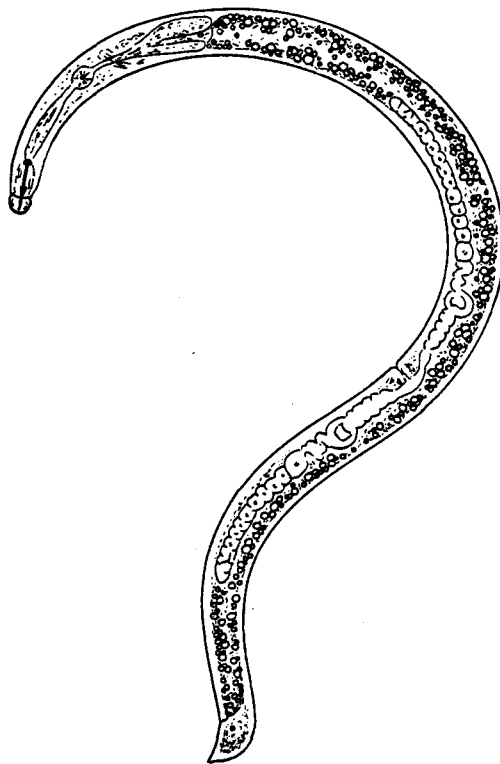# NEMAID 2.0

COMPUTER PROGRAM FOR IDENTIFICATION OF NEMATODES

USER'S MANUAL

R. FORTUNER
A. AHMADI

California Department of Food and Agriculture   *August 1986*

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NEMATODES

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*

RENAUD FORTUNER*/

Program Written By

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August 1986

NEMAID 2.0

Computer program for identification of nematodes.

USER'S MANUAL

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INTRODUCTION TO NEMAID.

The program NEMAID has been described in two publications:

-- Fortuner, R., 1983 - Computer assisted semi-automatic identification of Helicotylenchus species. California Plant Pest and Disease Report 2(2):45-48.

-- Fortuner, R. & Wong, Y. 1985 - Review of the genus Helicotylenchus Steiner, 1945.1: A computer program for identification of the species. Revue de Nematologie, (1984) 7(4):385-392.

NEMAID is designed as a tool to help identify the species in selected nematode genera.

To identify an unknown sample, the user enters its description in the program. NEMAID compares this description to that of every species in the database for the selected genus. Coefficients of similarity are calculated for every species. Coefficients range from 1.00 (species identical with the sample for all the characters considered), to 0.00 (all characters considered are dissimilar between the sample and the species). Species with coefficients closest to 1.00 are the most likely candidates for identification.

NEMAID 2.0 is available for IBM-PC and IBM-compatible (MS-DOS) microcomputers with 128K RAM or more.

With computers using different operating systems, it is possible to recompile the source codes of NEMAID 2.0 using a Turbo Pascal compiler. The source code's name is "NEMAID.PAS".

The following diskettes are available:

1. NEMAID 2.0: object code (48K) + source code (131K).

2. Genus database 1.02 : Helicotylenchus (= Rotylenchoides), 60K for 251 descriptions, November 1986.

Other genus databases will soon be available.

The 5-1/4 inch diskettes are available either single or double sided, and on either eight or nine tracks.

Never use the original diskettes you receive, but make copies for routine use. Format blank diskettes, and copy the source diskettes according to instructions from your microcomputer manuals.

BEFORE STARTING AN IDENTIFICATION...

1. Gather a good sized sample of the nematode to be identified (20 specimens of each sex if possible).

2. Identify the genus. Check if this genus is available with NEMAID.

3. Check which characters are used by NEMAID for this particular genus, decide which of these characters you accept as significant for identification (see documents attached to each genus database.)

4. Record these characters in your sample:

    -- Calculate the means of the measurements.

    -- Score separately each state of the morphological characters as 0 (state present) or 1 (state absent).

       For example, if head shape is coded for two states, rounded/ flattened, observe which shape(s) occur in your sample:

          Only rounded heads,   code: 1-0
          Only flattened heads, code: 0-1
          Both rounded and flattened heads observed, code: 1-1.

5. Have ready:

    -- The operating system diskette (for example, the DOS-diskette for an IBM-PC);

    -- The diskette with NEMAID program;

    -- The diskette with the genus database;

    -- The coded value of the characters in your sample;

    -- Eventually, which genus definition you recognize as valid (see page 31);

    -- Eventually the value you want to attribute to:

          character weights
          coefficients of correction (see page 40);

    -- Eventually a set of characters for a preselection of some species to which you want to compare your sample (see page 34).

USING THIS MANUAL

NEMAID: >   : This signal displayed by your terminal is a prompt
                 that indicates that the program expects an answer from
                 you.

[RETURN]   : Indicates that you must press the key marked RETURN or
                 RTRN on your keyboard.

JUMP   : The first choice of each frame is always: "1 Jump".
                 By typing "1 [RETURN]", you will be able to "jump"
                 directly to any frame in the program through a "jump
                 menu", as follows:

```
+------------------------------------------------------------------------+
|    JUMP TO:                                                             |
+------------------------------------------------------------------------+
| 1   Start                                                              |
| 2   Database information                                              |
| 3   Sample or species                                                 |
| 4   Selection of a subset of species                                 |
| 5   Entering label, data, and parameters                             |
| 6   Output                                                            |
| 7   End                                                              |
| 8   Wherever I was before                                            |
+------------------------------------------------------------------------+
```
NEMAID: >

                 Enter the number of the frame you want to go. For
                 example, enter "5 [RETURN]" to go to frame 5 and enter or
                 modify label, data, and parameters.

PREVIOUS SCREEN: The second choice of each frame is always: "2 Previous
                 screen". Type "2 [RETURN]" if you want to go back to the
                 previous frame and change your answers to the previous
                 question.

PROCEED   : The third choice of each frame is always "3 Proceed".
                 Type "3 [RETURN]"if you are done with the frame and you
                 want to go to the next frame and proceed with the
                 identification.

G   : G (go) is used throughout the program to go from one
                 screen to the next when the frame you are working with
                 necessitates several screenful of information. Type "G
                 [RETURN]" when you are done with the information on
                 one screen and you want to see more information on the
                 next screen.

GETTING STARTED WITH NEMAID 2.0

The following instructions may vary slightly with different computers. They refer to the mode of operation of an IBM-PC, single disc dive, 128K RAM. See the user's manual of your own computer for any conflicting instructions.

Don't forget: use copies of program and database (see page 4).

1. Insert operating system diskette into drive (or into drive A if you have a double disk drive);

2. Turn on the microcomputer. Wait about 2 minutes;

3. Enter time and date (optional);

4. Take O.S. diskette out of the drive;

5. Insert NEMAID 2.0 diskette into drive (or into drive A);

6. Type: NEMAID [RETURN]

Frame 1 will appear:

```
FRAME 1.
******************************************************************************
*                              NEMAID                                       *
*                                                                           *
*        A COMPUTER PROGRAM FOR IDENTIFICATION OF NEMATODES                 *
*                                 *                                         *
*                          RENAUD FORTUNER                                  *
*            CALIFORNIA DEPARTMENT OF FOOD AND AGRICULTURE                  *
*         1220 N STREET, SACRAMENTO,  CALIFORNIA 95814   USA                *
*                                 *                                         *
*              PROGRAM WRITTEN BY ABBAS AHMADI                              *
*                                 *                                         *
******************************************************************************
+--------------------------------------------------------------------------+
|    First insert the genus diskette in the drive A.                       |
|    Then  press RETURN to proceed  or type L to load previous             |
|          input file from diskette.                                       |
+--------------------------------------------------------------------------+


NEMAID: >
```

7. Take diskette out of drive;

8. Insert genus database diskette into drive (or into drive A);

9. Press [RETURN] or type L according to instructions of Frame 1. Use
    [RETURN] if you want to start a new identification; use L to recover
    data saved at the end of the previous session with the same genus
    database diskette (see page 49). This permits you to work on a sample
    during several sessions without having to reenter the sample data each
    time.

In either case (RETURN or L), you will see some information about the
database you are using. For example:

```
******************************************************************************
*                                                                          *
*   GENUS:        Helicotylenchus Steiner, 1945                            *
*   SYNONYM:      Rotylenchoides Whitehead, 1958                           *
*   AUTHOR OF DATABASE: Renaud Fortuner                                    *
*                California Department of Food and Agriculture             *
*                1220 N Street, Sacramento,   CA 95814   USA               *
*   VERSION:      1.01                                                     *
*   CREATED:      April 1984                                               *
*   UPDATED:      October 1985                                             *
*                                                                          *
******************************************************************************
Press RETURN to proceed  or type Q to quit the program
```

You have now the possibility to end the program (type "Q [RETURN]" to quit)
and return to system level. This option may be used for example if you
have loaded the wrong genus database.

If you want to continue with the identification, press [RETURN] to proceed
to Frame 2.

EXAMPLE OF A STRAIGHTFORWARD IDENTIFICATION

NEMAID has been designed to offer complete freedom to the users. You are not obligated to use all the characters proposed; you can change weights, correction factors, and ranges; you are free to select a list of species to compare with your sample; you can select one of the synonym genera included. The exercise of this freedom makes necessary the use of many options (selection of genus, change of parameters, and selection of species) that may bewilder the new user not familiar with the program. However, it is very easy to use NEMAID if you trust the author who proposed a genus in this identification program. The example below shows how you can go quickly through NEMAID.

Load NEMAID program and genus database according to instructions on pages 8 and 9. Follow instructions on pages 11 to 19.

```
FRAME 1.
******************************************************************
*                          NEMAID                               *
*                                                                *
*     A COMPUTER PROGRAM FOR IDENTIFICATION OF NEMATODES         *
*                            *                                   *
*                      RENAUD FORTUNER                           *
*        CALIFORNIA DEPARTMENT OF FOOD AND AGRICULTURE           *
*         1220 N STREET, SACRAMENTO,  CALIFORNIA 95814  USA      *
*                            *                                   *
*           PROGRAM WRITTEN BY ABBAS AHMADI                      *
*                            *                                   *
******************************************************************
+----------------------------------------------------------------+
|                                                                |
|    First insert the genus diskette in the drive A.             |
|    Then   press RETURN to proceed  or type L to load previous  |
|            input file from diskette.                           |
|                                                                |
+----------------------------------------------------------------+



NEMAID:  >




******************************************************************
*                                                                *
*    GENUS:          Helicotylenchus Steiner, 1945               *
*    SYNONYM:        Rotylenchoides Whitehead, 1958              *
*    AUTHOR OF DATABASE: Renaud Fortuner                         *
*                    California Department of Food and Agriculture *
*                    1220 N Street, Sacramento,  CA 95814  USA   *
*    VERSION:        1.01                                         *
*    CREATED:        April 1984                                   *
*    UPDATED:        October 1985                                *
*                                                                *
******************************************************************
Press RETURN to proceed  or type Q to quit the program



FRAME 2.   DATABASE INFORMATION
+----------------------------------------------------------------+
|  1   Jump                                                      |
|  2   Previous screen                                           |
|  3   Proceed                                                   |
|  4   Code names (all populations)                              |
|  5   Code names (only populations of one particular species)   |
|  6   Descriptions (all populations)                            |
|  7   Description (only one particular population)              |
|  8   Key to codes of database                                  |
+----------------------------------------------------------------+
NEMAID:  > 1
```

```
+----------------------------------------------------------------------+
|     JUMP TO:                                                          |
+----------------------------------------------------------------------+
| 1   Start                                                            |
| 2   Database information                                             |
| 3   Sample or species                                               |
| 4   Selection of a subset of species                                |
| 5   Entering label, data, and parameters                            |
| 6   Output                                                           |
| 7   End                                                             |
| 8   Wherever I was before                                          |
+----------------------------------------------------------------------+

NEMAID: > 5


FRAME 5.   ENTERING LABEL, DATA, AND PARAMETERS
+----------------------------------------------------------------------+
| 1   Jump                                                            |
| 2   Previous screen                                                  |
| 3   Proceed                                                         |
| 4   Entering label                                                  |
| 5   Entering data                                                   |
| 6   Entering parameters                                             |
+----------------------------------------------------------------------+

NEMAID: > 4


ENTERING LABEL :


1:
2:
3:
4:
5:


Type Q to quit.            (up to 60 characters per line)
For line:   text=
```

See page 37 for detailed explanations on now to label your identification job. For example, type: "1 [RETURN] Test NEMAID 2 [RETURN]" to enter text on the first line. Then type: "2 [RETURN] Population in Fortuner, 1979 [RETURN]" to enter text on the second line. Then type: "3 [RETURN] Revue Nematol 2:197-202 [RETURN]" to enter text on the third line. The screen now looks like this:

```
ENTERING LABEL :

1: Test NEMAID 2
2: Population in Fortuner, 1979
3: Revue Nematol. 2:197-202
4:
5:


Type Q to quit.            (up to 60 characters per line)
For line:q text=
```

FRAME 5.   ENTERING LABEL, DATA, AND PARAMETERS

+--+
| 1   Jump |
| 2   Previous screen |
| 3   Proceed |
| 4   Entering label |
| 5   Entering data |
| 6   Entering parameters |
+--+

NEMAID: > 5

ENTERING DATA :
No   CHARACTER   VALUE
----

    1. Body length? ....   ?
    2. Stylet length? ....   ?
    3. Distance stylet:dorsal gland opening? ....   ?
    4. Distance anterior end: excretory pore? ....   ?
    5. Width of one body annule? ....   ?
    6. Tail length? ....   ?
    7. Number of ventral tail annules? ....   ?
    8. Phasmids, in annules from anus?(anus level=20) .....   ?
    9. Ratio a (body length/body diameter)?................   ?
   10. Ratio c (body length/tail length)? ....   ?
   11. Ratio c'(tail length/tail diameter)? ....   ?
   12. Ratio m (cone/stylet length)? ....   ?
   13. Ratio v (head-vulva/body length)? ....   ?
   14. Spicule length? ....   ?

Q = Quit. G = Goto next screen. (? denotes missing value)
For Line number: Value is:

See page 38 for explanations on how to enter data for your sample. For
example, type: "1[RETURN] 671.0 [RETURN]" for character 1, type "2
[RETURN] 24.5 [RETURN]" for character 2, etc. The screen now looks
like this:

ENTERING DATA :
No   CHARACTER   VALUE
----

    1. Body length? 671.0
    2. Stylet length? 24.50
    3. Distance stylet:dorsal gland opening? 9.3
    4. Distance anterior end: excretory pore? ....   ?
    5. Width of one body annule? ....   ?
    6. Tail length? 20.9
    7. Number of ventral tail annules? 13.5
    8. Phasmids, in annules from anus?(anus level=20) 22.8
    9. Ratio a (body length/body diameter)?................   28.6
   10. Ratio c (body length/tail length)? ....   ?
   11. Ratio c'(tail length/tail diameter)? ....   ?
   12. Ratio m (cone/stylet length)? ....   ?
   13. Ratio v (head-vulva/body length)? 62.1
   14. Spicule length? ....   ?

Type "G" to go to next screen. Use Y (yes) or N (no) to describe whether a qualitative character is present:

```
ENTERING DATA :
No  CHARACTER                                                     VALUE
----------------------------------------------------------------------
15. Males present? ...................................... .....    ?
16. Labial disc visible in lateral view? ......................   ?
17. Canals (= fasciculi) present? ............................    ?
18. Habitus:   open circle to straight? ......................    ?
19.               closed circle to spiral ? ...................   ?
20. Lip anteriorly: rounded ? ................................    ?
21.                    flattened ? ...........................    ?
22. Fusion of incisures: y- or v-shaped? .....................    ?
23.                        u- or m-shaped? ...................    ?
24. Lip annulations: three or less ? .........................    ?
25.                   four to five ? .........................    ?
26.                   six or more  ? .........................    ?




Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:     Value is:
```

After you have entered your data (same method as above) the screen looks like this:

```
ENTERING DATA :
No  CHARACTER                                                     VALUE
----------------------------------------------------------------------
15. Males present? .......................................... ....   n
16. Labial disc visible in lateral view? .....................   n
17. Canals (= fasciculi) present? ............................   n
18. Habitus:   open circle to straight? ......................   n
19.               closed circle to spiral ? ..................   y
20. Lip anteriorly: rounded ? ................................   y
21.                    flattened ? ...........................   n
22. Fusion of incisures: y- or v-shaped? .....................   y
23.                        u- or m-shaped? ...................   n
24. Lip annulations: three or less ? .........................   ?
25.                   four to five ? .........................   ?
26.                   six or more  ? .........................   ?




Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:g    Value is:
```

Type "G [RETURN]" to go to next screen.

```
ENTERING DATA :
No  CHARACTER                                                          VALUE
------------------------------------------------------------------------------
27. Stylet knobs: indented? ..........................................    ?
28.                   flattened to rounded? ......................       ?
29.                   sloping backwards? .........................       ?
30. Tail: hemispherical and symmetrical? .....................          ?
31.       ventrally bent with rounded end? ..................          ?
32.       D and V sides joining at an angle? ...............          ?
33.       with projection or indented? ......................          ?
34. Female post. genital br. : functional? ...................          ?
35.                            degenerated? ..................          ?
36.                            reduced to a PUS? .............          ?




Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:      Value is:
```

```
ENTERING DATA :
No  CHARACTER                                                          VALUE
------------------------------------------------------------------------------
27. Stylet knobs: indented? ..................................         y
28.                   flattened to rounded? .....................      y
29.                   sloping backwards? .......................       n
30. Tail: hemispherical and symmetrical? ...................          n
31.       ventrally bent with rounded end? ..................          n
32.       D and V sides joining at an angle? ...............          y
33.       with projection or indented? ......................          y
34. Female post. genital br. : functional? ..................          y
35.                            degenerated? ..................          n
36.                            reduced to a PUS? ............          n




Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:q      Value is:




Type "Q [RETURN]" when all data has been entered.
```

FRAME 5.   ENTERING LABEL, DATA, AND PARAMETERS
+--+
| 1   Jump |
| 2   Previous screen |
| 3   Proceed |
| 4   Entering label |
| 5   Entering data |
| 6   Entering parameters |
+--+

NEMAID: > 3

FRAME 6.   OUTPUT
+--+
| 1   Jump |
| 2   Previous screen |
| 3   Proceed |
| 4   Summary of input |
| 5   General output |
| 6   Detailed output |
+--+

NEMAID: > 4

SUMMARY OF INPUT
==
SAMPLE OR SPECIES

  Comparison of sample to the species in the genus

SELECTION OF SUBSET OF SPECIES:
----

1   Definition of genus:
    A Helicotylenchus s. l. (including Rotylenchoides)
2   Description of species
    B Only valid descriptions and redescriptions
3   Selection of species based on the result of previous run
    NO
4   Selection of species based on the value of characters
    NO

Type G to go to next screen.   Type Q to quit listing :>   g

SUMMARY OF INPUT (CONTINUE)

LABEL:

    Test NEMAID 2
    Population in Fortuner, 1979
    Revue Nematol. 2:197-202

Type G to go to next screen.   Type Q to quit listing :>   g

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Type "G [RETURN]" to go to each successive frame and see a summary of all your input. After the last screen, the program will continue as follows:

FRAME 6.   OUTPUT

```
+--------------------------------------------------------------------------+
| 1    Jump                                                                |
| 2    Previous screen                                                     |
| 3    Proceed                                                             |
| 4    Summary of input                                                    |
| 5    General output                                                      |
| 6    Detailed output                                                     |
+--------------------------------------------------------------------------+
```

NEMAID: > 5

NEMAID   GENERAL OUTPUT

The species with the highest coefficients of similarity are listed
below with:
   - their coefficient of similarity
   - the number of characters used (weights not equal to 0.0)
   - the number of characters in agreement (score at least equal to 0.7)

LABEL:
     Test NEMAID 2
     Population in Fortuner, 1979
     Revue Nematol. 2:197-202

167 ORIGINAL DESCRIPTIONS
  2 COMPOSITE DESCRIPTIONS
 47 REDESCRIPTIONS

Type G to go to next screen.   Type Q to quit listing :>   g

CODE NAMES	SPECIES NAMES	COEFFICIENT OF SIMILARITY	NUMBER OF CHARACTERS USED	NUMBER OF AGREEMENTS
1BQ13	H.dihystera	1.00	17	17
1AA00	H.abunaamai	1.00	15	15
1BQ11	H.dihystera	1.00	12	12
1GT00	H.caudatus	1.00	14	14
1B099	H.dihystera	1.00	17	17
1HN00	H.interrogativus	1.00	16	15
1BQ00	H.dihystera	1.00	14	13
1BQ03	H.dihystera	0.99	15	14
1BP00	H.digonicus	0.99	13	12
1CS02	H.leiocephalus	0.99	17	16
1GI00	H.sagitovi	0.99	15	14
1BL00	H.densibullatus	0.99	14	13
1BU00	H.elegans	0.99	13	12
1DS00	H.persici	0.98	12	11
1BQ08	H.dihystera	0.97	16	14
1HR00	H.laevicaudatus	0.97	16	15

Type G to go to next screen.   Type Q to quit listing :>   g

-17-

Type "G [RETURN]" to see successive frames with the general results. See
as many screen as you wish.   Then type "Q [RETURN]" to continue with the
program.

FRAME 6.   OUTPUT

```
+-----------------------------------------------------------------------+
| 1   Jump                                                              |
| 2   Previous screen                                                   |
| 3   Proceed                                                           |
| 4   Summary of input                                                  |
| 5   General output                                                    |
| 6   Detailed output                                                   |
+-----------------------------------------------------------------------+
```

NEMAID: > 6

DETAILED OUTPUT

Enter description code name or type Q to quit.
NEMAID:> ObxOO

Use the option "Detailed output" (type "6 [RETURN]") to see a detailed
comparison between your data and one of the descriptions in the generic
database, for example here, OBXOO, the original description of H. flatus:

DETAILED OUTPUT. YOUR INPUT IS COMPARED TO DESCRIPTION FROM DATA BASE:
OBXOO   H.flatus   Roman, 1965

No	CHARACTER	INPUT	DESCRIP	SCORE	WEIGHT	SW
1	Body length	671.0	620.0	1.00	0.70	0.70
2	Stylet length	24.5	26.5	1.00	1.00	1.00
3	Distance stylet: dorsal gland opening	9.3	10.0	1.00	0.30	0.30
4	Distance anterior end: excretory pore	?	?	0.00	0.00	0.00
5	Width of one body annule	?	?	0.00	0.00	0.00
6	Tail length	20.9	?	0.00	0.00	0.00
7	Number of ventral tail annules	13.5	?	0.00	0.00	0.00
8	Phasmids, in annules from anus	22.8	26.0	1.00	0.70	0.70
9	Ratio a (body length/body diameter)	28.6	29.0	1.00	0.30	0.30
10	Ratio c (body length/tail length)	?	37.0	0.00	0.00	0.00
11	Ratio c'(tail length/tail diameter)	?	?	0.00	0.00	0.00
12	Ratio m (cone/stylet length)	?	?	0.00	0.00	0.00
13	Ratio v (head-vulva/body length)	62.1	63.5	1.00	1.00	1.00
14	Spicule length	?	?	0.00	0.00	0.00

Type G to go to next screen.   Type Q to quit listing :> g

Type "G [RETURN]" to see successive frames with comparison of all
characters. After the last frame, "G" will return to the menu:

FRAME 6.   OUTPUT
+--+
| 1   Jump |
| 2   Previous screen |
| 3   Proceed |
| 4   Summary of input |
| 5   General output |
| 6   Detailed output |
+--+

NEMAID: > 3

FRAME 7.   END
+--+
| 1   Jump |
| 2   Previous screen |
| 3   New run: keeping all input of present run. |
| 4   New run: discarding all input of present run. |
| 5   Exit program: saving the present input on the diskette. |
| 6   Exit program: not saving the present input on the diskette. |
+--+

NEMAID: > 5

****
*   *
*   THANK YOU FOR USING NEMAID   *
*   *
****

A>

You are now out of NEMAID, and back to the operating system level.

NEMAID gives you much more freedom than used in this first example. Each
available option will now be presented frame by frame and option by option.

Reload NEMAID 2.0 (page 7, 8) and go to Frame 2.

FRAME 2: DATABASE INFORMATION

After pressing [RETURN] at Frame 1 (see page 8), or when selecting option 2
on jump menu (see page 5), you will see the Frame 2 menu:

```
FRAME 2.   DATABASE INFORMATION
+------------------------------------------------------------------------------+
!  1    Jump                                                                    !
!  2    Previous screen                                                         !
!  3    Proceed                                                                 !
!  4    Code names (all populations)                                            !
!  5    Code names (only populations of one particular species)                 !
!  6    Descriptions (all populations)                                          !
!  7    Description (only one particular population)                            !
!  8    Key to codes of database                                                !
+------------------------------------------------------------------------------+
NEMAID: >
```

Choices 1 and 2 are explained page 5.

Choice 3 (proceed) will take you directly to Frame 3 (see page 28).

Choices 4 to 8 provide you with information on:

4: Species' names, code names, and literature references to all descrip-
    tions and redescriptions included in the generic database (see page
    21).

5: List of all the descriptions and redescriptions of a particular species
    that have been included in the database (see page 23).

6: Coded data of all the descriptions and redescriptions included in the
    genus database (see page 24).

7: Detailed description of a particular population (see page 25).

8. Information on the codes (validity, code name, coded characters) used
    in the genus database (see page 26).

Note that all this information is included in the documents attached to
each genus database.

Type the number of your choice and press [RETURN]

FRAME 2, OPTION 4: LIST OF CODE NAMES OF ALL POPULATIONS

Each genus database in NEMAID includes descriptions of:

1. Every new species described in the genus, including synonym species,
    but excluding species now in a different genus.

    The original author and date are noted. This information appears
    between parentheses if the species was originally proposed in a dif-
    ferent genus. The complete reference is not given (see database
    NOMEN).

    When type material has been redescribed by a latter author, his
    conclusions are included in the description of the species. In the
    list, such descriptions are noted: "original author + Smith, 1976"
    when the redescription by Smith, 1976 is included. The code name of
    all original descriptions includes a group of 2 letters and a double
    zero: by00.

2. Descriptions of populations of known species, other than the type
    population.

    Only redescriptions from good sized samples (n > 10), with mean values
    given for the measurements, and with intraspecific variability noted,
    are included. Reference include only the author's name(s) and the year
    of publication. See the database NOMEN for more information. The code
    names for the redescriptions use the same two letters as the original
    description followed by a two-digit number: by01, by02, by03, etc.

3. Composite descriptions.

    When at least five to ten good descriptions are known for a species, a
    composite description can be made with measurements given as the mean
    of the successive sample means, and morphological characters described
    including the variability observed in the successive samples.

    The code names uses the same two letters as the original description
    followed by the number 99: by99.

For example, type "4 [RETURN]" at Frame 2 menu (page 20) using
Helicotylenchus database to see the following information:

CODE NAMES (ALL POPULATIONS)

CODE	SPECIES NAME	REFERENCE
1AA00	H.abunaamai	Siddiqi, 1972
1FU00	H.acunae	Fernandez et al., 1980
1GB00	H.acutucaudatus	Fernandez et al., 1980
1HI00	H.acutus	Teben'kova, 1983
1HC00	H.affinis	(Luc, 1960)
1AC00	H.africanus	topotypes in Sher, 1966
1AC02	H.africanus	in Van den Berg & Heyns, 1975
1AD00	H.agricola	Elmiligy, 1970 + Ali, 1976
1GW00	H.amplius	Anderson & Eveleigh, 1982
1HF00	H.angularis	Mulk & Siddiqi, 1982
1AE00	H.anhelicus	Sher, 1966
0AF00	H.annobonensis	(Gadea, 1960)
0AG00	H.apiculus	Roman, 1965
1AH00	H.aquili	Khan & Nanjappa, 1972
1AI00	H.arachisi	Mulk & Jairajpuri, 1975

Type G to go to next screen. Type Q to quit listing :>

The program displays only that part of the list that can fit into one
screen frame. You must type "G [RETURN]" (go) to see each successive
frame. After the last frame has been displayed, or if you want to stop the
listing, type "Q [RETURN]", and the program will return to Frame 2 menu
(page 20).

FRAME 2, OPTION 5: LIST OF CODE NAMES OF ALL POPULATIONS OF A PARTICULAR SPECIES

For example, type "5 [RETURN]" at Frame 2 menu (page 20) to see the following message:

```
CODE NAMES (ONE PARTICULAR SPECIES)
-------------------------------------------------------------
Enter only species name (omit genus name).   Type Q to quit.
NEMAID:>
```

Type, for example, "DIHYSTERA" to obtain the list of all the descriptions of H. dihystera in the generic database Helicotylenchus:

```
CODE NAMES (ONE PARTICULAR SPECIES)
-------------------------------------------------------------
Enter only species name (omit genus name).   Type Q to quit.
NEMAID:> dihystera
```

```
CODE NAMES (ONE PARTICULAR SPECIES)
-------------------------------------------------------------------------------
CODE      SPECIES NAME              REFERENCE
-------------------------------------------------------------------------------
1BQ00     H.dihystera               topotypes in Sher, 1966
1BQ03     H.dihystera               in Siddiqi, 1972
1BQ05     H.dihystera               in Anderson, 1974
1BQ08     H.dihystera               in Van den Berg & Heyns, 1975
1BQ11     H.dihystera               in Zavaleta-Meija & Sosa-Moss, 1979
1BQ13     H.dihystera               in Fortuner, 1979
1BQ99     H.dihystera               composite description
```

If there are more than 15 descriptions for the species (one screen full), type "G [RETURN]" to see the next screen.

Type "Q [RETURN]" to stop the listing, or after the last screen, to return to Frame 2 menu (page 20).

```
Type G to go to next screen.   Type Q to quit listing :>   q
```

```
CODE NAMES (ONE PARTICULAR SPECIES)
-------------------------------------------------------------
Enter only species name (omit genus name).   Type Q to quit.
NEMAID:> q
```

FRAME 2, OPTION 6: DESCRIPTIONS OF ALL POPULATIONS

This option permits you to see how the author entered the descriptions of
the species in the genus database.

Because of the great number of species involved, the descriptions are
given in coded form with:

  -- the validity of the description (1 = valid; 0 = nonvalid), according
     to the author of the genus database;

  -- the code name of the species: two letters and a two-digit number;
     this code is given in Frame 2, option 4 (page 21);

  -- the measurements entered as mean values (or mid-range if means are
     not known);

  -- the coded value (0 or 1) of the morphological characters.

The characters are listed in the same order as given in option 8 (page 26),
and the descriptions are listed in the same order as in option 4 (page
21).

To obtain these descriptions, type "6 [RETURN]" at Frame 2 menu (page 20)
to see the following message:

DESCRIPTIONS (ALL POPULATIONS)

CODE   DESCRIPTION

```
1AA00   056021.6    0871.4    092327381.34761.5    000011010110110011100
1FU00   063829.8              11272338       61.5   000011001010100011100
1GB00   084733.5              09252932       65.3   000011010010100001100
1HI00   080030.0071061.5      27570.95260.0  000   1001010010001100
1HC00   040826.0080771.314    1922311.5  85.2 000101010010100010001
1AC00   080029.0              152637312.04461.0231001010  010010001100
1AC02   080027.6  1021.422112437391.64760.0251001010  010110001100
1AD00   051524.008     1.5    092625321.2  63.0  000011001010110011100
1GW00   076128.0141251.92211  27361.24361.0  000011001010100001100
1HF00   060024.5111001.7      092530491.24663.0  0000110  110110001100
1AE00   067530.5              112229401.55060.5241001010  010100100100
0AF00   0750                  13162835       65.0      01      0010001100
0AG00   055024.010            242536    63.5231000110010111000001100
1AH00   062523.5              09302758       64.0  000011010010100100100
1AI00   053522.0090951.5      2428431.24762.5  000011010010110110100
```

Type G to go to next screen. Type Q to quit listing :> g

After each screen frame, the listing stops and you are asked if you
want to see the next frame (type "G [RETURN]") or if you want to quit
listing (type "Q [RETURN]") and return to Frame 2 menu (page 20).

FRAME 2, OPTION 7:   DESCRIPTION OF ONE PARTICULAR POPULATION

Detailed descriptions are easier to read than the coded descriptions you obtain when using option 6.

Because a detailed description will need several screens to be displayed, only one population can be described at a time.   The program asks for the coded name of the description you want to see in details.   This coded name (5 digits) can be found in the documents attached to each genus database. It can also be obtained on line using options 4 or 5 of Frame 2 (pages 21 and 23).

To use this option, type "7 [RETURN]" at Frame 2 menu (page 20) to see the following message:

```
DESCRIPTION (ONE PARTICULAR POPULATION)
--------------------------------------------------------------------------------


Enter description code name or type Q to quit.
NEMAID: >
```

Type the code name of a description (as given in options 4 or 5).   For example, type "1BQ03" to see the description of this population of H. dihystera.

```
DESCRIPTION ( ONE PARTICULAR POPULATION):
1BQ03   H.dihystera              in Siddiqi, 1972
--------------------------------------------------------------------------------

No    CHARACTER                                      VALUE
--------------------------------------------------------------------------------

  1   Body length                                   670.0
  2   Stylet length                                  26.0
  3   Distance stylet: dorsal gland opening           ?
  4   Distance anterior end: excretory pore           ?
  5   Width of one body annule                        ?
  6   Tail length                                     ?
  7   Number of ventral tail annules                 10.0
  8   Phasmids, in annules from anus                 29.0
  9   Ratio a (body length/body diameter)           30.0
 10   Ratio c (body length/tail length)             48.0
 11   Ratio c'(tail length/tail diameter)            1.2
 12   Ratio m (cone/stylet length)                    ?
 13   Ratio v (head-vulva/body length)              63.0
 14   Spicule length                                 22.0


Type G to go to next screen.   Type Q to quit listing : >
```

After each screen, type "G [RETURN]" to see the next screen.   Type "Q [RETURN]" to quit and return to Frame 2 menu (page 20).

FRAME 2, OPTION 8: INFORMATION ON CODES USED IN THE DATABASE

This option explains how was coded the data for each description as read
from the documents attached to the genus database or as obtained through
Frame 2, option 6 (page 24).

The first column gives the taxonomic status (valid = 1; nonvalid = 0) of
each description, according to the opinion of the author of the genus
database. Later (see page 32), you can decide to compare your sample to
all descriptions (coded 1 and 0) or only to the valid descriptions (coded
1). If you disagree with the author about the validity of a particular
description, you can modify the code by changing 1 to 0 or vice versa
in the genus database.

The next four columns give the coded name of the species (two letter) and
of the description (two-digit number) as explained page 21.

The characteristics of each population are given in the rest of the
columns. Numerical characters are entered as the mean, or as midrange if
mean is unknown for a measurement. Qualitative characters are entered as
presence (1) or absence (0) of each character state.

To see this information on screen, type "8 [RETURN]" at Frame 2 menu (page
20):

KEY TO CODES
==

A. SPECIES CODE NAME

No	FIELD	FORMAT	COLUMNS	CONTENTS
1	Validity of description	X	1 - 1	valid=1/nonvalid=0
2	Species	XX	2 - 3	letters
3	Description	XX	4 - 5	00 = original
				99 = composite
				01, 02, 03, etc=
				redescriptions

B. SPECIES CHARACTERISTICS

No	CHARACTER	FORMAT	COLUMNS	CONTENTS
1	Body length	XXXX	8 - 11	numerical value
2	Stylet length	XX.X	12 - 15	numerical value

Type G to go to next screen. Type Q to quit listing :> g

Type "G [RETURN]" to go to the next screen.

SPECIES CHARACTERISTICS (continue)

No	CHARACTER	FORMAT	COLUMNS	CONTENTS
3	Distance stylet:dorsal gland opening	XX	16 - 17	numerical value
4	Distance anterior end: excretory pore	XXX	18 - 20	numerical value
5	Width of one body annule	X.X	21 - 23	numerical value
6	Tail length	XX	24 - 25	numerical value
7	Ventral tail annules	XX	26 - 27	numerical value
8	Phasmids, in annules from anus	XX	28 - 29	numerical value
9	Ratio a (body length/body diameter)	XX	30 - 31	numerical value
10	Ratio c (body length/tail length)	XX	32 - 33	numerical value
11	Ratio c'(tail length/tail diameter)	X.X	34 - 36	numerical value
12	Ratio m (cone/stylet length)	XX	37 - 38	numerical value
13	Ratio v (head-vulva/body length)	XX.X	39 - 42	numerical value
14	Spicule length	XX	43 - 44	numerical value
15	Male present?	X	45 - 45	yes=1/no=0
16	Labial disc visible in lateral view?	X	46 - 46	yes=1/no=0
17	Canals (= fasciculi) present?	X	47 - 47	yes=1/no=0

Type G to go to next screen.   Type Q to quit listing :> g

SPECIES CHARACTERISTICS (continue)

No	CHARACTER	FORMAT	COLUMNS	CONTENTS
18	Habitus :			
	closed circle to spiral?	X	48 - 48	yes=1/no=0
	open circle to straight?	X	49 - 49	yes=1/no=0
19	Lip shape:			
	anteriorly rounded?	X	50 - 50	yes=1/no=0
	anteriorly flattened	X	51 - 51	yes=1/no=0
20	Incisure shape:			
	Y- or V-shaped?	X	52 - 52	yes=1/no=0
	U- or M-shaped?	X	53 - 53	yes=1/no=0
21	Lip annulation:			
	three or less?	X	54 - 54	yes=1/no=0
	four to five?	X	55 - 55	yes=1/no=0
	six or more?	X	56 - 56	yes=1/no=0

Type G to go to next screen.   Type Q to quit listing :> g

The whole list takes several screens. After each screen, type "G [RETURN]"
to see the next screen or type "Q [RETURN]" to return to Frame 2 menu (page
20).

FRAME 3:   SAMPLE OR SPECIES?

NEMAID is primarily designed to compare an unknown sample to the described
species of a genus.

NEMAID can also be used to study the taxonomic status of one of the
descriptions in the genus database. NEMAID will in this case compare this
description to the rest of the descriptions in the database. Frame 3 gives
you the possibility to study an unknown sample (default option) or a
description in the database.

```
FRAME 3.   SAMPLE OR SPECIES?
+-----------------------------------------------------------------------------+
|  1   Jump                                                                   |
|  2   Previous screen                                                        |
|  3   Proceed                                                                |
|  4   Sample                                                                 |
|  5   Species                                                                |
+-----------------------------------------------------------------------------+
NEMAID: >
```

Choices 1 and 2 are explained page 5.

Choice 3 (proceed) will take you to Frame 4 menu (page 29). The program
will utilise the default option (sample) or it will use species if you had
used option 5 for a previous run of the program.

Choose option 4 if you want to study your own sample; choose option 5 if
you want to study one of the descriptions of the database.

If you choose option 4 (sample), you will have to enter the values of
the characters in your sample later (Frame 5, option 5, see page 38).

If you choose option 5 (species), you will be asked to choose one of the
descriptions, redescriptions, or composite descriptions available in the
genus database for the species you selected. Enter the code name (5
digits) of the description you want to study. The code names are given in
the documents attached to each genus database, or can be seen from Frame
2, option 4 (see page 21). For example, enter lac00 for the description of
the type population of H. africanus. Enter lac02 for the population of
this species described by Van den Berg and Heyns.

Once you have selected a population, its description is read from the
genus database and is used by the program as input for the identifi-
cation.

Type the number of your choice and press [RETURN].

FRAME 4:   SELECTION OF A SUBSET OF SPECIES

After answering the question asked at Frame 3 (page 28), you arrive at
Frame 4 menu:

```
FRAME  4.    SELECTION OF A SUBSET OF SPECIES
+--------------------------------------------------------------------------------+
|  1   Jump                                                                      |
|  2   Previous screen                                                           |
|  3   Proceed                                                                   |
|  4   Selection of a subset of species                                         |
+--------------------------------------------------------------------------------+
NEMAID:  >
```

Choices 1 and 2 are explained page 5.

Choice 3 (proceed) will take you to Frame 5 (page 36) using the default
option of the program if you are running it for the first time during the
current session.   If you have already used NEMAID and if you have changed
the default options in any way, choice 3 will proceed, keeping whatever
choice you have made before.   Everytime you exit NEMAID and unless you
decide to save your input for the next session (see page 49), the program
reverts to the default options as below:

   1: Genus defined "sensu lato" (= in the widest sense).

   2: Utilization of all the descriptions and redescriptions that are
       noted as valid in the database.

   3 and 4: Options not used.

Choice 4 (selection of a subset of species) will permit you to change some
of these options.

Type the number of your choice and press [RETURN].

Type "4 [RETURN]" to see the following table.

```
SELECTION OF A SUBSET OF SPECIES
1  Which definition of genus do you want to use?                              A
        A   Helicotylenchus s. l. (including Rotylenchoides)
        B   Helicotylenchus s. str. (excluding Rotylenchoides)
        C   Rotylenchoides  sensu Siddiqi & Husain, 1964
        D   Rotylenchoides sensu Luc, 1960

2  Which description do you want to use?                                       B
        A   All descriptions and redescriptions
        B   Only valid descriptions and redescriptions
        C   All original descriptions (valid and nonvalid)
        D   Only valid original descriptions

3  Selection of species based on the result of previous run? (Y/N)           NO
        If YES, enter the coefficient of similarity                          0.7

4  Selection of species based on the value of sample characters? (Y/N)       NO




Type G to go to next screen.   Type Q to quit.
For Question No:          Answer=
```

The right hand column shows you that the program is currently using the
default options. See following pages on how to change these options.

FRAME 4, QUESTION 1:   SELECTION OF A GENUS DEFINITION

The widest possible definition has been accepted for every genus in NEMAID, including all their synonym genera, even if the synonymizations are controversial.   For example Rotylenchoides is accepted as a synonym of Helicotylenchus and the species of both genera are found in the same genus database in NEMAID.

However, NEMAID can be used by users who do not accept such synonymizations.

For example, you can compare an unknown sample to:

A -- Helicotylenchus s.1. (including Rotylenchoides); default option;

B -- Helicotylenchus s. str. (excluding Rotylenchoides);

C -- Rotylenchoides sensu Siddiqi & Husain, 1964;

D -- Rotylenchoides sensu Luc, 1960 and Sher, 1965.

The list of genera and synonym genera included in NEMAID can be found in the documents attached to each genus database.

*

To change the default option (A, Helicotylenchus s. 1.) to one of the other options, for example B, enter 1, press [RETURN] then type B and press [RETURN] again:

For question no.:   1 [RETURN] Answer = B [RETURN].

If you do not wish to use any of the other options (pages 32 to 35), type "Q [RETURN]" to return to Frame 4 menu (page 29).

See following pages if you want to use one of these options.

FRAME 4, QUESTION 2:   SELECTION OF SPECIFIC DESCRIPTIONS

You may also decide against which set of descriptions you want to compare
your sample(s):

A -- all the descriptions and redescriptions in the genus database.

B -- only the descriptions and redescriptions considered as valid by the
     author of the database default option.

C -- only the original and composite descriptions whether or not they are
     considered as valid.

D -- only the original and composite descriptions of the species considered
     as valid by the author of the genus database.

To change the default option (B: all valid descriptions and redescrip-
tions) to one of the other options, for example D, enter 2, press [RETURN],
then type D and press [RETURN] again.

For question no. 2 [RETURN] Answer = D [RETURN].

Type "Q [RETURN]" to go back to Frame 4 menu (page 29), or see following
pages to use other options.

FRAME 4, QUESTION 3: SELECTION OF DESCRIPTIONS FROM A PREVIOUS RUN OF THE
                      PROGRAM

If you use only a few characters, you will find that NEMAID will:

-- discard all the species that do not fit your sample description for
   these characters

-- do poorly in differentiating between your samples and all the species
   that do share these characteristics. Many species will have a
   coefficient of similarity equal to 1. It is impossible to decide
   which is the most similar to your sample.

NEMAID permits to overcome this difficulty in the following manner:

1. Run the identification program a first time, using very selective
    conditions (a few characters, heavy weights).

2. The results of this first run are stored in a temporary memory (list of
    all species with decreasing similarity coefficients.

3. Then, you may decide to run the program again. Use choice 3 on Frame 7
    menu (page 49). This will save all your input and return you to Frame
    2 menu (page 20).

4. When you run the program a second time, and you arrive at Frame 4, you
    need to change the default answer (no) at question 3 to a yes, and you
    need to set the coefficient of similarity you want to use as a
    cut-point. The default value is set at 0.7. This means that only the
    descriptions with a coefficient of similarity at least equal to 0.7 as
    calculated during the first run of the program will be used for the
    second run. You can change 0.7 to any value you prefer.

    Enter 3, press [RETURN], then type Y (for yes), press [RETURN], then
    you will see that a new question appears at the end of the line, and
    you are asked to enter the value of the coefficient of similarity you
    want to use (for example 0.8):

For question no. 3 [RETURN] Answer = Y [RETURN] and coefficient = 0.8
[RETURN].

5. When you press [RETURN], the program takes you directly to Frame 4,
    question 4 (page 34) where you can change your previous selections.
    For the second run of the program, you will have to choose less
    restrictive conditions: a larger set of characters, different
    character weights (see Frame 5 to modify the parameters, page 40).

FRAME 4, QUESTION 4: SELECTION OF DESCRIPTIONS BASED ON THE VALUE OF SOME
CHARACTERS

You can select a set of species from the genus database, that share one
or several morphological characters with your sample. You will have to
decide which characters you want to use.

If you use TAIL and your sample has TAIL = 1100, it will be compared
only to species with TAIL = 1100, 0100, and 1000. If you use a measure-
ment, only species with similar measurement will be used. For example, if
you use STY and if your sample has a stylet length of 25 um (mean value),
the sample will be compared only to species with STY = 25 + 3 (3 um is
the correction factor).

To change the default answer (no), enter 4, press [RETURN], then type Y
(for yes), and press [RETURN]:

For question no. 4 [RETURN] Answer = Y [RETURN].

Then type "G [RETURN]" to see the following table:

SELECTION OF A SUBSET OF SPECIES BASED ON THE CHARACTER(S)
===

No	CHARACTER	USE	NO	CHARACTER	USE
1	Body length	NO	13	Ratio v (head-vulva/body len.	NO
2	Stylet length	NO	14	Spicule length	NO
3	Distance stylet:gland opening	NO	15	Presence male	NO
4	Distance anterior end:excr. pore	NO	16	Labial disc visible	NO
5	Width of one body annule	NO	17	Presence canals (= fasciculi)	NO
6	Tail length	NO	18	Habitus	NO
7	Number of ventral tail annules	NO	19	Lip shape	NO
8	Phasmids, in annules from anus	NO	20	Incisure shape	NO
9	Ratio a (body len./body diam.)	NO	21	Lip annulation	NO
10	Ratio c (body len./tail len.)	NO	22	Stylet knobs shape	NO
11	Ratio c'(tail len./tail diam.)	NO	23	Tail shape	NO
12	Ratio m (cone/stylet length)	NO	24	Female post. genital branch	NO

Type Q to quit.
Change usage (NO to YES or vice versa) for character No:

This table lists all the characters available for the genus. The "USE"
colum shows whether a character is used (YES) or not used (NO) to select
descriptions. In the default option, none of the characters are used.
Change the NO into YES for those characters you want to use by entering the
reference number of the character:

Change usage (NO to YES or vice versa) for character No: 2 [RETURN].

You will see that the second character (stylet length in the example above) change from NO to YES on the screen. You can revert your choice by entering again the character number:

Change usage (NO to YES or vice versa) for character No: 2 [RETURN].

This time the YES of stylet lenght changes back to NO.

Type "Q [RETURN]" (quit) when you are satisfied with the options selected. You will then go back to Frame 4 menu (page 29). Type "3 [RETURN]" to proceed to Frame 5.

FRAME 5: ENTERING LABEL, DATA, PARAMETERS

When you are through with Frame 4, type "3 [RETURN]" at Frame 4 menu (page 29) or use option 5 in jump menu (page 6) to see Frame 5 menu:

```
FRAME 5.   ENTERING LABEL, DATA, AND PARAMETERS
+------------------------------------------------------------------------+
|  1   Jump                                                              |
|  2   Previous screen                                                   |
|  3   Proceed                                                           |
|  4   Entering label                                                    |
|  5   Entering data                                                     |
|  6   Entering parameters                                               |
+------------------------------------------------------------------------+
NEMAID: >
```

Choices 1 and 2 are explained page 5.

Choice 3 (proceed) will take you directly to Frame 6 (see page 43). Use this choice if you have already entered and saved the sample data in a previous run of the program, or if you are studying a description from the database (Frame 3, choice 5, see page 28), and if you do not wish to modify the parameters.

Choices 4 to 6 allow you to:

4: enter a sample label, i.e. a short title for your sample (see page 37).

5: enter the values of the characters in your sample (see page 38).

6: modify the parameters (see page 40).

Type the number of you choice and press [RETURN].

FRAME 5, OPTION 4:   ENTERING LABEL

For an easy record keeping, you may want to note some information about
your sample.   This sample label will be displayed with the results of the
identification.

If, for any reason, you do not want to record sample data, type Q then
press the RETURN key to go back to Frame 5 menu (page 36).

```
ENTERING LABEL :


1:
2:
3:
4:
5:




Type Q to quit.          (up to 60 characters per line)
For line:  text=
```

To enter data, type "1 [RETURN]", then start typing using a maximum of 60
characters on line no. 1 (including spaces and punctuation marks), then
type "2 [RETURN]" and enter the text for line no. 2, etc.   Use 5 lines
maximum:

```
ENTERING LABEL :

1: Test NEMAID 2
2: Population in Fortuner, 1979 ·
3: Revue Nematol. 2:197-202
4:
5:




Type Q to quit.          (up to 60 characters per line)
For line:q text=
```

When all the data has been entered, type Q, then press the RETURN key to go
back to Frame 5 menu (page 36).

FRAME 5, OPTION 5:   ENTERING SAMPLE DATA

Do not use this option if you are comparing a description from the database
to the other descriptions (Frame 3, choice 5, page 28).

To enter the description of your sample, type "5 [RETURN]" at Frame 5
menu (page 36) to obtain the following table:

ENTERING DATA :
No   CHARACTER   VALUE
----
  1. Body length? ....   ?
  2. Stylet length? ....   ?
  3. Distance stylet:dorsal gland opening? ....   ?
  4. Distance anterior end: excretory pore? ....   ?
  5. Width of one body annule? ....   ?
  6. Tail length? ....   ?
  7. Number of ventral tail annules? ....   ?
  8. Phasmids, in annules from anus?(anus level=20) ....   ?
  9. Ratio a (body length/body diameter)?.....................   ?
 10. Ratio c (body length/tail length)? ....   ?
 11. Ratio c'(tail length/tail diameter)? ....   ?
 12. Ratio m (cone/stylet length)? ....   ?
 13. Ratio v (head-vulva/body length)? ....   ?
 14. Spicule length? ....   ?

Q = Quit. G = Goto next screen. (? denotes missing value)
For Line number: Value is:

Question marks at the right column of the table show that all character
values are missing until you enter these values. You may leave some
characters with missing values.

Enter numerical values as mean of each measurement in your sample.

The format is free, you may use decimals at will. For example, this is how
you would enter body length = 671 μm, stylet length = 24.5 μm, etc:

For line number : 1 [RETURN] value is: 671 [RETURN]
For line number : 2 [RETURN] value is: 24.5 [RETURN]
etc.

The screen now looks as follows:

```
ENTERING DATA :
No   CHARACTER                                                          VALUE
-------------------------------------------------------------------------------
   1. Body length? .................................................    671.0
   2. Stylet length? ...............................................     24.5
   3. Distance stylet:dorsal gland opening? ........................      9.3
   4. Distance anterior end: excretory pore? .......................      ?
   5. Width of one body annule? ....................................      ?
   6. Tail length? .................................................     20.9
   7. Number of ventral tail annules? ..............................     13.5
   8. Phasmids, in annules from anus?(anus level=20) ...............     22.8
   9. Ratio a (body length/body diameter)?..........................     28.6
  10. Ratio c (body length/tail length)? ...........................      ?
  11. Ratio c'(tail length/tail diameter)? .........................      ?
  12. Ratio m (cone/stylet length)? ................................      ?
  13. Ratio v (head-vulva/body length)? ............................     62.1
  14. Spicule length? ..............................................      ?




Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:g    Value is:
```

Type "Q [RETURN]" to return to Frame 5 menu (see page 36). Type "G [RETURN]" to see the next frame, which includes qualitative characters:

```
ENTERING DATA :
No   CHARACTER                                                          VALUE
-------------------------------------------------------------------------------
  15. Males present? ...............................................      ?
  16. Labial disc visible in lateral view? .........................      ?
  17. Canals (= fasciculi) present? ................................      ?
  18. Habitus:  open circle to straight? ...........................      ?
  19.           closed circle to spiral ? .........................      ?
  20. Lip anteriorly: rounded ? ....................................      ?
  21.                 flattened ? ..................................      ?
  22. Fusion of incisures: y- or v-shaped? .........................      ?
  23.                      u- or m-shaped? .........................      ?
  24. Lip annulations: three or less ? .............................      ?
  25.                  four to five ? ..............................      ?
  26.                  six or more  ? ..............................      ?



Q = Quit. G = Goto next screen. ( ? denotes missing value)
For Line number:    Value is:
```

For each character (unless missing) enter character state line number, [RETURN], then indicate if the state is present (Y for yes) in at least one specimen in your sample or absent (N for no). Type "G [RETURN]" to see the next frame. Type "Q [RETURN]" to return to Frame 5 menu (p. 36).

FRAME 5, OPTION 6:   ENTERING PARAMETERS

The computation of the coefficients of similarity by NEMAID utilizes
several quantities:

-- range: difference between the highest and the lowest specific value
            in the genus database.   This value is computed automatically
            from all the values of the characters in the descriptions you
            have selected.

            If you are using a restricted generic definition (Frame 4,
            question 1, page 31), only the descriptions that fit this
            generic definition are used to calculate ranges.   For example,
            if you selected answer C in the example page 31, only Helico-
            tylenchus spp. with posterior genital branch reduced to a PUS
            are used to calculate the range.

            Frame 4 also permits you to select only some of the descrip-
            tions included in the database.   This selection does not
            influence the computation of the range.   For example, if
            descriptions in Helicotylenchus s. l. are selected from Frame
            4, question 4 (page 34) with character No. 24, female pos-
            terior genital branch reduced to a PUS, ranges are calculated
            from all descriptions in Helicotylenchus s. l. and not only
            from those with PUS.

            Range values calculated by the program cannot be modified.

-- correction factor: maximum difference in measurements that can be
            explained by the intraspecific variability.   A difference in
            measurement between your sample and a species will be
            considered as indicating a specific dissimilarity only if it
            exceeds the correction factor.   You may change the values of
            the correction factors proposed by the author of the generic
            database (page 41, 42).

-- weight: the intermediate coefficient of similarity for each succes-
            sive character can be given a weight from 0 (character
            neutralized) to 1 (character taken at full value).   You may
            change the weights proposed by the author of the genus
            database (page 41, 42).

To see the values of the parameters used in the program, type "6 [RETURN]"
at Frame 5 menu (page 36) to obtain the following table:


```
ENTERING PARAMETERS :
NO CHARACTER                                            WEIGHT    CORRECTION    RANGE
--- -------------------------------------------------   --------  ----------    -------
  1 Body length                                          0.7       150.0        827.0
  2 Stylet length                                        1.0         3.0         21.5
  3 Distance stylet:dorsal gland opening                 0.3         5.0         13.0
  4 Distance anterior end: excretory pore                0.6        10.0         72.0
  5 Width of one body annule                             0.1         1.0          2.4
  6 Tail length                                          0.3         3.0         22.0
  7 Ventral tail annules                                 0.5        13.0         19.0
  8 Phasmids, in annules from anus                       0.7         6.0         24.0
  9 Ratio a (body length/body diameter)                  0.3         8.0         24.0
 10 Ratio c (body length/tail length)                    0.1        15.0         71.0
 11 Ratio c'(tail length/tail diameter)                  0.6         0.5          2.0
 12 Ratio m (cone/stylet length)                         0.8         4.0         13.0
 13 Ratio v (head-vulva/body length)                     1.0         2.0         39.4
 14 Spicule length                                       0.7         3.0         20.0


Press RETURN to skip a field.  Q = Quit.  G = Goto next screen
For Char No:    Weight=        Correction=
```


If you accept these values, type "G [RETURN]" to see each successive screen
or type "Q [RETURN" to go back to Frame 5 menu (page 36).

You can also change any weight and any correction factor. To change the
parameters of body length (#1) to weight = 0.5 and correction factor = 75,
type: "1 [RETURN] 0.5 [RETURN] 75 [RETURN]":

For Char. No: 1 [RETURN] Weight = 0.5 [RETURN] Correction = 75 [RETURN].

You may change only the correction factor. To change the correction factor of tail length (No. 6) to 1.5 without changing the weight, type " 6 [RETURN] [RETURN] 1.5 [RETURN]":

For Char. No. 6 [RETURN] Weight = [RETURN] Correction = 1.5 [RETURN].

For qualitative characters, there are no correction factors or ranges:

```
ENTERING PARAMETERS :
NO CHARACTER                                     WEIGHT
___ _____     _____
15 Presence male                                   0.9
16 Labial disc visible (in lateral view)           0.8
17 Presence canals (= fasciculi)                   0.9
18 Habitus                                          0.9
19 Lip shape                                        0.9
20 Incisure shape                                   0.8
21 Lip annulation                                   0.3
22 Stylet knobs shaoe                               0.1
23 Tail shape                                       0.6
24 Female post. genital br.                         1.0




Press RETURN to skip a field. Q = Quit. G = Goto next screen
For Char No:    Weight=
    :
```

You can only modify weights as above. For example, to change weight of habitus (No. 18) to 1.0, type "18 [RETURN] 1".

Type "Q [RETURN]" at any time to return to Frame 5 menu (page 36).

FRAME 6: OUTPUT

When you have entered label and sample data, and when you are satisfied
with the parameters, go back to Frame 5 menu (type "Q [RETURN]") and
proceed (option 3) to Frame 6:

```
FRAME 6.   OUTPUT
+-------------------------------------------------------------------------------+
:  1   Jump                                                                     :
:  2   Previous screen                                                          :
:  3   Proceed                                                                  :
:  4   Summary of input                                                         :
:  5   General output                                                           :
:  6   Detailed output                                                          :
+-------------------------------------------------------------------------------+

NEMAID: >
```

Choices 1 and 2 are explained page 5.

Choice 3 (Proceed) will take you directly to Frame 7 (see page 49).

Choice 4 recapitulates the input (page 44).

Choice 5 gives the results in an abbreviated form (page 45).

Choice 6 gives more detailed results (page 47).

Type the number of your choice and press [RETURN].

FRAME 6: OPTION 4: SUMMARY OF INPUT

Choice 4 at Frame 6 menu (page 43) gives on screen a summary of all your
input including:

  -- sample label.

  -- values of sample characters.

  -- parameters.

  -- eventually selection of a subset of descriptions.

The input is presented in several screens. After seeing each screen type
"G [RETURN]" to go to the next one or type "Q [RETURN]" to quit and return
to Frame 6 menu, (page 43).

If you notice any error and you want to change your input, type "Q
[RETURN]" to go back to Frame 6 menu (43). Then type "2 [RETURN]" to
return to Frame 5. From Frame 5, you can change label, data, or
parameters.

If you want to change your selection of a subset of descriptions you
need to go back to Frame 4 (page 29). You can go to Frame 4 by typing "2
[RETURN]" at Frame 5 menu (page 36). You can also "jump" (page 6) directly
from Frame 6 menu to Frame 4. From Frame 6 menu, type "1 [RETURN]" to go
to jump menu, then type "4 [RETURN]" to jump to Frame 4 menu. You can use
jump again to return to Frame 6.

FRAME 6: OPTION 5: GENERAL OUTPUT

Once you are satisfied with your input, go back "Q [RETURN]" to Frame 6 menu (page 43) and type "5 [RETURN]" to obtain the results. The computations will take a few seconds then you will see the first screen of the general output:

NEMAID   GENERAL OUTPUT

The species with the highest coefficients of similarity are listed below with:
- their coefficient of similarity
- the number of characters used (weights not equal to 0.0)
- the number of characters in agreement (score at least equal to 0.7)

LABEL:
   Test NEMAID 2
   Population in Fortuner, 1979
   Revue Nematol. 2:197-202

167 ORIGINAL DESCRIPTIONS
  2 COMPOSITE DESCRIPTIONS
 47 REDESCRIPTIONS

Type G to go to next screen. Type Q to quit listing :>

This screen repeats your sample label, and the numbers of selected sets of descriptions with which you compared your sample.

Type "G [RETURN]" to see the next screen or "Q [RETURN]" to quit and return to Frame 6 menu (page 43).

In the general output, the descriptions are given by decreasing values of their coefficient of similarity with your sample. For each successive description, the number of characters used for the comparison and the number of characters that were similar in your sample and in the description are also given.

CODE NAMES	SPECIES NAMES	COEFFICIENT OF SIMILARITY	NUMBER OF CHARACTERS USED	NUMBER OF AGREEMENTS
1BQ13	H.dihystera	1.00	17	17
1AA00	H.abunaamai	1.00	15	15
1BQ11	H.dihystera	1.00	12	12
1GT00	H.caudatus	1.00	14	14
1BQ99	H.dihystera	1.00	17	17
1HN00	H.interrogativus	1.00	16	15
1BQ00	H.dihystera	1.00	14	13
1BQ03	H.dihystera	0.99	15	14
1BF00	H.digonicus	0.99	13	12
1CS02	H.leiocephalus	0.99	17	16
1GI00	H.sagitovi	0.99	15	14
1BL00	H.densibullatus	0.99	14	13
1BU00	H.elegans	0.99	13	12
1DS00	H.persici	0.98	12	11
1BQ08	H.dihystera	0.97	16	14
1HR00	H.laevicaudatus	0.97	16	15

Type G to go to next screen. Type Q to quit listing :>

Type "G [RETURN]" to see each successive screen. When you consider that the coefficients of similarity of the descriptions have become too low, type "Q [RETURN]" to quit the listing and go back to Frame 6 menu (page 43).

FRAME 6, OPTION 6:   DETAILED OUTPUT

The general output give the coefficient of similarity between your sample
and each description. It is very informative to know how was this
coefficient calculated for some descriptions.

From Frame 6 menu (page 43), type "6 [RETURN]" to see the following
question:

DETAILED OUTPUT

Enter description code name or type Q to quit.
NEMAID:> 1bq03

Enter the code name (5 digits) of the description you are interested in and
press return. You may take this code name from the general results of
Frame 6, option 5; or you may obtain it from Frame 2, options 4 and 5; or
from the documents attached to each genus database.

Enter, for example, 1bq03 [RETURN]. The computations will take a few
seconds, then you will see:

DETAILED OUTPUT. YOUR INPUT IS COMPARED TO DESCRIPTION FROM DATA BASE:
1BQ03 H.dihystera   in Siddiqi, 1972

No	CHARACTER	INPUT	DESCRIP	SCORE	WEIGHT	SW
1	Body length	671.0	670.0	1.00	0.70	0.70
2	Stylet length	24.5	26.0	1.00	1.00	1.00
3	Distance stylet: dorsal gland opening	9.3	?	0.00	0.00	0.00
4	Distance anterior end: excretory pore	?	?	0.00	0.00	0.00
5	Width of one body annule	?	?	0.00	0.00	0.00
6	Tail length	20.9	?	0.00	0.00	0.00
7	Number of ventral tail annules	13.5	10.0	1.00	0.50	0.50
8	Phasmids, in annules from anus	22.8	29.0	0.99	0.70	0.69
9	Ratio a (body length/body diameter)	28.6	30.0	1.00	0.30	0.30
10	Ratio c (body length/tail length)	?	48.0	0.00	0.00	0.00
11	Ratio c'(tail length/tail diameter)	?	1.2	0.00	0.00	0.00
12	Ratio m (cone/stylet length)	?	?	0.00	0.00	0.00
13	Ratio v (head-vulva/body length)	62.1	63.0	1.00	1.00	1.00
14	Spicule length	?	22.0	0.00	0.00	0.00

Type G to go to next screen. Type Q to quit listing :>

For each character is given:

   -- the value in your sample (or in a description if you are using option
      SPECIES from Frame 3, page 28);
   -- the value in the description you just selected (lbq03 in the example
      above);
   -- the score (s) for this character;
   -- the weight (w) attributed to the character;
   -- the final score (sw) for the character.

At the end, the following sums are given:

   -- the sum of all the weights ($\sum w$) and of all the final scores ($\sum sw$).
   -- the computation of the coefficient of similarity:

$$SG = \sum sw \ / \ \sum w$$

The detailed output takes several screens. After each screen, type "G
[RETURN]" to go to the next screen or "Q [RETURN]" to quit and return to
Frame 6 menu (page 43).

You can use this option as many times as you wish, to study successively
any number of detailed results and decide which particular description fits
best your sample.

FRAME 7: END

After studying the general results and as many detailed results you want,
type "Q [RETURN]" to quit and return to Frame 6 menu (page 43), then use
option 3 to proceed to Frame 7:

```
FRAME 7.  END
+----------------------------------------------------------------------------+
|  1   Jump                                                                   |
|  2   Previous screen                                                        |
|  3   New run: keeping all input of present run.                             |
|  4   New run: discarding all input of present run.                          |
|  5   Exit program: saving the present input on the diskette.                |
|  6   Exit program: not saving the present input on the diskette.|           |
+----------------------------------------------------------------------------+
NEMAID: >
```

Choices 1 and 2 are explained page 5.

Choices 3 and 4 will go back to Frame 2 menu (page 20). With choice 3 all
your input is saved including choice of sample vs. species, sample label
and data, parameter values, and subset of species. You can then either
keep these values or change any of then and try to identify your sample
under different conditions.

With choice 4, all input is discarded and the program reverts to the
original default options. You can start a new identification without
having to reload the genus database.

Choices 5 and 6 will exit the program and return to operating system
level.

Choice 5 is equivalent to choice 3 above. All your input is saved into a
special file stored in the generic diskette. When you start a new session
with NEMAID you can reload this input from the diskette (see page 9, use
L).

Choice 6 is equivalent to choice 4 and discards all input.

Type the number of you choice and press [RETURN]. For example, type "6
[RETURN]" to see the last message:

```
****************************************************************************
*                                                                         *
*                    THANK YOU FOR USING NEMAID                           *
*                                                                         *
****************************************************************************
A:\ >
```

"A>" indicates that you are back to operating system level.