

**NEMAID
COMPUTER PROGRAM FOR IDENTIFICATION
OF
NEMATODES**

USER'S MANUAL

**RENAUD FORTUNER
Program Written by
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CALIFORNIA DEPARTMENT OF FOOD AND AGRICULTURE

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NEMAID
 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. - Review of the genus Helicotylenchus Steiner, 1945.1: A computer program for identification of the species. Proposed for publication in Revue de Nématologie.

NEMAID is designed as a tool to help identify the species in selected 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 selected genus datafile. Coefficients of similarity are calculated for every species. Coefficients range from 1 (species identical with the sample for all the characters considered), to 0 (all characters considered are dissimilar between the sample and the species). Species with coefficients closest to 1 are the most likely candidates for identification.

BEFORE STARTING AN IDENTIFICATION...

1. Gather a good sized sample of the nematode to be identified (20 specimens of each sex or more if possible).
2. Identify the genus. Check if this genus is in NEMAID (Annex 2, page 41).
3. Check which characters are used by NEMAID for this particular genus, decide which of these characters you accept as significant for identification (Annex 3, page 42).
4. Record these characters in your sample:

-- Calculate the means of the measurements; be sure to use the correct format (decimals, how many numerals for each movement, etc.; for example for Helicotylenchus, body length must be given as 0752, not 752 or 752.5).

-- 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 head, code: 1-0

Only flattened head, code: 0-1

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

-- Write the coded identification in one line; include blanks for any missing characters.

5. Have ready:

-- The program password (page 6)

-- The name of the genus (page 41)

-- The coded value of the characters in your sample (pages 10 and 42)

-- Eventually the value you want to attribute to:

coefficients of correction (page 26)

ranges (page 28)

character weights (page 24)

-- Eventually a set of characters for a preselection of some species to which you want to compare your sample (page 32).

USING THIS MANUAL

- Underlining : In the examples, any text that must be typed by you, the user, is underlined.
- > : The signal ">" displayed by your terminal is a prompt that indicates that the program expects an answer from you.
- [RETURN] : Indicates that you must punch the key marked RETURN or RTRN on your keyboard.
- You must know that you have to punch the RETURN key at the end of every line you enter. Consequently, [RETURN] is not normally repeated in the examples.
- HELP : Whenever the program asks you to choose one of several options, the last option is "HELP". By typing: HELP, you will obtain a short explanation of the different options proposed.
- [CONTROL] S : Punching these two keys together will stop temporarily the text being displayed on your screen. Punch the space bar to resume the display.
- Capital letters: In the present manual, the examples are written in capital letters. However NEMAID also accepts entries typed in low case letters.

CONNECTING WITH NEMAID

- a. Connect with DIALCOM or with your national public data network according to the instructions from the network.
- b. Type "NEMAID"
- c. The program will ask you the secret NEMAID password. This is NOT the password needed to connect with DIALCOM.
- d. Unit March 1984, the NEMAID password is "LAUREL", after my wife to whom this program is dedicated.

After March 1984, a new secret password will be disclosed only to subscribers of the program NEMAID (see Annex 1 at the end of this manual for details).

- e. The program comes up with a title page.

Example:

(phone network access number)

[RETURN] [RETURN]

TELENET

916 19D

TERMINAL=

[RETURN]

@

C 301 363 [RETURN]

301 363 CONNECTED

PRIMECOM NETWORK 18.4D SYSTEM 63

PLEASE SIGN ON

>

ID DFA001 xxx

ITT DIALCOM COMPUTER SERVICES 18.4D(63)

ON AT 13:26 12/13/83 EST

NEMAID

WELCOME TO NEMAID

PLEASE ENTER THE PASSWORD FOR NEMAID :

>

LAUREL

NEMAID

COMPUTER PROGRAM FOR IDENTIFICATION OF NEMATODES

*

RENAUD FORTUNER

CALIFORNIA DEPARTMENT OF FOOD & AGRICULTURE

1220 N STREET, SACRAMENTO, CA 95814 USA

*

PROGRAM WRITTEN BY YINPO WONG

*

PLEASE SELECT A GENUS AND ENTER ITS NAME OR TYPE "HELP":

>

SELECTION OF A GENUS

NEMAID was first proposed in December 1983 with only one genus: Helicotylenchus. It is hoped that other genera will soon be added to NEMAID.

The widest possible definition has been accepted for every genus in NEMAID. Synonym genera are included in the genera in NEMAID, even if this synonymization is controversial. For example Rotylenchoides is accepted as a synonym of Helicotylenchus and the species of both genera are found in the same genus datafile in NEMAID.

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

For example, users can compare an unknown sample to:

- Helicotylenchus s.l. (including Rotylenchoides)
- Helicotylenchus s. str. (excluding Rotylenchoides)
- Rotylenchoides sensu Siddiqi & Husain, 1964
- Rotylenchoides sensu Sher, 1965

See page 32 of this manual for selection of the genus.

The list of genera and synonym genera included in NEMAID can be found in Annex 3 of this manual. It can also be obtained on-line by asking for: "HELP".

*

The program gives you the opportunity to know more on how the genus you selected is entered in its genus datafile.

You can request:

- the list of the criteria used to describe the species. Type: CHAR
- the list of the species included in the genus datafile. Type: LIST
- the descriptions of these species in the genus datafile. Type: DESCR

*

If you already know how these informations about the genus datafile, you can proceed to the next question by typing: PROC

Example:

```
*****  
PLEASE SELECT A GENUS AND ENTER ITS NAME OR TYPE "HELP":  
>  
HELICOTYLENCHUS  
THE GENUS YOU REQUESTED IS HELICOTYLENCHUS  
SYNONYM : ROTYLENCHOIDES  
CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP  
>  
*****
```

CHARACTERS USED FOR IDENTIFICATION

NEMAID uses three kinds of characters:

- Measurements: any character that can be described by a number: distance, ratio, number of annules, etc.

Measurements are given with format, range, and correction factor.

- Format is how the measurement is entered in the genus datafile. The format is given as two numbers separated by a period.
- The first number represents how many digits you must enter as the integer part of the measurement.
- The second number represents how many decimals you must enter.

For example, 4.0 is entered as a four digit integer with no decimal: (0730, 1582, etc.).

2.1 is entered as a two digit integer plus one decimal: (10.5, 09 0, etc.).

- Range is the difference between the highest and the lowest specific values for a measurement in the genus datafile.
- Correction factor is the maximum difference in measurements that can be explained by the intraspecific variability.

You can later change range and correction factors and substitute your own values. See pages 26-28.

- Nonvariable morphological characters: any morphological character that exists in only one of two possible states in a given species.

- Variable morphological characters: any morphological character that may exist in two or several states in a given species.

The format gives the number of digits used to describe each morphological character.

The program displays only the part of the list that can fit into one screen frame. You must punch [RETURN] to see each successive frame.

After the last frame has been displayed, the program offers you some information about format, range, and correction factors. Then it returns to the previous question (choose between: PROC/CHAR/LIST/DESCR/HELP).

Example:

```
*****  
CHOOSE ONE:  PROC/CHAR/LIST/DESCR/HELP  
>
```

CHAR

LIST OF CHARACTERS FOR THE GENUS HELICOTYLENCHUS (SYNONYM: ROTYLEN-
CHOIDES) PREPARED BY R. FORTUNER, 1983.

	CODE NAME	CHARACTER NAMES	FORMAT	RANGE	CORRECTION
MEASUREMENTS	: LGT	= BODY LENGTH	4.0	0830	0150
	: STY	= STYLET LENGTH	2.1	22.0	03
	: DGO	= POSITION DGO	2.0	10	05
	: EXPO	= POSITION EXCRE. PORE	3.0	050	010
	: BAW	= BODY ANNULE WIDTH	1.1	2.5	1.0
	: TLG	= TAIL LENGTH	2.0	22	03
	: TAN	= TAIL ANNULES /	2.0	19	13
	: PHAS	= POSITION PHASMIDS	2.0	24	06
	: RAA	= RATIO A	2.0	24	08
	: RAC	= RATIO C	2.0	71	15
	: RCC	= RATIO C'	1.1	1.7	0.5
	: RAM	= RATIO M	2.0	12	04
	: RAV	= RATIO V	2.1	40.0	02
	: SPI	= SPICULE LENGTH	2.0	20	03

[HIT RETURN TO CONTINUE]

>

NON VARIABLE CHAR : MALE = PRESENCE MALES 1.0
: DISC = LABIAL DISC VISIBLE 1.0
: CAN = PRESENCE CANALS 1.0

VARIABLE CHAR : HAB = HABITUS 2.0
: LIP = LIP SHAPE 2.0
: INC = INCISURE SHAPE 2.0
: LANN = LIP ANNULES 3.0
: KBS = KNOBS SHAPE 3.0
: TAIL = TAIL SHAPE 4.0
: GENB = GENITAL BRANCH 3.0

CHOOSE ONE : INFO/PROC

>

PROC

CHOOSE ONE : PROC/CHAR/LIST/DESCR/HELP

>

```
*****
```

LIST OF SPECIES INCLUDED IN THE GENUS DATAFILE

The genus datafiles in NEMAID include descriptions of:

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

In the list "n.sp" means original description. The complete reference is not given.

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: "n.sp. + Smith, 1976" when the redescription by Smith, 1976 is included. The code name of these descriptions includes a group of 2 letters and a double zero: AA00.

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 program NEMAS for more information. The code names for the redescriptions uses the same two letters as the original description followed by a two-digit number: AA01, AA02, AA03, etc.

3. Composite descriptions.

When at least ten good descriptions are known for a species, a composite description can be made with:

- measurements as the means of the successive sample means
- morphological characters including the variability of the successive samples

The code names uses the same two letters as the original description followed by the number 99: BY99.

The program displays only the part of the list that can fit into one screen frame. You must punch [RETURN] to see each successive frame. You may also punch "Q" to stop the listing. After the last frame has been displayed, or if you punch "Q", the program returns to the previous question (choose between PROC/CHAR/ LIST/DESCR/HELP

Example:

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

LIST

LIST OF SPECIES IN THE GENUS HELICOTYLENCHUS
SYNONYM: ROTYLENCHOIDES

180 NEW SPECIES
49 REDESCRIPTIONS
1 COMPOSITE DESCRIPTION.

PREPARED BY R. FORTUNER, 1983.

<u>CODE</u>	<u>SPECIES NAME</u>	<u>REFERENCE</u>
AA00	H. ABUNAAMAI	N. SP.
AB00	H. AEROLATUS	N. SP.
AC00	H. AFRICANUS	TOPOTYPES IN SHER, 1966
AD00	H. AGRICOLA	N. SP. + ALI, 1976
AE00	H. ANHELICUS	N. SP.
AG00	H. APICULUS	N. SP.
AH00	H. AQUILI	N. SP.
AI00	H. ARACHISI	N. SP.
AJ00	H. ASTRIATUS	N. SP.
AK00	H. AUSTRALIS	N. SP.
AL00	H. BAMBESAE	N. SP.
AM00	H. BELLI	N. SP.
FO00	H. BELURENSIS	N. SP.
AN00	H. BIHARI	N. SP.

[HIT RETURN TO CONTINUE LISTING OR "Q" TO STOP LISTING]

>

Q

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

DESCRIPTION OF THE SPECIES

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

You can ask to see all the description (ask: ALL) or only the description of one particular species (ask: ONE).

1. Descriptions of all the species in the genus datafile (ALL)

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

- the code name of the species; this code is given in LIST
- the measurements entered as mean values (or mid-range if means are not known), according to the format given in CHAR
- the coded value (0 or 1) of the morphological characters. The number of digits used to describe each character is given in CHAR

The characters are listed in the same order as in CHAR, and the species are listed in the same order as in LIST.

After each screen frame, the listing stops and you are asked if you want to quit (Q) or see the next frame [RETURN].

2. Detailed description (ask ONE)

Detailed descriptions are easier to read. You must give the name of the species and the code name of the particular description you want to see (Example page 16).

An additional option (BACK) permits you to go back to the previous question (choose one: PROC/CHAR/LIST/DESCR/HELP).

Example 1:

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

DESCR

CHOOSE ONE: ALL/ONE/BACK/HELP

>

ALL

DESCRIPTIONS OF SPECIES IN THE GENUS HELICOTYLENCHUS
SYNONYM: ROTYLENCHOIDES

180 NEW SPECIES
49 REDESCRIPTIONS
1 COMPOSITE DESCRIPTIONS

PREPARED BY R. FORTUNER, 1983

CODE
NAMES CODED DESCRIPTIONS

AA00	056021.6	0871.4	092327381.34761.5	0000110101101100011100
AB00	050023.7	0851.012102424451.04764.0	0000110	
AC00	080029.0	152637		
AD00	051524			

(etc., the program gives the descriptions of about 20 species, then...)

				100111100110100
		737	62.0 000 10	0111000001100
	009	3.0 08252235	61.0 0000110	0101000001100
AR00	071427.4101201.51608252345	61.0 0000101	0101000010100	
AS00	065525.6 1121.4 092131381.55361.4211000110	0101001100100		

[HIT RETURN TO CONTINUE LISTING OR "Q" TO STOP LISTING]

>

Q

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

Example 2:

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

DESCR

CHOOSE ONE: ALL/ONE/BACK/HELP

>

ONE

ENTER: SPECIES NAME/HELP

>

PSEUDOROBUSTUS

PLEASE CHOOSE ONE:

TOPOTYPES IN SHER, 1966 + FORTUNER ET AL, 1984	TYPE DY00
COMPOSITE DESCRIPTION IN FORTUNER ET AL, 1984	TYPE DY99
IN VAN DEN BERG & HEYNS, 1975	TYPE DY08
TO CHOOSE ANOTHER SPECIES INSTEAD,	TYPE "SPEC"
TO RETURN TO MENU	TYPE "MENU"

>

DY00

<u>CHARACTERS</u>	<u>VALUES</u>
BODY LENGTH	0764
STYLET LENGTH	27.1
POSITION DGO	09
POSITION EXCRET. PORE	114
BODY ANNULE WIDTH	

(etc., the program gives the values of all the characters, then...)

KNOBS SHAPE	110
TAIL SHAPE	0001
GENITAL BRANCH	100

PLEASE CHOOSE ONE:

TOPOTYPES IN SHER, 1966 + FORTUNER ET AL, 1984	TYPE DY00
COMPOSITE DESCRIPTION IN FORTUNER ET AL, 1984	TYPE DY99
IN VAN DEN BERG & HEYNS, 1975	TYPE DY08
TO CHOOSE ANOTHER SPECIES INSTEAD,	TYPE "SPEC"
TO RETURN TO MENU	TYPE "MENU"

>

MENU

CHOOSE ONE: PROC/CHAR/LIST/DESCR/HELP

>

SAMPLES OR SPECIES?

NEMAID is primarily designed to compare one or several unknown SAMPLES to the described species of a genus.

NEMAID can also be used to study the taxonomic status of one of the described species of the genus. NEMAID will in this case compare one of the SPECIES to the other species in the genus datafile.

Choose SAMPLES if you want to study your own sample; choose SPECIES if you want to study one of the species in the genus.

*

If you ask "SPECIES", you will be asked to choose one of the description, redescrptions, or composite description available in the genus datafile for the species you selected.

You may also change your mind and decide to study a different species (type "SPEC") or your own samples (type "SAMP").

Example:

```
*****
  CHOOSE ONE:  PROC/CHAR/LIST/DESCR/HELP
  >
  PROC

  CHOOSE ONE:  SAMPLES/SPECIES/HELP
  >
  SPECIES

  ENTER SPECIES NAME/HELP
  >
  PSEUDOROBUSTUS

  PLEASE CHOOSE ONE:

  TOPOTYPES IN SHER, 1966 + FORTUNER ET AL, 1984      TYPE DY00
  COMPOSITE DESCRIPTION IN FORTUNER ET AL, 1984      TYPE DY99
  IN VAN DEN BERG & HEYNS, 1975                      TYPE DY08
  TO CHOOSE ANOTHER SPECIES INSTEAD,                TYPE "SPEC"
  TO INPUT SAMPLES INSTEAD,                          TYPE "SAMP"
  >
  DY00

  DO YOU ACCEPT PARAMETERS? : Y/N/INFO
  >
  *****
```

RECORD OF SAMPLE DATA

For an easy record keeping, you may want to identify your sample. This sample data will be displayed with the results of the specific identification.

The data you enter is stored in a temporary memory. The contents of this memory are rubbed out when you exit the program. To protect your privacy, NEMAID is not designed to permit an outsider to tap this memory.

If, for any reason, you do not want to record sample data, type an asterisk "*" then punch the RETURN key to go to next question.

To enter data, start typing using a maximum of 50 characters per line (including spaces and punctuation marks). Punch RETURN for each new line.

When all the data has been entered, type an asterisk "*", then punch the RETURN key to go to next question.

If you have several samples, enter data for the first sample only. You will have later the opportunity to enter data for the next sample, when it is time to enter its characteristics.

Example:

CHOOSE ONE: SAMPLES/SPECIES/HELP

>

SAMPLES

SAMPLE # 1

CHOOSE ONE: SAMPLE DATA/*/HELP

>

ORYZA SATIVA

CALIFORNIA

YOLO COUNTY EXPERIMENTAL RESEACH STATION

20 DECEMBER 1983

*

CHOOSE ONE: PROC/AID/CHAR/HELP

>

PROC

ENTER ALL VALUES.

>

070022.0151011.5 121820400.95062.9 0100101110010101100100

DO YOU HAVE ANOTHER SAMPLE? : Y/N

>

ENTERING THE SAMPLE CHARACTERISTICS (quick method)

The list CHAR gives the order which must be followed to enter the characteristics of the sample. CHAR also gives the format.

This order and format MUST be followed to enter the sample characteristics.

To see this format on-line type CHAR. Preferably see the annexes at the end of this manual.

Measurements

The list "CHAR" gives the format as 2 digits separated by a period: 4.0; 2.1; etc.

The first digit indicates how many numerals must be entered before the period.

The second digit indicates the number of decimals to be used.

For example: LGT = 4.0; the body length must be entered as a four-digit number with no decimals. A mean value of 753.8 μ m is entered as 0754, not 754, not 754.0, not 753.8.

STY = 2.1; the stylet length must be entered as a two-digit number plus a decimal. A mean value of 25 μ m is entered as 25.0, not 25.

Do not leave spaces between the successive characters.

Enter only mean values.

Enter missing values by pressing the space bar as many times as the character has digits, plus the period. Press bar 4 times for 4.0; 4 times for 2.1; 3 times for 1.1; etc.

Morphological characters

Every state is coded 0 (state absent, nonvisible, etc.) or 1 (state present, visible, etc.).

The list CHAR gives the number of digits used to code each morphological character.

Two-state nonvariable characters are entered with a single digit: 0 or 1.

Two- and multi-state variable characters are entered with two or more digits, one digit per state. Each state is coded separately 0 or 1. When two or several states of a character are observed in a sample, every state observed is coded 1.

Enter missing characters by pressing the space bar as many times as the character has digits.

ENTERING THE SAMPLE CHARACTERISTICS (slow method)

The above method for entering the sample characteristics is quick, but it is easy to make mistakes.

Ask AID for a slower, safer method.

By entering the AID option at this state, you can:

- obtain the list of the characters used in the genus datafile, with their format, type CHAR
- obtain on-line some informations on how to record these characters, type INFO
- quit the program NEMAID if you are not yet ready to enter your sample characteristics, type END
- when you are ready, type PROC

NEMAID will ask you to enter each character one by one. It will give you an example of the format you must follow.

Missing values must be entered by pressing [Return] once.

Example:

CHOOSE ONE: PROC/AID/HELP

>

AID

CHOOSE ONE: CHAR/INFO/END/PROC/HELP

>

PROC

ENTER EACH CHARACTER ON SAME FORMAT AS GIVING IN EXAMPLE.

ENTER BODY LENGTH AS IN 0500/INFO

>

0750

ENTER STYLET LENGTH AS IN 50.0/INFO

>

22.5

ENTER POSITION DGO AS IN 50/INFO

>

[RETURN]

ENTER POSITION EXCRET. PORE AS IN 500/INFO

>

097

ENTER BODY ANNULE WIDTH AS IN 5.0, 2.1, ETC/INFO

>

[RETURN]

(etc., the program ask you to enter the values of all the characters in your sample.
remember: missing values, press bar an equal number of times)

ENTER TAIL SHAPE AS IN 0001, 1000,0110, ETC/INFO

>

0011

ENTER GENITAL BRANCH AS IN 001, 100, 110, ETC/INFO

>

100

DO YOU HAVE ANOTHER SAMPLE? : Y/N

>

MULTIPLE SAMPLES

NEMAID offers you the possibility to identify several samples simultaneously.

The descriptions of all the samples will be added temporarily to the genus datafile. When your first sample is compared to the species in the genus datafile, it is also compared to your other samples. If they are similar to your first sample, they will appear in the final results.

This feature may be helpful if you suspect a mixture of species in a population. Enter as a separate sample each subsample suspected to be of specific status. The similarity of the subsamples will be evaluated in the final results.

When you have several samples [answer Y (yes) to the question], the program goes back to "Record of sample data", page 18.

You may enter as many samples as you want.

Example:

```
*****
DO YOU HAVE ANOTHER SAMPLE? : Y/N
>
Y

      SAMPLE # 2

      CHOOSE ONE:  SAMPLE DATA/* /HELP
>
*****
```

CHOICE OF 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 datafile
- correction factor: maximum difference in measurements that can be explained by the intraspecific variability. A difference in measurement between your sample on a species will be considered as indicating a specific dissimilarity only when it exceeds the correction factor.

NEMAID takes all characters as equal to each other. The assigned character weights is equal to 1. Only missing characters have a weight equal to 0, which neutralize them.

You may see the parameters assigned by NEMAID to the measurement by typing N (for no) then CHAR.

If then you decide to accept the assigned parameters, and if you do not want to weight the characters, type PROC to proceed with the program without change.

If you want to change any parameter or attribute character weights, type WEIGHT, CORR, or RANGE accordingly.

Example:

```
*****
DO YOU ACCEPT THE PARAMETERS? Y/N/INFO
>
N
CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
>
```

WEIGHT

```
*****
```

WEIGHTS

You can attribute different weights to the various characters. Weights must be taken from 0 (character neutralized) to 1 (character taken at full value).

Weights must be entered according to the format below:

0.0	0.6
0.1	0.7
0.2	0.8
0.3	0.9
0.4	1.0
0.5	

If you do not attribute weights, NEMAID utilizes all characters at the same value (all weights equal to 1) except missing characters that are neutralized ($w = 0$)

You can give weights to all the characters (type ALL) or to only one or a few characters (type FEW).

If you weight all the characters, you can enter all the weights without help. Type PROC then, when the program asks you to enter the weights, enter the weights of all characters, without spaces between the successive weights.

If you prefer a slower, safer method, type AID. The program will give you the names of the successive characters to be weighted.

If you want to weight only one or a few characters, the program will ask you to give the code name of the first character to be weighted. If you do not know the code name of this character, type CHAR to see the list of characters and their code names.

Enter the code names of the successive characters. After you have entered the last weight, type PROC to go back to the previous question. You can now change the other parameters, type: CORRECT or RANGE;

or, if you have no more modifications to enter, type PROC to go to the next question.

Example 1:

```
*****
DO YOU ACCEPT PARAMETERS? : Y/N/INFO
>
N
CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
>
WEIGHT
CHOOSE ONE: ALL/FEW/HELP
>
ALL
CHOOSE ONE: PROC/AID/INFO/HELP
>
PROC
ENTER ALL WEIGHTS:
>
0.51.00.00.10.10.30.30.90.50.10.30.91.00.70.70.50.70.50.90.70.30.20.51.0
CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP /
>
*****
```

Example 2:

```
*****
CHOOSE ONE: ALL/FEW/HELP
>
FEW
ENTER CHARACTER CODE NAME/SEE/PROC/HELP
>
DGO
DORSAL GLAND OPENING WEIGHT = ?
>
0.0
ENTER ANOTHER CHARACTER CODE NAME/SEE/PROC/HELP
>
KBS
KNOBS SHAPE WEIGHT = ?
>
0.2
ENTER ANOTHER CHARACTER CODE NAME/SEE/PROC/HELP
>
PROC
CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
>
*****
```

CORRECTION FACTOR

See definition of correction factors on page 23.

Correction factors were attributed by the author of the genus datafile.

The values attributed by the author to the correction factors were explained in a published article. Type SEE to see these values. If you accept these values, type PROC to return to the last question.

If you do not agree with the author, NEMAID allows you to use your own set of correction factors. Type CHANGE.

Use the same format as used in the program for the author's values of the correction factors. You can change all the correction factors (type ALL) or only one or a few factors (type FEW).

If you change all the correction factors, you can enter the new factors without help. Type PROC the, when the program asks you to enter the correction factors, enter the factors of all the measurements in one line, without spaces between the successive factors.

If you prefer the slower, safer method, type AID. The program will give you the names of the successive factors to enter, and the format you must follow.

If you change only one or a few factors, the program will ask you to give the code name of the first character whose correction factor you want to change. If you do not know the code name of this character, type CHAR to see the list of the measurements and their code names.

After you have entered your last change, type PROC to go back to the previous question. You can then change the other parameters by typing RANGE or WEIGHT,

or, if you have no more modifications to enter, type PROC to go to the next question.

Example 1:

```
*****
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  >
  CORRECT
  CHOOSE ONE:  SEE/CHANGE/PROC/HELP
  >
  CHANGE
  CHOOSE ONE:  ALL/FEW/HELP
  >
  ALL
  CHOOSE ONE:  PROC/AID/INFO/HELP
  >
  PROC
  OLD CORRECTION FACTORS:  015003.0050101.003130608150.5040203
  ENTER NEW CORRECTION FACTORS:
  >
  010002.5050101.003130709150.9040103
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  *****
```

Example 2:

```
*****
  CHOOSE ONE:  PROC/AID/INFO/HELP
  >
  AID
  BODY LENGTH          OLD CORRECTION FACTOR = 0150          NEW FACTOR = ?
  >
  0100
  STYLET LENGTH        OLD CORRECTION FACTOR = 03.0          NEW FACTOR = ?
  >
  02.5
  (etc., the program asks new correction factors for all the measurements)
  *****
```

Example 3:

```
*****
  CHOOSE ONE:  ALL/FEW/HELP
  >
  FEW
  ENTER:  CHARACTER CODE NAME/CHAR/PROC/HELP
  >
  STY
  STYLET LENGTH        OLD CORRECTION FACTOR =  3.0          NEW FACTOR = ?
  >
  2.0
  ENTER:  ANOTHER CHARACTER CODE NAME/CHAR/PROC/HELP
  >
  PROC
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  >
  *****
```

RANGES

See definition of the range on page 23.

The range is an objective value, and it should be accepted by most users as entered by the author of the genus datafile. Type SEE to see the range values. If you accept these values, type PROC to return to the last question.

The range of a measurement can be changed if your sample value for this measurement is over the limits previously recognized for the genus.

Calculate a new range by using the sample value as the lower or the higher specific limit.

The range should also be changed when you want to compare your sample only to one of the synonym genus included in the genus datafile.

Substitute the range in the genus you want to use to the range of the broader genus used by the author.

Type CHANGE.

You must use the same format as used in the program for the author's values of the ranges.

You can change all the ranges (type ALL) or only one or a few ranges (type FEW).

If you change all the ranges, you can enter the new ranges without help. Type PROC then, when the program asks you to enter the ranges, enter the ranges of all the measurements in one line, without spaces between the successive ranges.

If you prefer the slower, safer method, type AID. The program will give you the names of the successive ranges to enter, and the format you must follow.

If you change only one or a few ranges, the program will ask you to give the code name of the first character whose range you want to change. If you do not know the code name of this character, type CHAR to see the list of the measurements and their code names. After you have entered your last change, type PROC to go back to the previous question. You can then change the other parameters, type WEIGHT or CORRECT;

or, if you have no more modifications to enter, type PROC to go to the next question.

Example 1:

```
*****
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  >
  RANGE
  CHOOSE ONE:  SEE/CHANGE/PROC/HELP
  >
  CHANGE
  CHOOSE ONE:  ALL/FEW/HELP
  >
  ALL
  CHOOSE ONE:  PROC/AID/INFO/HELP
  >
  PROC
  OLD RANGES:  083022.0100502.522192424711.7124020
  ENTER NEW RANGES:
  >
  080022.0100502.518192421711.5121817
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  >
  *****
```

Example 2:

```
*****
  CHOOSE ONE:  PROC/AID/INFO/HELP
  >
  AID
  BODY LENGTH                OLD RANGE = 0830                NEW RANGE = ?
  >
  0800
  (etc., the program asks new range for all the measurements)
  *****
```

Example 3:

```
*****
  CHOOSE ONE:  ALL/FEW/HELP
  >
  FEW
  ENTER:  CHARACTER CODE NAME/SEE/PROC/HELP
  >
  LGT
  BODY LENGTH                OLD RANGE = 0830                NEW RANGE = ?
  >
  0800
  ENTER:  ANOTHER CHARACTER CODE NAME/SEE/PROC/HELP
  >
  TLG
  TAIL LENGTH                OLD RANGE = 22                NEW RANGE = ?
  >
  18
  ENTER ANOTHER CHARACTER CODE NAME/SEE/PROC/HELP
  >
  PROC
  CHOOSE ONE:  PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP
  >
  *****
```

CHECKING THE DATA

When all the values for your sample(s), and all the changes for the parameters, have been entered, NEMAID presents you with a recapitulating table so you can check the accuracy of the data.

After a first display of the data, you may:

- ask to obtain the same data again, type AGAIN
- decide to change some data (either sample character values or parameters), type CHANGE
- when you are satisfied with the data for the first sample, type PROC to see the data of the second sample, or to go to the next question when all the samples have been checked

Note that the same set of parameters must be used for all the samples entered. If you change parameters while checking the second sample, the new parameter value will be used for the first sample, and for all the other samples.

CHANGING THE DATA

If you decide to change the data, type CHANGE at the previous question. The program will ask you if you want to change character values in your sample (type SAMPLE), or parameters (type RANGE, WEIGHT, or CORRECT accordingly).

In any case, you will then be asked if you want to change ALL values or only a FEW.

If you want to change all values, you can enter the new values without help. Type PROC then, when the program asks you to enter the new values, enter the values in one line, without spaces between the successive values.

If you prefer a slower, safer method, type AID. The program will give you the names of the successive values to enter, and the format you must follow.

If you change only one or a few values, the program will ask you to give the code name of the first character you want to change. If you do not know this code name, type SEE to see the list of characters and their code names.

After you have entered your last change, type PROC. You can then decide to change another set of values: sample characters (SAMPLE) or parameters (RANGE, WEIGHT, CORRECT).

When all the corrections have been made and you are satisfied with the sample values, type PROC to go to the next question.

Example:

CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP

>

PROC

<u>CHARACTERS</u>	<u>CODE</u>	<u>RANGE</u>	<u>WEIGHT</u>	<u>CORR</u>	<u>SAMPLE #</u>
	<u>NAME</u>				<u>1</u>
BODY LENGTH	: LGT	830.0	1.0	150.0	0700
STYLET LENGTH	: STY	22.0	1.0	3.0	22.0
POSITION DGO	: DGO	10.0	1.0	5.0	
POSITION EXCRET. PORE	: EXPO	50.0	1.0		
BODY ANNULE WIDTH					

(etc., the program gives the value of all the characters)

					010
	: TAIL		1.0		1100
GENITAL BRANCH	: GENB		1.0		100

CHOOSE ONE: INFO/AGAIN/CHANGE/PROC/HELP

>

CHANGE

CHOOSE ONE: RANGE/WEIGHT/CORREC/PROC/HELP

>

RANGE

CHOOSE ONE: ALL/FEW/HELP

>

FEW

ENTER CHARACTER CODE NAME/SEE/PROC/HELP

>

BAW

BODY ANNULE WIDTH RANGE = 2.5 NEW RANGE = ?

>

2.0

ENTER: ANOTHER CHARACTER CODE NAME/CHAR/PROC/HELP

>

PROC

CHOOSE ONE: RANGE/WEIGHT/CORREC/PROC/HELP

>

PROC

CHOOSE ONE: INFO/AGAIN/CHANGE/PROC/HELP

>

PROC

SELECTION OF SPECIES; GENUS

You must decide against which set of species you want to compare your sample(s):

- all the descriptions in the genus datafile (see page 12), plus eventually your other samples. Type ALL
- only the original and composite descriptions (see page 12), plus eventually your other samples, type ORIG
- a set of species from the genus datafile, selected by one or several morphological characters. Your other samples will be added to this set of species if they agree with the characters you have selected. Type CHAR

When you use the option CHAR, the program will ask you to enter the code name of the first character you want to use, then the coded values (0,1: absent, present) of the successive states of this character.

After you have typed CHAR, if you decide not to use this option, type BACK to return to the last question.

You can obtain the list of available morphological character, type LIST.

You can recapitulate the characters you have used so far, type SUM.

*

The option CHAR permits you to compare your sample to only the species in one of the genera included by the author as a synonym genus.

For example, to select the species in Rotylenchoides treated as a synonym of Helicotylenchus, use the option CHAR, with the character genital branch, GENB, equal to 001 or 011 (depending if you accept Siddiqi & Husain's or Sher's definition of Rotylenchoides).

- The option PREVIOUS cannot be used during the first run of the program. See page 38 for use of this option.

Example:

CHOOSE ONE: INFO/AGAIN/CHANGE/PROC/HELP

>

PROC

TO WHICH SET OF SPECIES DO YOU WANT TO COMPARE YOUR SAMPLE(S)?

CHOOSE ONE: ALL/ORIG/CHAR/PREV/INFO/HELP

>

CHAR

ENTER ONE: CHARACTER CODE NAME/LIST/BACK/HELP

>

MALE

MALE: ENTER 0 (ABSENT) OR 1 (PRESENT):

>

0

CHOOSE ONE: ANOTHER CODE NAME/SUM/PROC/LIST/HELP

>

TAIL

TAIL HEMISPHERICAL : ENTER 0 (ABSENT) OR 1 (PRESENT):

>

1

TAIL ROUNDED BENT : ENTER 0 (ABSENT) OR 1 (PRESENT):

>

1

TAIL ANGLED : ENTER 0 (ABSENT) OR 1 (PRESENT):

>

0

TAIL WITH PROJECTION : ENTER 0 (ABSENT) OR 1 (PRESENT):

>

0

CHOOSE ONE: ANOTHER CODE NAME/SUM/PROC/LIST/HELP

>

SUM

CHARACTERS USED SO FAR:

<u>MORPHOLOGICAL CHARACTERS</u>	<u>CODE NAME</u>	<u>VALUE</u>
PRESENCE MALE	MALE	0
TAIL SHAPE	TAIL	1100

CHOOSE ONE: ANOTHER CODE NAME/SUM/PROC/LIST/HELP

>

PROC

OUTPUT

NEMAID calculates the coefficients of similarity of Gower S.G. between your sample and all the selected species.

The species with S.G. > 0.7 are retained and arranged by descending values.

The output consists in:

- the sample data (see page 18)
- the code name of the species (see page 12)
- the actual name of the species
- the coefficient of similarity of this species with your sample
- the number of characters used to calculate the S.G. (characters with missing values, and characters weighted w=0 are not used)
- the number of characters in agreement (character score > (.7) between your sample and the species

The output is given one screen frame at a time.

After each frame you may continue to the next frame, punch [RETURN]; or quit the listing and go to the next question, type Q.

You can then:

- see the same results again, type RESULTS
- examine in detail the comparison of a particular species type the code name of this species
- run the program again with the same sample but with a different set of characters/parameters (see page 38), type SECOND
- proceed to the next question, type PROC

Example:

TO WHICH SET OF SPECIES DO YOU WANT TO COMPARE YOUR SAMPLE(S)?

CHOOSE ONE: ALL/ORIG/CHAR/PREV/INFO/HELP

>

ALL

CALCULATIONS ARE NOW BEING MADE, PLEASE WAIT ...

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)

SAMPLE #1: ORYZA SATIVA
CALIFORNIA
YOLO COUNTY EXPERIMENTAL RESEARCH STATION
20 DECEMBER 1983
COMPARED TO: SPECIES SELECTED BY MALE 0
TAIL 1100

CODE NAMES	SPECIES NAMES	COEFFICIENTS OF SIMILARITY	NUMBER OF CHARACTERS USED	NUMBER OF AGREEMENTS
B100	H. CRENATUS	1.00	14	14
GFO0	H. LEUCERNIS	1.00	11	11
CT00	H. LOBUS	1.00	18	18
FF00	H. OLAAE	1.00	10	10
DT00	H. PHALERUS	1.00	23	23
DY00	H. PSEUDOROBUSTUS	1.00	23	23
AQ00	H. BRASSICAE	.98	6	6
DY99	H. PSEUDOROBUSTUS	.98	23	22
DZ01	H. PTERACERCUS	.98	22	21
AD00	H. AGRICOLA	.97	20	19
GW00	H. AMPLIUS	.97	22	21

[HIT RETURN TO CONTINUE, OR "Q" TO STOP]

>

Q

CHOOSE ONE: SPECIES CODE NAME/RESULTS/SECOND/PROC/LIST/HELP

>

END OF PROGRAM

After the results have been presented, you can examine how the program compared your sample to a particular species.

Enter the code name of the species you want to see (this code name is given in the main output, or ask LIST). The program gives you the character values in your sample and in the selected species, the score and weight of each character, and the computation of the coefficient of similarity de bower S.G.

You can examine as many species as you want.

When you have seen enough species, you can decide to run the program again with the same sample, but with a different set of characters and/or parameters (see page 38) type SECOND

Or you can proceed to the next point in the program (type PROC)

The program will then present the results of the identification of your second sample, if any. After the last sample has been processed NEMAID gives you the possibility to enter new samples or quit the program.

Example:

CHOOSE ONE: SPECIES CODE NAME/RESULTS/SECOND/PROC/LIST/HELP

>

CROO

CHARACTERS	SAMPLE	H.LABIODISCINUS CROO	SCORE	WEIGHT	SW
BODY LENGTH	0700	0565	1.00	1.0	1.00
STYLET LENGTH	22.0	25.0	1.00	1.0	1.00
POSITION DGO	15				
POSITION EXCRET. PORE	101				

(etc., the program compares each successive couplet of characters.)

LIP ANNULES	001				
KNOBS SHAPE	010	110	.50	1.0	.50
TAIL SHAPE	1100	0110	.33	1.0	.33
GENITAL BRANCH	100	100	1.00	1.0	1.00

TOTAL 17.00 15.82

SG = 15.82/17.00

= .93

CHOOSE ONE: SPECIES CODE NAME/RESULTS/SECOND/PROC/LIST/HELP

>

PROC

THE PROGRAM NEMAID CANNOT HELP YOU ANY MORE. PLEASE SEARCH THE LITERATURE FOR DESCRIPTION AND REDESCRIPTIONS OF THE PROPOSED SPECIES BEFORE FINAL IDENTIFICATION.

AT THIS POINT, YOU MAY EITHER

- ENTER MORE SAMPLES OR CHECK A SPECIES, TYPE "AGAIN"
- OR TYPE "BYE" TO EXIT THE PROGRAM.

>

BYE

THANK YOU FOR USING NEMAID

>

OFF

OFF AT 13:27 12/13/83 EST

CONNECT MINS = 5

COMPUTE SECS = 6/5

301 363 DISCONNECTED

(hang up your phone to complete the disconnect)

SUCCESSIVE RUNS OF THE PROGRAM; option PREVIOUS

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 S.G. > 0.7).
3. You then decide to run the program again. Type SECOND after the results of the first run have been displayed. The program will go back to the choice of parameters (p. 23).
4. You will have to choose less restrictive conditions: a larger set of characters, different character weights.
5. When the program asks you "To which set of species do you want to compare your sample(s)?", use the option PREVIOUS (p. 32).

Your sample is then compared only to the species selected by the first run.

You may decide to run the program a third time, using still another set of conditions. The option PREVIOUS will still compare your sample to the set of species selected during the first run of the program, not during the second.

If during the second, third, etc. run of the program, you use one of the other options (ALL, ORIG, CHAR) the comparison will be made with the set of species selected, drawn from the main genus datafile, not from the temporary set of species selected during the first run.

Example:

CHOOSE ONE: SPECIES CODE NAME/RESULTS/SECOND/PROC/LIST/HELP

>

SECOND

DO YOU ACCEPT THE PARAMETERS? Y/N/INFO

>

N

CHOOSE ONE: PROC/INFO/CHAR/WEIGHT/CORRECT/RANGE/HELP

>

(here you must change weights and/or correction factors.

The program then lets you check the new data, then asks:)

TO WHICH SET OF SPECIES DO YOU WANT TO COMPARE YOUR SAMPLE(S)?

CHOOSE ONE: ALL/ORIG/CHAR/PREV/INFO/HELP

>

PREV

Annex 1

AVAILABILITY OF NEMAID

NEMAID is deposited at ITT-DIALCOM, Inc. It can be accessed by phone via a public data network (TELENET, TYMNET, DATAPAC, IPSS, etc.), from many U.S. cities and from many foreign countries.

Prospective users in the U.S. must open an account with ITT-DIALCOM, Inc., 600 Maryland Avenue SW, Suite 455, Washington, D.C. 20024, (202) 488-0550. There is no initial fee and no monthly minimum fee. Users are charged (about \$20 per hour) only for the time they access the system.

Users in other countries must contact their national administration. Subscription and access fees vary for each country.

Please contact Mr. Tony Kemper at ITT-DIALCOM, and mention that you intend to use NEMAID.

To access the programs, only a terminal is needed with the following transmission characteristics:

- Communications protocol: Asynchronous TTY
- Code: ASCII, EBCD, CORRESPONDENCE (SELECTRIC)
- Speed: 110 to 1200 bps
- Interface: RS-232C
- Modem: For 110-300 bps, BELL 103, 113, 212A, VADIC 3400, or compatible modems
For 1200 bps, BELL 212A, VADIC 3400, or compatible FULL DUPLEX modems

In addition to the fee charged by the public data networks, the California Department of Food and Agriculture requires the users of NEMAS and NEMAID to pay a yearly subscription fee of 30 U.S. dollars to contribute to the storage cost of the two programs at DIALCOM.

Prospective users should write to the following address after having made the necessary arrangements with a public data network:

Renaud Fortuner
Nematology Laboratory - Room 340
California Department of Food and Agriculture
1220 N Street
Sacramento, California 95814
U.S.A.

NOTE: Access to the program is free until March 1984. Just send me a note to receive the current passwords and the user's guides. However, you will have to pay for using the public data networks.

Annex 2

LIST OF THE GENERA INCLUDED IN NEMAID

<u>GENUS</u>	<u>SYNONYM GENERA</u>	<u>AUTHOR</u>
Helicotylenchus	Rotylenchoides	Fortuner, 1983

No other genus for the moment

Annex 3

GENUS HELICOTYLENCHUS
INCLUDING SYNONYM GENUS ROTYLENCHOIDES.

Genus datafile prepared by R. Fortuner, December 1983.

The characters used in the genus datafile have been evaluated in:

Fortuner, R. - Morphometrical variability in Helicotylenchus Steiner, 1945. 6: Value of the characters used for specific identification. To be published in Revue de Nématologie 7(3).

List of characters used:

Code	Character	Format (with examples)	Range	Correction Factor
LGT	Body length	4 digits: 0756; 1182;	0830	0150
STY	Stylet length	3 digits, 1 decimal: 19.0; 25.6	22.0	03.0
DGO	Distance stylet - dorsal gland opening	2 digits: 08; 12;	10	05
EXPO	Distance anterior end - excretory pore	3 digits: 097; 112;	050	010
BAW	Width of one body annule	2 digits, 1 decimal: 0.9, 1.0, 1.6	2.5	1.0
TLG	Tail length	2 digits: 09; 15;	22	03
TAN	Ventral tail annule	2 digits: 05; 25;	19	13
PHAS	Phasmids, in annules from anus	anus level: 20 5 ann. anterior: 25 5 ann. posterior: 15	24	6
RAA	Ratio a (LGT/body diameter)	2 digits: 27;	24	08
RAC	Ratio c (LGT/TLG)	2 digits: 38;	71	15
RCC	Ratio c' (TLG/tail diameter)	2 digits, 1 decimal: 0.9; 1.0; 1.6;	1.7	0.5
RAM	Ratio m (STY/cone)	2 digits: 47;	12	04
RAV	Ratio v (head-vulva/LGT)	3 digits, 1 decimal: 59.6; 62.0;	40.0	02.0
SPI	Spicule length	2 digits: 23;	20	03
MALE	presence of males	2 states, 1 digit: males (or sperms) present/absent = 1/0		
DISC	Labial disc	2 states, 1 digit: disc visible/not visible in lateral view = 1/0		
CAN	Canals or fasciculi	2 states, 1 digit: canals present/absent = 1/0		

Code	Character	Format	Range	Correction Factor
HAB	Habitus	2 states, 2 digits:	- habitus open circle to straight, present/absent = 1/0 - habitus closed circle to spiral, present/abs = 1/0	
LIP	Lip shape	2 states, 2 digits:	- lip anteriorly rounded, pres/abs = 1/0 - lip anteriorly flattened, pres/abs = 1/0	
INC	Fusion of incisures	2 states, 2 digits:	- fusion y or v-shaped, pres/abs = 1/0 - fusion u, /u, m-shaped, pres/abs = 1/0	
LANN	Lip annulation	3 states, 3 digits:	- few annules (2,3), pres/abs = 1/0 - many annules (6 and more), pres/abs = 1/0	
KBS	Stylet knobs	3 states, 3 digits:	- indented, pres/abs = 1/0 - flattened to rounded, pres/abs = 1/0 - sloping backwards, pres/abs = 1/0	
TAIL	Tail shape	4 states, 4 digits:	- hemispherical, symmetrical, pres/abs = 1/0 - ventrally bent with rounded end, pres/abs = 1/0 - D and V side joining at an angle, pres/abs = 1/0 - with projection, or indented, pres/abs = 1/0	
GENB	Female posterior-genital branch	3 states, 3 digits:	- functional, equal to anterior branch, pres/abs = 1/0 - degenerated but present as a row of cells, pres/abs = 1/0 - reduced to a PUS, pres/abs = 1/0	

Selection of group of species.

The genus datafile Helicotylenchus includes the species of the synonym genus Rotylenchoides.

To use the entire datafile (Helicotylenchus s.p.) ask for ALL the species (or only the ORIGINAL descriptions).

To use only Helicotylenchus s.str., not including Rotylenchoides spp., ask to select a group of species according to a CHARACTER (see page 32). This character is female genital branch GENB = 100.

You can also select only the species in Rotylenchoides

- according to the definition of Siddiqi & Husain, 1964: (only species with posterior branch reduced to a PUS); use female genital branch GENB=001
- according to the definition of Sher, 1965: species with PUS and/or with posterior branch degenerated: use female genital branch GENB=011