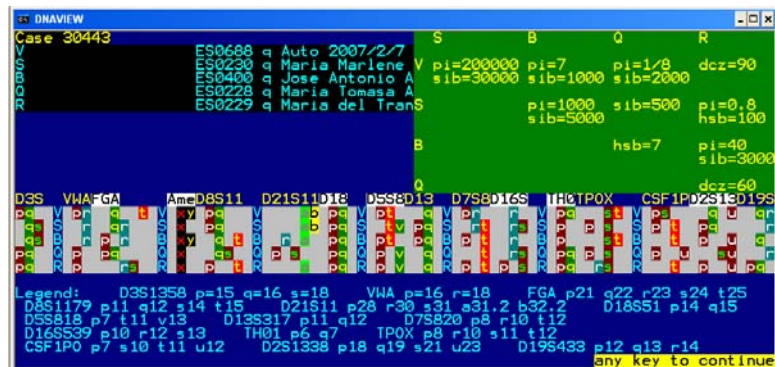
`pi`=paternity index (duo)

`si`=sibling index

`cuz`=cousin index

`hsb`=half sib/avuncular/grandparent index (they're all the same)

`dcz`=double cousin index.



However, the chart will show at most the largest one of the last four. Also, in no case will any  $LR < 1/100$  be shown. Therefore any blank cells in the upper triangle, or role letters omitted entirely, mean that all  $LR < 1/100$ .

#### IV.F.2. Kinship – Show pairwise relations

This option is similar to *Estimate likely relations*, but it lists every LR (that is  $\geq 1/100$ ) for every role pair and for every one of the six relationships. The listing is presented as a menu-chart with special key-strokes available to rearrange the chart. Hit one of the lower-case letters **abcdef** to sort according to the values in one of the columns id, pi, etc. Hit the same key again to sort in the opposite order. Sort according to the largest LR in the row with **+**. Put the red bar on a line (e.g. by single-left-click) and then **del** to remove a row. Example: **a** sorts the combinations **A,A B,B ...** to the top (since they have the large ID=matching odds figures); **down-arrow** to move to the first of them; **del del del ...** to remove them from the chart.

### IV.G. Kinship Simulation

#### IV.G.1. Simulation does [not] complete partial profiles

When running a simulation for a case for which some DNA profiles already exist, there are two kinds of additional data that one might consider obtaining and therefore want to simulate:

1. Additional people
2. Additional loci.

In either case, there may some loci for some of the previously typed people for which types were not obtained. This option allows you to specify whether the program should assume that you will re-assay and obtain genotypes to fill out those profiles, or not.

### IV.H. Import/Export

To import DNA profiles into DNA·VIEW, the data file be tab-delimited Ascii – see manual.

Import DNA profile data with one of two *Import/Export* options depending on the format of the file.

#### IV.H.1. Genotyper import

The input is one row per sample, such as can be produced by the ABI Genotyper® “Allele Table” macro. See the DNA·VIEW manual for details & procedure.

#### IV.H.2. Genemapper import

By this DNA·VIEW means an ABI format that is tall and narrow. It may be an option from the Genotyper for output as well. See the DNA·VIEW manual, §X.C.6, for an example.

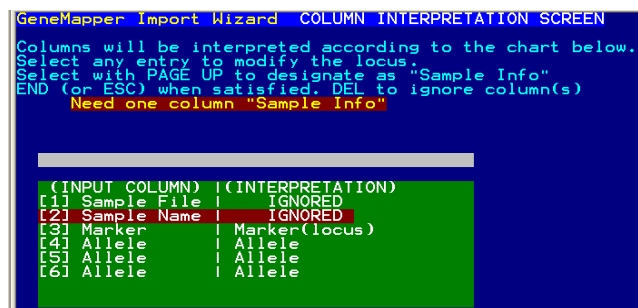
**added feature:** The import wizard allows a fair amount of flexibility for the input file:

##### IV.H.2.a. Column headings

Depending on how it is configured, GeneMapper® can produce some variation of the output columns. DNA·VIEW guesses how the GeneMapper columns correspond to information that DNA·VIEW is interested in. To guarantee complete flexibility, a *column interpretation screen* allows the user to override any incorrect guesses.

The critical (recognized and imported columns) are

IV.H.2.a.i.) Sample Info – means the column containing DNA·VIEW sample names in any of the various allowed formats (DNA·VIEW manual, §X.C.4).



(If there is a column names "Sample Info" or only one column named "Sample" anything, DNA·VIEW guesses that it is the Sample Info column. Otherwise, DNA·VIEW requires the user to choose.)

IV.H.2.a.ii.) Marker – the column with locus names. The word “Category” is recognized as an alternative.

IV.H.2.a.iii.) Allele – a column or columns with the allele sizes. The word “Peak” is permitted as an alternative to “Allele” for the heading of the columns containing the locus names. “Allele 1”, “Allele 2” etc are ok. If you were wondering, no, it is *not* ok to call some of the Allele and some Peak!

IV.H.2.a.iv.) Height – optional column or columns with peak heights.

If present, they must be equinumerous with Allele columns.

**Esc** if all column interpretations are ok; select any row to change the interpretation for that row.

