User's guide to Intkey: a program for interactive identification and information retrieval

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M.J. Dallwitz, T.A. Paine and E.J. Zurcher

Abstract

Intkey is an interactive program for identifying a specimen by comparing it with stored descriptions. The program can also be used to interrogate the stored data.

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Introduction

Introduction

Intkey is an interactive program for identifying a specimen by comparing it with stored descriptions. The program can also be used to interrogate the stored data.

Intkey has two modes of operation: Normal and Advanced. We recommend that you start with Normal mode, even if you know how to use conventional identification keys.

In Normal mode, the program is operated via the toolbars. Most of the menu system, many dialog-box buttons, and the command line are disabled.

In Advanced mode, which is set by the 'Advanced Mode' option of the 'File' menu, the program can be operated via the toolbars, the menu system, or the command line. Before using this mode, you should become thoroughly familiar with Normal mode, and read the 'Introduction' which becomes available upon entering Advanced mode.

To display the Help for an active toolbar button (one that is not grey), first press the '?' button at the right of the main toolbar (which is just below the menu bar), then click on the button for which help is required. Basic instructions for using the program for identification are in the help for the 'Restart identification' button. The author of a data set may also have supplied other help accessible via the leftmost button of the main toolbar.

This documentation is intended for users of Advanced mode. It is not available in Normal mode, for which the Help provided with the toolbar buttons should be adequate.

Identification

To identify a specimen:

1. In the 'Characters' toolbar (top-left pane), press the 'Restart identification' button.
2. The top-left pane shows a list of characters. Normally, the pane is headed 'Best Characters' and the best characters are at the top (if not, you can restore this setting by pressing the 'Best order' button). Click on a character.
3. The program displays a list of character states, or a box for entering values such as lengths. If there is an illustration for the character, it will be normally be displayed automatically (if not, press the 'Images' button). Most characters have explanatory notes, which may be viewed by pressing the 'Notes' button. Click on the state, or enter the value, that applies to your specimen, and press 'OK'. *If you are not sure, do not guess a single state or value*. Instead, click on more than one state, enter a range of values, or press 'Cancel' and try another character. To deselect a previously selected state, click on it again.
4. The 'Taxa Remaining' (top-right) pane shows the taxa that match the information that you have entered. The 'Taxa Eliminated' (bottom-right) pane shows the taxa that do not match, with the number of mismatches in parentheses. Repeat from step 2 until 'Identification complete' or some other message is displayed in the top-left pane. A 'Help' button is also displayed; press this to obtain information on how to proceed (for example, how to confirm the identification).

If, at any stage, you think you have made a mistake and want to correct it, click on the appropriate character in the 'Used Characters' (bottom-left) pane. The program again displays the box for selecting character states or entering values, and you can change the information you previously entered. You can remove the character from the identification by clearing all the information.

Checking an Identification

You should check your identification against the information that can be obtained by pressing the 'Information' button, in the 'Taxa' toolbar (top-right pane). The information usually includes full and

diagnostic descriptions. A diagnostic description aims to distinguish the taxon from all the others, using only characters that have not already been used in the identification. Illustrations may also be available.

If the descriptions or illustrations are inconsistent with the tentative identification, you can increase the 'error tolerance', by means of the 'Error tolerance' button in the 'Characters' toolbar (in the top-left pane). This allows a greater number of mismatches before taxa are eliminated, so some taxa that were previously in the 'Eliminated Taxa' pane move to the 'Remaining Taxa' pane. The identification process can then be continued exactly as before, until only a single taxon remains.

Increasing the error tolerance may also be used directly to confirm or increase your confidence in a tentative identification. Continuing the identification after increasing the error tolerance should again lead to a single remaining taxon. This may or may not be the same as the original remaining taxon, but, in either case, it will be more strongly separated from the eliminated taxa, and so you can have more confidence in the result. The advantage of this method over using a diagnostic description is that you have full control over the extra characters used.

In Advanced mode (see 'Help' menu), an increased error tolerance can be used in conjunction with the 'Separate a given taxon' button, which orders the available characters according to how well they separate a given taxon from the other remaining taxa. This can lead to a quicker confirmation or rejection of the tentative identification. If the extra information that you enter is inconsistent with the original identification, you should switch back to using the 'Best' order.

Not Enough Characters to Complete an Identification

In some circumstances, you may be unable to use any of the available characters (for example, if your specimen is incomplete), or the program may report that there are no characters that separate the remaining taxa.

If you have used the 'Use subsets of the characters' button to exclude some characters, you could try using the button again to include all the characters. Other possibilities are as follows.

If you have used the 'Error tolerance' button to allow mismatches between the specimen and the remaining taxa, you could try reviewing the information you have entered, which is displayed in the 'Used Characters' (bottom-left) pane. If you can see an obvious error, click on the relevant character. The program displays the box for selecting character states or entering values, and you can change the information you previously entered.

(1) The specimen information that you have entered may be too broad. You can find out which characters separate the remaining taxa by selecting all the remaining taxa, and pressing the 'Differences' button in the 'Taxa' toolbar. These differences may include characters that you have already used. If so, you may be able to separate the taxa by selecting fewer states or entering smaller ranges for those characters. To do this, click on the required character in the 'Used Characters' (bottom-left) pane. The program displays the box for selecting character states or entering values, and you can change the information you previously entered.

(2) The author may have set 'reliabilities' of zero for some characters that were considered to be generally inappropriate for use in identification (for example, number of chromosomes). This prevents the characters appearing in the 'Best Characters' pane. You can find out whether such characters separate the remaining taxa by selecting all the remaining taxa, and pressing the 'Differences' button in the 'Taxa' toolbar. If a useful character is found, you can access it by first pressing the 'Natural order' button in the 'Characters' toolbar.

(3) It may be that the taxa really cannot be separated by the comparative information in the database. Information available via the 'Information' button in the 'Taxa' toolbar, may help to distinguish them. The information may include descriptions, illustrations, and links to Web pages. The descriptions may contain supplementary free-text information and/or references, in addition to the comparative information from the database.

Selecting Taxa

The taxa on which an operation is to be carried out (for example, displaying the differences between taxa) may be selected in the 'Taxa' (right-hand) panes of the main window before specifying the operation. In Advanced mode, other selection methods are also available (see 'Dialog Boxes and List Boxes').

The 'Remaining Taxa' and 'Eliminated Taxa' lists behave as a single list when taxa are being selected. Clicking on a taxon selects that taxon and deselects all others. Multiple taxa can be selected in the usual ways, that is, by holding down the Shift and/or Ctrl keys while clicking.

The 'Find text in taxon names' button in the 'Taxa' toolbar allows you to search for text in the taxon names in the 'Taxa' panes. The authorities are also searched, although they are not normally displayed in these panes. The names found are selected, allowing them to be used in subsequent operations (for example, in requesting information about the taxa). By default, all the matching names are selected; 'Next' and 'Previous' buttons allow all the selections to be seen, if they cannot all be displayed together. Clicking the radio button 'Select one' cause the names to be selected one by one; the 'Next' and 'Previous' buttons then move the selection to the next or previous matching name.

By default, only the names in the 'Remaining Taxa' (top-right) pane) are searched. Check boxes allow the search to be extended to the 'Eliminated Taxa' (bottom-right) pane and to the synonyms (if available).

Information retrieval

The 'Remaining Taxa' and 'Eliminated Taxa' lists behave as a single list when taxa are being selected. Clicking on a taxon selects that taxon and deselects all others. Multiple taxa can be selected in the usual ways, that is, by holding down the Shift and/or Ctrl keys while clicking.

The 'Information' button in the 'Taxa' toolbar (top-right pane) provides access to descriptions and illustrations of taxa. Before pressing the button, you may select the required taxon or taxa in either or both of the 'Taxa' panes; if no taxa are selected, the 'Remaining' taxa are used.

When the button is pressed, the 'Information' dialog box is displayed. This initially shows the name of the first (or only) selected taxon, and lists the descriptions and/or images that are available for it. Any or all of these can be selected and displayed. The information for the other selected taxa (if any) can be shown by navigating the list of taxa by means of 'Back' and 'Forward' buttons, or by selecting from a drop-down list. A completely new selection of taxa can be made by means of the 'Select new taxa' button.

The information usually includes a diagnostic description, which aims to distinguish the taxon from all the others in at least a certain number of characters. This number is called the 'diagnostic level'. Intkey gives it a default value of 1, but a larger value may have been set by the author of a particular dataset. The diagnostic description includes messages showing the diagnostic levels that were actually attained. If an identification is in progress, the diagnostic description uses only characters that have not already been used in the identification.

Images are scaled to fit the available area; to turn scaling off or on, click 'Scaled' in the image's 'Window' menu. To view an image or description at the maximum possible size, press its 'maximize' button.

The 'Differences between taxa' button in the 'Taxa' toolbar (top-right pane) displays the differences between selected taxa. Two or more taxa must be selected in either or both of the 'Taxa' panes before pressing the button. Differences in free-text characters are not shown, and unrecorded or inapplicable attributes are not treated as being different from recorded attributes.

Taxa having a specified set of attributes can be found by using the ordinary identification procedure to specify the attributes. The natural order of the character list (obtained by pressing the 'Natural order' button in the 'Characters' toolbar) should be used. The 'Match' setting used for identification is

usually inappropriate, because taxa for which the specified characters are unrecorded or inapplicable are not eliminated. The setting can be changed by means of the 'Set match' button, which is in the 'Characters' toolbar in Advanced mode. For details, see the help for the 'Set Match' command, which is available via the main 'Help' menu, or by pressing the 'Help' button in the 'Set Match' dialog box.

To find the taxa for which a given character is unrecorded, set 'Match' to 'Overlap Inapplicables', and select all the states of the character; the taxa for which the character is unrecorded are displayed in the 'Eliminated Taxa' pane.

The Queries menu contains other commands useful for information retrieval: Describe, Diagnose, Differences, Similarities, and Summary. Using the Differences command from this menu instead of from the 'Taxa' toolbar allows more flexibility — free-text attributes may be compared, and matching is defined by the current 'Match' setting.

Modes of Operation

Intkey has two modes of operation: Normal and Advanced.

In Normal mode, the program is operated via the toolbars. Most of the menu system, many dialog-box buttons, and the command line are disabled. There are three toolbars: the main toolbar, just under the menu bar; the 'Characters' toolbar, at the top of the 'Best/Available Characters' (top-left) pane; and the 'Taxa' toolbar, at the top of the 'Remaining Taxa' (top-right) pane. The main toolbar is usually defined by the author of a data set, and invoked in the program's initialization file (usually INTKEY.INI or INTKEY.INK).Advanced mode, which is set by the 'Advanced Mode' option of the 'File' menu, the program can be operated via the toolbars, the menu system, or the command line.

The program works the same in both modes, with the following exceptions.

1. Different main-toolbar buttons may be available in the two modes, and buttons which look the same may have been defined differently (see 'Define').
2. In Normal mode, there are no 'Separate' and 'Set match' buttons in the 'Characters' toolbar (top-left pane).
3. In Normal mode, the following keywords are not shown in keyword-selection dialogs: remaining, eliminated, selected, available, used.
4. In Normal mode, character images are automatically displayed during identification. In Advanced mode, you must press the 'Images' button to display images. See 'Display Images'.
5. In Normal mode, Autotolerance is off; in Advanced mode, it is on. See 'Set Autotolerance'.

Keywords

A keyword is a word or phrase associated with a group of characters or taxa. The keyword can be used to refer to those characters or taxa (instead of using a list of character or taxon numbers).

The set of characters or taxa denoted by a keyword is normally restricted to the 'included' characters or taxa. See the 'Include' command for details and an example.

Keywords are defined by means of the 'Define' command. Most sets of data will incorporate keywords defined by the person who prepared the data. You can add further definitions for your own convenience.

Several keywords are predefined by the program itself. The actual sets of characters and taxa defined by these may change as you use certain commands.

Four character keywords are predefined:
    all – all the (included) characters;
    none – none of the characters;
    used – the characters used in the current identification;
    available – the characters still usable in the current identification (characters which have not been used, and which are not inapplicable because of a dependency on used characters).

Five taxon keywords are predefined:
    all – all the (included) taxa;
    none – none of the taxa;
    remaining – the taxa remaining in the current identification;
    eliminated – the taxa eliminated from the current identification.
    selected – the taxa currently selected in the 'Taxa' panes of the main window..

Dialog Boxes and List Boxes

Many commands require you to specify the taxa and/or characters upon which the command is to act, and some also require you to specify character states. These commands automatically display a 'dialog box' from which you can make your selection. Inside the dialog box are various buttons, and a 'list box' containing taxa, characters, or states. Clicking on an item in the list selects the item (or deselects it if it was already selected). You can also drag the cursor to select or deselect multiple items. Some dialog boxes contain 'SelectAll' and 'DeselectAll' buttons, which select or deselect all the items in the list.

The item currently at the 'focus' of a list box is enclosed in a dotted rectangle, and is also indicated by an arrow. If you press the 'OK' button (or its equivalent) without having selected any items from the list, then the item at the focus is automatically selected.

Taxa and characters may be selected in groups from 'keyword' dialog boxes, or individually from taxon and character dialog boxes. To switch between these dialog boxes, use the 'Keywords' and 'List' buttons.

Using the keyboard in list boxes

You can move the focus in list boxes by pressing the up-arrow, down-arrow, PageUp, PageDown, Home, and End keys, or by typing the number of the required item. The space bar selects or deselects the item at the focus.

Advanced selection methods

A set of taxa or characters may be built up by repeated selections or deselections in the keyword and taxon or character dialog boxes. The rules governing the process are as follows.

1. When a keyword dialog box is deactivated by pressing an 'OK' or 'List' button, the taxa or characters corresponding to the selected keywords are added to the set.
2. When a taxon or character dialog box is deactivated by pressing an 'OK' or 'Keywords' button, the selected taxa or characters are added to the set, and the deselected taxa or characters are removed from the set.

Note that taxa or characters cannot be *removed* from the set via the keyword dialog box. As control passes to and fro between the keyword and taxon or character dialog boxes, the keywords and taxa or characters that are currently in the set are automatically marked as selected. The fact that a keyword is *not* automatically marked as selected implies only that at least one of its taxa or characters is not in the set.

Buttons in Dialog Boxes

All Images. Select all the images in the list.
Cancel. Cancel the command (or the current part of a repetitive command).
Change. Equivalent to 'OK' in 'Change' dialog box.
Delete. Equivalent to 'OK' in 'Delete' dialog box.
Deselect All. Deselect all the items in a list.
Display. Display the selected information.
*Done.*Close the dialog box.
Full Text. Display the full text of a character or taxon name.
Help. Obtain information about using the program.

Images. Display image(s) for the character currently being used, or for the taxon or character at the
    focus.
Keywords. Open or return to the keyword dialog box.
List. Open a dialog box containing the taxa or characters corresponding to the keyword at the focus.
Notes. Display notes about the character currently being used or at the focus.
OK. Proceed with the command.
Search. Search for text in a list.
Select All. Select all the items in a list.
Stop. Stop a repetitive command.

The Command Line

Intkey commands may be typed in on the 'command line' at the bottom of the screen. Commands
consist of a command word, or a command word followed by parameters. You can learn to use the
command line by observing the commands which are built up by the program when you use the menu
system.

Command words and parameters may be abbreviated, as long as the abbreviations are not ambiguous
(the program will tell you if they are).

You can edit the command line by using the left and right arrow keys, and the Backspace, Delete, and
Insert keys.

If a keyword (q.v.) containing blanks is used on the command line, it must be enclosed in quotation
marks ("), or the blanks must be omitted. All taxon names can be used as keywords on the command
line.

Commands may also be read from a file. See the 'File Input' command for details.

Saving Output

Program output can be saved in files, or copied to the clipboard and pasted into other applications.

Output from commands such as 'Describe', 'Diagnose', and 'Differences' is normally displayed in
separate windows. The contents of these windows can be printed, saved, or copied to the clipboard by
the usual Windows mechanisms.

The contents of the 'log', which can be displayed by means of the command 'Display Log On' in the
'Settings' menu, can also be printed, saved, or copied to the clipboard by the usual Windows
mechanisms; they can also be saved via the 'File Log' command in the 'File' menu.

The 'File Output' and 'Output' commands in the 'File' menu produce output in special formats for
input to other programs.

Data-Sets Index and Startup Parameters

Data sets are normally selected from a dialog box, which the program displays on startup or when the
New Data Set option of the 'File' menu is invoked. The program generates this dialog box from a file
INTKEY.IND which is normally in the same directory as the program. Entries in this file can be added
or removed using Intkey dialog boxes which are automatically displayed at appropriate times. Also,
the file can be edited with any text editor (e.g. Notepad, which is supplied with Windows).

If there is a file INTKEY_.IND in the same directory as the program, the name of a data-set
initialization file (usually INTKEY.INI or INTKEY.INK) is read from this file, and the data set is
immediately loaded. This feature can be used to simplify the starting of an Intkey package on a CD-
ROM.

Some aspects of the program's behaviour on startup can be controlled by adding parameters to the
shortcut target line, as follows. Press the Windows 'Start' button. Select 'Settings'. Select 'Taskbar';

the 'Taskbar Properties' dialog box appears. Select the 'Start Menu Programs' tab. Press the 'Advanced' button; an 'Exploring ...' window appears. In the right-hand part of the window, double click on Programs, then double click on DELTA. Click the right mouse button on 'Intkey'; a menu appears. Click on 'Properties'; the 'Intkey Properties' dialog box appears. Click on the 'Shortcut' tab. Click near the end of the 'Target' text box, and type in the required parameters, separated by blanks.

The available parameters are as follows.

filename
  Specifies the name of an initialization file (for example, C:\ANGIO\INTKEY.INI). The corresponding data set is then automatically loaded when the program starts, and the data-set selection box is not displayed.
–A
  Sets Advanced mode.
–G=*filename*
  Specifies the name of the (global) index file. The default is INTKEY.IND in the same directory as the program. You will need to use this option if Intkey is on a network drive for which you do not have write permission.
–H=*filename*
  Specifies the name of the 'Help' file. The default is INTKEN.HIN in the same directory as the program.
–I
  Suppresses display of startup images.
–P=*filename*
  Specifies the name of a preferences file — see help for the 'Preferences' command. The default directory is the one containing the program.
–R=*filename*
  Specifies the name of the DELTA registration file. The default is DELTA.INI in the same directory as the program.

Hardware and Operating-System Requirements

Intkey requires Windows 95, NT, or later.

The program will work on any hardware capable of running Windows. However, for good image quality, we recommend a display card with at least 32768 colours at 800x600 or 1024x768 resolution, and a refresh rate of at least 70Hz.

Conditions of Use

If the use of the program leads to a publication, you must include appropriate citations (see below), and send a copy of the publication to the authors.

Use or distribution of the program for financial gain is prohibited unless you have entered into a License Agreement for such use or distribution.

Details of the conditions of use are contained in the file USE.TXT, which accompanies the the DELTA program suite (see http://delta-intkey.com).

Commands

CHANGE

This command is no longer available in the menus, but is retained for use in the command line.

The command allows the user to change previously entered information about the specimen being identified.

See also USE, DELETE.

Syntax of command line

CHANGEc_1,v_1 c_2,v_2 ...

where c_1, c_2, ... are character numbers, ranges, or keywords, and v_1, v_2, ... are state values (or numerical or text values, depending on the character type). The state values and the preceding commas are optional; if they are not specified, the program prompts for them.

CHARACTERS

This command displays the character list.

See also OUTPUT CHARACTERS, and Keywords.

Syntax of command line

CHARACTERS c_1 c_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords.

COMMENT

This command allows the insertion of comments in INPUT and LOG files. The command is ignored (except for inclusion in LOG and JOURNAL files).

See also OUTPUT COMMENT, SHOW.

Syntax of command line

COMMENT *text*

CONTENTS

This command displays a dialog box for selecting and executing an Intkey command, or an Intkey input file (see FILE INPUT) associated with the current data set.

The list presented in the dialog box is normally defined by the author of the data, but the Intkey user can also create or add to the list. It is defined in a file, usually contents.ind, each line of which has the syntax

    description *command
    or
    description input-file-name

Example of 'contents' file

    References *FILE DISPLAY refs.tps
    Genera of the Australian Capital Territory act.tax

Syntax of command line

CONTENTS *filename*

DEFINE

This command defines the following entities.

Keywords. These are names representing sets of characters or taxa (see Keywords in the general help).

Toolbar buttons. The command associates Intkey commands with a button.

Intkey commands to be executed at the end of an identification. The commands are executed only if DISPLAY IMAGES AUTO is set. N.B. This feature was designed for use with older versions of Intkey. We recommend against using it with the current version, as it usually obscures other important information which the program displays at the end of an identification.

Intkey commands to be executed as part of the INFORMATION command.

Words or phrases to be used for selection of taxon images by subject.

Syntax of command line – keywords

DEFINE CHARACTERS *keyword* c_1 c_2 ...
DEFINE TAXA *keyword* t_1 t_2 ...
DEFINE NAMES *keyword* n_1, n_2, ...

where c_1, c_2 ... are character numbers, ranges or previously defined keywords, t_1, t_2 ... are taxon numbers, ranges or previously defined keywords, and n_1, n_2 ... are taxon names. Taxon names must be separated by a comma or the end of a line. If the keyword contains spaces, it must be enclosed in quotation marks ("). If a keyword is defined in terms of a previously defined keyword, the meaning of the new keyword is fixed at the time of its definition – that is, it is not affected by subsequent changes in the meaning of the previously defined keyword. The NAMES form of the command is mainly intended for use in INPUT files.

Examples

DEFINE CHARACTERS "reproductive organization" 12 23–24

RESTART
USE 13,2 27,1
DEFINE TAXA g1 remaining

The keyword 'g1' continues to represent those taxa with attributes '13,2 27,1', even though the set of taxa represented by the keyword 'remaining' may change later in the session.

DEFINE NAMES cereals Echinochloa, Eleusine, Oryza, Panicum, Zea

Syntax of command line – buttons

DEFINE BUTTON *switches bitmap*.BMP "c_1; c_2; ..." "*shorthelp*" "*fullhelp*"
DEFINE BUTTON CLEAR
DEFINE BUTTON SPACE

where *bitmap*.BMP is the image to be displayed on the button, c_1, c_2, ... are commands, *shorthelp* is a short help message ('hint') for the button, and *fullhelp* is detailed help for the button (optional). The buttons are added to the toolbar in the order in which they are defined.

The optional switches are as follows.
/A displays the button only in Advanced mode.
/N displays the button only in Normal mode.
/U makes the button inactive (grey) unless there are USED characters.

The special parameters '?', '?K', '?L', and '?L1' can be used in place of predetermined sets of taxa or characters in the commands invoked by the button. They cause an appropriate dialog box to be displayed, so that the user can make a selection. '?' causes the default dialog box to be displayed (keyword or character/taxon selection depending on the DISPLAY KEYWORDS setting). '?K' causes

the keyword selection dialog box to be displayed. '?L' causes the character or taxon selection dialog box to be displayed. '?L1' is applicable only to taxa. It has the same effect as '?L', except that the dialog is not displayed if it would contain only a single taxon – that taxon is automatically selected.

DEFINE BUTTON CLEAR clears all the buttons, and DEFINE BUTTON SPACE puts a space between buttons.

Example

> DEFINE BUTTON START.BMP "INCLUDE TAXA CEREALS; RESTART" "Start a new identification, including only cereals"
> DEFINE BUTTON /U CHANGE.BMP "CHANGE ?L" "Change previously entered information about the specimen being identified" "This button allows you to change previously entered information about the specimen being identified."

Syntax of command line – end of identification

N.B. This feature was designed for use with older versions of Intkey. We recommend against using it with the current version, as it usually obscures other important information which the program displays at the end of an identification.

DEFINE ENDIDENTIFY *switch* "c_1; c_2; ..."

where c_1, c_2, ... are commands.

The optional switch /T=n causes the output to be produced in n tiled windows.

Example

> DEFINE ENDIDENTIFY "DESCRIBE REMAINING BRIEF"

Syntax of command line – information

DEFINE INFORMATION "s" "c"

where s is the subject to be displayed in the INFORMATION dialog, and c is an Intkey command. The subjects are added to the list box in the dialog in the order in which they are defined, and after any subjects which were defined when the Intkey data files were generated.

The special parameter '?S' should be used in place of a set of taxa in the command c. It means 'the taxon currently selected in the INFORMATION dialog'.

Example

> DEFINE INFORMATION "Diagnostic description" "diagnose ?S none"

Syntax of command line – subjects

DEFINE SUBJECTS w_1 w_2 ...

where w_1, w_2, ... are words, or phrases enclosed in quotation marks (").

The words or phrases are placed in the 'Subjects' list box in the 'Select Multiple Images' dialog box, which is invoked by the 'Multiple Images' option of the 'Control' menu in taxon-image windows. The images displayed are restricted to those whose 'subjects' contain any of the words or phrases selected in the list box.

Example

> DEFINE SUBJECTS anatomy "distribution map" "habit " habitat inflorescence type
>
> The space in "habit " prevents it from matching 'habitat' in a subject. "type" matches 'holotype' and 'isotype', but " type" would not.

DELETE

This command is no longer available in the menus, but is retained for use in the command line.

The command allows the user to remove previously entered information about the specimen being identified.

See also CHANGE, USE.

Syntax of command line

DELETE *switch* c_1 c_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords.

The optional switch /M suppresses the warning message when unused characters are specified.

DESCRIBE

This command displays descriptions of taxa, or the description of the specimen being identified.

See also OUTPUT DESCRIBE, DISPLAY, Keywords.

Syntax of command line

DESCRIBE (t_1 t_2 ...) c_1 c_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords, which may include the word SPECIMEN, and c_1, c_2 ... are character numbers, ranges or keywords. If there is only one taxon number, range or keyword, the parentheses may be omitted.

DIAGNOSE

This command generates diagnostic descriptions of taxa. You may specify 'preset' characters to be included in all the descriptions: specify NONE if you want the diagnostic characters to be selected entirely by the program.

Each diagnostic description will (if possible) differ in at least DIAGLEVEL characters from the full description of every other INCLUDEd taxon (not just the taxa specified in this command) (see SET DIAGLEVEL, INCLUDE TAXA). The current MATCH setting (see SET MATCH) is ignored: the setting used is almost equivalent to O U I, but see SET DIAGTYPE. The characters are selected from the AVAILABLE characters (see Keywords).

See also OUTPUT DIAGNOSE, DISPLAY CHARACTERORDER SEPARATE.

Syntax of command line

DIAGNOSE (t_1 t_2 ...) c_1 c_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords, and c_1, c_2 ... are character numbers, ranges or keywords. If there is only one taxon number, range or keyword, the parentheses may be omitted.

DIFFERENCES

This command displays the differences between taxa, or between taxa and the specimen being identified.

See also SET MATCH, SIMILARITIES, OUTPUT DIFFERENCES, DISPLAY, Keywords.

Syntax of command line

DIFFERENCES *switches* (t_1 t_2 ...) c_1 c_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords, which may include the word SPECIMEN, and c_1, c_2 ... are character numbers, ranges or keywords. If there is only one taxon range or keyword, the parentheses may be omitted.

The optional switches /O, /S, /E, /U, and /I set the corresponding values of the MATCH parameter (see SET MATCH) for the current command only. The optional switch /X causes text characters to be omitted from the comparison.

DISPLAY

This command sets options for controlling the screen display.

Syntax of command line

DISPLAY *option value*

DISPLAY CHARACTERORDER BEST
DISPLAY CHARACTERORDER NATURAL
DISPLAY CHARACTERORDER SEPARATE *t*

> where *t* is a taxon number, or a keyword representing a single taxon.

> Causes the list of characters to be displayed in 'Best' order, natural order, or the most appropriate order to 'Separate' the specified taxon, respectively.

> In 'Best' and 'Separate' orders, the merit of a character is calculated partly from its separating power, and partly from its 'reliability' or ease of use. Characters are displayed in order of merit, and their separating powers are shown at the left of the display. A separating power of 1 corresponds to a division of the group of remaining taxa into halves, and a value of 0 indicates very poor separation. See Section 5.4 of the DELTA User's Guide for more details.

> See also SET RELIABILITIES, SET RBASE.

DISPLAY COMMENTS ON|OFF

> Determines whether comments in taxon names are displayed in list boxes and in the output of the TAXA command. The default is OFF.

DISPLAY CONTINUOUS ON|OFF

> When CONTINUOUS is ON, the main text display does not pause between 'pages', images are displayed in a continuous loop, and the 'Multiple Images' option in taxon-image windows is unavailable. The default is OFF.

DISPLAY ENDIDENTIFY ON|OFF

> When ENDIDENTIFY is ON, the commands specified by DEFINE ENDIDENTIFY are executed at the end of an identification. The default is ON for Normal mode, and OFF for Advanced mode.

DISPLAY IMAGES *options*

> where *options* are one of AUTO, MANUAL, and OFF, and/or one of MISSING_IMAGE_LIST, CHARACTER_IMAGE_LIST, and TAXON_IMAGE_LIST.

> When AUTO is set, images are displayed automatically after a state-selection menu is displayed; MANUAL cancels this option. OFF suppresses all references to images; this option is intended for use with data sets whose images have not been installed (for example, because of lack of disk space). The default is AUTO in Normal mode, and MANUAL in Advanced mode.

> The MISSING_IMAGE_LIST option checks local disks for the presence of all images, and lists missing ones (images on the Internet are not checked). The CHARACTER_IMAGE_LIST and TAXON_IMAGE_LIST options list the images which are linked to INCLUDEd characters or taxa (the *presence* of the images is not checked).

DISPLAY INAPPLICABLES ON|OFF

> Determines whether inapplicable characters are displayed in the output of the DESCRIBE command. The default is ON.

DISPLAY INPUT ON|OFF

> Determines whether the contents of an input file are displayed (and included in the LOG and JOURNAL files) as it is executed (see FILE INPUT). The default is OFF.

DISPLAY KEYWORDS ON|OFF

> If KEYWORDS is OFF, the display does not pause at keyword menus, but immediately displays the default character or taxon menu. The default is OFF in Normal mode, and ON in Advanced mode.

DISPLAY LOG ON|OFF

> Determines whether the log window is displayed. The default is OFF.

DISPLAY NUMBERING ON|OFF

> Determines whether taxon and character numbers are displayed in some contexts. The default is OFF.

DISPLAY SCALED ON|OFF

> DISPLAY SCALED ON causes taxon images to be automatically scaled to fit within the image window. DISPLAY SCALED OFF turns this option off. The default is ON.

DISPLAY UNKNOWNS ON|OFF

> Determines whether unknown characters are displayed in the output of the DESCRIBE command. The default is ON.

DISPLAY WINDOWING ON|OFF

> Determines whether output is displayed in separate windows. The default is ON.

EXCLUDE

This command is used to exclude characters or taxa from consideration by other commands. It is equivalent to an INCLUDE command specifying those characters or taxa not specified in the EXCLUDE command. See INCLUDE for more details.

Syntax of command line

EXCLUDE CHARACTERS c_1 c_2 ...
EXCLUDE TAXA t_1 t_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords, and t_1, t_2 ... are taxon numbers, ranges or keywords.

FILE

This command specifies the names of input and output files, and causes input files to be read. If a specified output file already exists (that is, was present before the Intkey run) and the command came from the keyboard, a warning is given and there is an opportunity to abort the command; if the command came from an input file, the existing output file is overwritten without warning.

Syntax of command line

FILE *option filename*

FILE INPUT *filename*

> This command reads and executes a file of Intkey commands. Commands in an input file take the same form as commands entered interactively on the command line, or generated by the menus, except that they must be preceded by a * (e.g. *SET), and the parameters may extend over more than one line. Each command must start on a new line.

To facilitate the location of errors in an input file, put a DISPLAY INPUT ON command at the start of the file.

FILE OUTPUT *filename*

This command specifies the name of a file to which output lines generated by the OUTPUT command will copied when the program terminates, or when a FILE CLOSE command is given. Up to 16 output files may be specified, and the same file may be specified more than once.

FILE LOG *filename*

This command specifies the name of a file to which the log (see DISPLAY LOG) will be saved when the program terminates. The command may be used at any time during a session. Log files are saved in RTF format if the specified file type is .rtf,and otherwise as plain text.

FILE JOURNAL *filename*

This command specifies the name of a file to which all input lines will be copied when the program terminates. See also DISPLAY INPUT.

FILE CLOSE *filename*

This command causes a file previously named in a FILE OUTPUT command to be output and closed.

FILE CHARACTERS *filename*

This command specifies the name of the Intkey characters file, and is normally used only in the initialization file, INTKEY.INI. If the command has not been specified by the time the program needs information from the data files, the name ICHARS is used.

Intkey cannot be used to prepare or alter its characters file. This is done via the DELTA system – see M.J. Dallwitz (1980), 'A general system for coding taxonomic descriptions', Taxon 29, 41–6.

FILE TAXA *filename*

This command specifies the name of the Intkey taxa (items) file, and is normally used only in the initialization file, INTKEY.INI. If the command has not been specified by the time the program needs information from the data files, the name IITEMS is used.

Intkey cannot be used to prepare or alter its taxa file. This is done via the DELTA system – see M.J. Dallwitz (1980), 'A general system for coding taxonomic descriptions', Taxon 29, 41–6.

FILE DISPLAY *filename*

This command displays the specified file in a separate window.

FIND

This command is used to search for text in taxon names or characters. The taxon-names search also searches attributes which have been designated by the author of the data to contain synonymy. The search is not case sensitive.

Syntax of command line

FIND TAXA *text*
FIND CHARACTERS *text*

ILLUSTRATE

This command displays illustrations of characters or taxa (if available). Images of any size, and containing any number of colours or grey levels, can be displayed, but the results will usually be poor

if Windows is running in a 16-colour mode (see 'Hardware' under 'Introduction' for more information). Various options are available through the menu system in the illustration window.

Ctrl+DownArrow and Ctrl+UpArrow move between illustrations of the same character or taxon, and Ctrl+PageDown and Ctrl+PageUp move between illustrations of different characters or taxa. This can also be done via the menus. A bell indicates that there are no more illustrations.

Ctrl+End displays all the remaining illustrations (of those specified in the command). Esc interrupts this display. '+' increases and '−' decreases the length of time each image is displayed.

See also Keywords.

Syntax of command line

ILLUSTRATE CHARACTERS c_1 c_2 ...
ILLUSTRATE TAXA t_1 t_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords, and t_1, t_2 ... are taxon numbers, ranges or keywords.

INCLUDE

This command is used to specify the set of characters or taxa on which subsequent commands operate. If another command also specifies ranges of characters or taxa, the ones used are normally those specified in both the current command and the last INCLUDE command. For example, INCLUDE CHARACTERS 1–5 9–20 followed by CHARACTERS 5–10 would display characters 5, 9, and 10. However, the INCLUDE command completely overrides previous INCLUDE commands.

The currently INCLUDEd characters or taxa can be overridden in any command by means of a checkbox in the keyword selection dialog box. The same thing can be achieved on the command line by means of the switch /C (for characters) and /T (for taxa). Example: DESC REMAINING /C ALL will display a complete description regardless of which characters are currently INCLUDEd.

See also EXCLUDE, Keywords.

Syntax of command line

INCLUDE CHARACTERS c_1 c_2 ...
INCLUDE TAXA t_1 t_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords, and t_1, t_2 ... are taxon numbers, ranges or keywords.

INFORMATION

This command displays various information about selected taxa. After a taxon or set of taxa have been selected in the usual way, a dialog is displayed. This allows the further selection of a single taxon (if more than one was originally specified), and the selection, by subject, of the information to be displayed for the currently selected taxon. The dialog remains open, allowing the selection and display of further information, until explicitly closed or a command which potentially changes the number of taxa remaining, is executed.

The kinds of information which may be displayed are as follows: (1) output of other commands such as DESCRIBE and DIAGNOSE; (2) images; (3) RTF files; (4) Intkey startup/initialization files (.ink); (5) any other external files with a registered type (i.e. for which a viewer is known to Windows, for example, HTML files, Word documents, Windows help files). The generation of output by means of other Intkey commands is specified by the Intkey command DEFINE INFORMATION. The other kinds of information are specified when the Intkey data files are generated by the author – see directives TAXON IMAGES and TAXON LINKS in the DELTA User's Guide for details.

The 'Web Search' button in the 'Information' dialog can be used to search for the selected taxon using a nominated general-purpose search engine (e.g. Google) or taxonomic database (e.g. ITIS). The queries sent to the search engines are normally specified in a file websearch.ind, which is supplied with Intkey. If you want specify your own set of queries and avoid having them overwritten when new versions of Intkey are installed, put them in a file mywebsearch.ind; Intkey will use this instead of websearch.ind.

The SET INFOPATH command allows specification of the path to be searched for 'information' files.

Syntax of command line

INFORMATION *switches* t_1 t_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords.

The optional switches are as follows.

/I=*text* causes the display of all images which are attached to the currently selected taxon, and whose subjects contain '*text*'. If '=*text*' is omitted, all images are displayed.

/O=*text* causes the display of all other (non-image) information which is attached to the currently selected taxon, which is contained in an RTF file or is generated from Intkey commands, and whose subjects contain '*text*'. If '=*text*' is omitted, all such information is displayed, regardless of subject.

/X causes the 'information' dialog to be closed when operations specified in other switches are complete.

NEWDATASET

This command displays a dialog box for selecting a new set of data.

New data sets can also be invoked by means of the FILE INPUT command. In input files, these commands are synonymous.

OUTPUT

This command is available only if an OUTPUT file (see FILE OUTPUT) has been opened. It provides alternative versions of the commands CHARACTERS, TAXA, DESCRIBE, SUMMARY, DIAGNOSE, DIFFERENCES, SIMILARITIES, and COMMENT. These versions format the output differently (in formats designed for input to other programs).

OUTPUT commands, except for COMMENT, normally output a heading identical with the first two words of the command. This heading is suppressed if the preceding command was an OUTPUT COMMENT command. This enables the construction of complete directives for other programs. For example, 'OUTPUT COMMENT *INCLUDE ITEMS' followed by 'OUTPUT TAXA REMAINING' would produce an INCLUDE ITEMS directive suitable for CONFOR.

Syntax of command line

OUTPUT *option parameters*

OUTPUT CHARACTERS *parameters*

> The same as the CHARACTERS command, except that the output consists only of the specified character numbers. This command can be used to generate INCLUDE or EXCLUDE CHARACTERS directives for CONFOR.

OUTPUT TAXA *parameters*

> The same as the TAXA command, except that the output consists only of the specified taxon numbers. This command can be used to generate INCLUDE or EXCLUDE ITEMS directives for CONFOR.

OUTPUT DESCRIBE *parameters*

The same as the DESCRIBE command, except that the output is in DELTA format.

OUTPUT SUMMARY *parameters*

The same as the SUMMARY command, except that the output is in DELTA format.

OUTPUT DIAGNOSE *parameters*

The same as the DIAGNOSE command, except that the output is in a format suitable for the CONFOR directives ADD or EMPHASIZE CHARACTERS.

OUTPUT DIFFERENCES *parameters*

The same as the DIFFERENCES command, except that the output consists only of the character numbers for which the taxa are different. This command can be used to generate INCLUDE or EXCLUDE CHARACTERS directives for CONFOR.

OUTPUT SIMILARITIES *parameters*

The same as the SIMILARITIES command, except that the output consists only of the character numbers for which the taxa are similar. This command can be used to generate INCLUDE or EXCLUDE CHARACTERS directives for CONFOR.

OUTPUT COMMENT *text*

The same as the COMMENT command, except that the text is written to the OUTPUT file.

PREFERENCES

This command displays a dialog box for selecting an input file (see FILE INPUT) specifying preferred parameter settings. This input file is executed immediately, and again after the initialization file (INTKEY.INI) of each new data set. The default file type is .PRF, and the default directory is the one containing the program.

The settings associated with the operating mode initially selected by the user (see 'Modes of Operation', under 'Introduction') are also reset at the start of each new data set. The order of setting parameters is: initialization file, operating mode, preferences file.

You can also specify a preferences file to be automatically invoked when the program starts: see 'Data-Sets Index and Startup Parameters' under 'Introduction'.

Example of 'preferences' file

```
*SHOW Preferences: SET AUTOTOLERANCE ON, DISPLAY NUMBERING ON
*SET AUTOTOLERANCE ON
*DISPLAY NUMBERING ON
```

Syntax of command line

PREFERENCES *filename*

QUIT

This command terminates the program.

RESTART

This command prepares the program for a new identification or query.

See also SET FIX, SET TOLERANCE, SET AUTOTOLERANCE.

Syntax of command line

RESTART *switches*

The optional switches are as follows.

    /I sets parameters for identification. MATCH is set to O I U. DIAGTYPE is set to SPECIMENS.

    /Q sets parameters for information retrieval (queries). MATCH is set to O. DIAGTYPE is set to TAXA.

    /T causes the error tolerance to be set to 0.

SET

Sets the values of various parameters.

Syntax of command line

SET *parameter value*

SET AUTOTOLERANCE ON|OFF

> When AUTOTOLERANCE is ON, then TOLERANCE (see SET TOLERANCE) is decreased automatically by the program to the smallest value such that the number of taxa remaining is non-zero; the value is never automatically increased. The default is ON in Normal mode, and OFF in Advanced mode.

> See also SET EXACT.

SET DEMONSTRATION ON|OFF

> When DEMONSTRATION is ON, the RESTART command restores the SET, DISPLAY, and INCLUDE parameters to the values they had when demonstration mode was turned on, or the values associated with the selected operation mode (automatic or manual).

> When DEMONSTRATION is turned ON from an input command file it cannot subsequently be turned OFF except from another input file.

> This option is intended for running unattended demonstrations of the program. The default is OFF.

SET DIAGLEVEL *n*

> Sets the required level of diagnostic descriptions (see DIAGNOSE). Each diagnostic description will (if possible) differ in at least DIAGLEVEL characters from the full description of every other INCLUDEd taxon. The default value is 1.

SET DIAGTYPE SPECIMENS|TAXA

> Specifies whether DIAGNOSE will generate specimen- or taxon-diagnostic descriptions. A specimen-diagnostic description must be able to distinguish any specimen belonging to the diagnosed taxon from any specimen belonging to any other taxon. A taxon-diagnostic description must be able to distinguish the diagnosed taxon from any other taxon. When generating specimen-diagnostic descriptions, the program will not include characters which may be inapplicable to specimens in the diagnosed taxon, because, for some specimens, such characters cannot contribute to the desired separation. The default is SPECIMENS.

SET EXACT c_1 c_2 ...

> where c_1, c_2 ... are character numbers, ranges or keywords.

> Specifies characters which are to be regarded as not subject to error. When such a character is USEd, taxa inconsistent with the specified value are eliminated, regardless of the TOLERANCE value. Furthermore, any intra-taxon variability inconsistent with the specified value is subsequently ignored, and does not appear in descriptions.

> See also Keywords.

SET FIX ON|OFF

SET FIX ON fixes the attributes that have currently been USEd, so that they are not cleared by the RESTART command. SET FIX OFF cancels the SET FIX ON command: fixed characters are cleared and the identification is restarted.

SET IMAGEPATH *path*

Specifies the directory path which will be searched for the character and taxon images. The default is the current directory. Example: SET IMAGEPATH .;IMAGES;B:\ will cause the program to search for images in the current directory, its subdirectory IMAGES, and the root directory of the B drive. Components of the imagepath may be URL's, e.g. http://biodiversity.uno.edu/delta/angio/images.

See also ILLUSTRATE.

SET INFOPATH *path*

Specifies the directory path which will be searched for files specified in the INFORMATION dialog. The default is the current directory. Example: SET INFOPATH .;INFO;B:\ will cause the program to search for files in the current directory, its subdirectory INFO, and the root directory of the B drive. Components of the infopath may be URL's, e.g. http://biodiversity.uno.edu/delta/angio/info.

SET MATCH option1 option2 ...

where *option1*, *option2*, ... are chosen from Overlap, Subset, Exact, Unknowns, and Inapplicables.

Specifies which character values are to be regarded as equal – that is, 'match' – in the commands USE, DIFFERENCES, or SIMILARITIES.

SET MATCH O specifies that two sets of values match if they overlap, that is, if they have any values in common (e.g. 1/2 matches 2/3; 2–5 matches 4–10). (S and O cannot be used together.)

SET MATCH S specifies that two sets of values match if one set (usually the values of the specimen) is a subset of the other. (E.g. 1/2 matches 1/2/4 but not 2/3; 2–5 matches 1–6 but not 4–10).

SET MATCH E specifies that two sets of values match only if they are identical.

SET MATCH U specifies that 'unknown' matches any value.

SET MATCH I specifies that 'inapplicable' matches any value.

The default setting is O U I, which is usually the most appropriate for identification. For information retrieval, the most appropriate setting is usually O.

The U and I settings do not affect text characters, for which unknown and inapplicable attributes are never treated as matches.

N.B. Regardless of the current 'Match' settings, the 'Differences between the specimen and the remaining taxa' button always uses settings equivalent to 'Match exact', and the 'Differences between taxa' button always uses settings equivalent to 'Match Unknowns Inapplicables'. To obtain differences in terms of the current 'Match' settings, use the 'Differences' option in the 'Queries' menu.

SET RBASE *r*

where *r* is a real number in the range 1 to 5. Sets the base of the logarithmic character-reliability scale, which is used in determining the 'best' characters during an identification. The default value is 1.1. A value of 1 causes character reliabilities to have no effect on character merit. See Section 5.4 of the DELTA User's Guide for more details.

See also DISPLAY CHARACTERORDER BEST, SET RELIABILITIES, SET VARYWT.

SET RELIABILITIES c_1,v_1 c_2,v_2 ...

where c_1, c_2 ... are character numbers, ranges or keywords, and v_1, v_2, ... are reliability values in the range 0 to 10. The values and their preceding commas are optional.

Specifies character reliabilities, which are used in determining the 'best' characters for separating taxa.

If character numbers, ranges, or keywords are entered without following commas and values, the program prompts for a value, which is applied to all the specified characters.

The default reliabilities are those that were specified when the Intkey data files were generated. See Sections 3.6 and 5.4 of the DELTA User's Guide for more details.

See also DISPLAY CHARACTERORDER BEST, SET RBASE, Keywords.

SET STOPBEST *n*

Specifies the number of characters which a DIAGNOSE command must find before it stops searching for acceptable characters. Characters are processed in order of decreasing reliability. If *n* is 0, which is the default, all the characters are examined.

SET TOLERANCE *n*

Sets the maximum number of differences between a taxon and the specimen which still allows the taxon to remain under consideration in an identification. The default value is 0.

If AUTOTOLERANCE is ON (see SET AUTOTOLERANCE), then TOLERANCE is altered automatically by the program to the smallest value such that the number of taxa remaining is non-zero. Regardless of the AUTOTOLERANCE setting, TOLERANCE is reset to 0 by the RESTART command.

SET VARYWT *r*

where *r* is a real number in the range 0 to 1. Sets the value of a parameter which determines the treatment of intra-taxon variability in selecting the 'best' characters during an identification. The default value is 1. If VARYWT is 1, there is no special penalty for intra-taxon variability; if it is 0, characters with intra-taxon variability are ranked lowest. See Section 5.4 of the DELTA User's Guide for more details.

See also DISPLAY CHARACTERORDER BEST, SET RBASE.

SHOW

SHOW causes the specified text to be displayed on the screen.

See also COMMENT, OUTPUT COMMENT.

Syntax of command line

SHOW *text*

SIMILARITIES

This command displays the similarities (that is, the character values they have in common) between the specified taxa, for the specified characters. (However, characters which are unknown or inapplicable for all taxa are not displayed.)

See also SET MATCH, DIFFERENCES, OUTPUT SIMILARITIES, DISPLAY, Keywords.

Syntax of command line

SIMILARITIES switches (t_1 t_2 ...) c_1 c_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords, which may include the word SPECIMEN, and c_1, c_2 ... are character numbers, ranges or keywords. If there is only one taxon range or keyword, the parentheses may be omitted.

The optional switches /O, /S, /E, /U, and /I set the corresponding values of the MATCH parameter (see SET MATCH) for the current command only.

STATUS

This command displays the values of various program parameters.

Syntax of command line

STATUS *option*

where *option* is ALL, or one of the command words DISPLAY, INCLUDE, EXCLUDE, FILES, FUNCTION, or SET.

SUMMARY

This command displays a summary of the character values exhibited by the specified set of taxa, for the specified set of characters. The output line labelled 'U/I/Recorded' gives, for each character, the numbers of taxa for which the character is unknown, inapplicable, or recorded. Multistate and integer numeric values are summarized as a 'distribution of values'. Each value is followed by the number (in parentheses) of taxa which exhibit the value. If this number is the same for consecutive values of a character, the values are expressed as a range; note that this does not imply that the range occurs as such in any of the members of the set. Real numeric values are summarized as a 'mean' and 'standard deviation'. The standard deviation is calculated from the within-taxon means, that is, the variation within taxa is not included. If difficulties arise with interpretation of the output, comparison with DESCRIBE output may be helpful.

See also OUTPUT SUMMARY, Keywords.

Syntax of command line

SUMMARY (t_1 t_2 ...) c_1 c_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords, and c_1, c_2 ... are character numbers, ranges or keywords. If there is only one taxon number, range or keyword, the parentheses may be omitted.

TAXA

This command displays the names of specified taxa. If any of the taxa differ from the specimen being identified (see USE), the number of differences is displayed, in parentheses, for each taxon.

See also OUTPUT TAXA, Keywords.

Syntax of command line

TAXA t_1 t_2 ...

where t_1, t_2 ... are taxon numbers, ranges or keywords.

USE

This command is no longer available in the menus, but is retained for use in the command line.

The command allows the user to enter information about a specimen, in terms of characters selected according to categories (e.g. leaves, fruit, inflorescence, 'available' – see Keywords). After the characters have been selected, the program prompts for the character value(s) exhibited by the specimen.

Character values can be changed at any stage by specifying the character in a CHANGE command or another USE command, and characters can be completely removed from the specimen description by means of the DELETE command.

The characters currently in use are represented by the keyword USED (see Keywords). These characters, and the values that have been entered for them, are displayed in the main window, and can be displayed again by entering DESCRIBE SPECIMEN USED.

Syntax of command line

USE *switch* c_1,v_1 c_2,v_2 ...

where c_1, c_2, ... are character numbers, ranges, or keywords, and v_1, v_2, ... are state values (or numerical or text values, depending on the character type). The state values and the preceding commas are optional; if they are not specified, the program prompts for them.

The optional switch /M suppresses the warning message when characters that have already been used are specified.

The command-word ('USE') is optional (unless c_1 is a keyword): any input line starting with a number is assumed to be a USE command. Examples:

    17
    USE 3 10–12
    USE lemmas
    4,1 7,2–4/7 26,1.2–2.6 biochemistry,1/2 104,tundra
'/' indicates alternative values ('or'), and '–' indicates a range of values ('to'). If the value of a text character contains spaces, it must be enclosed in quotation marks ("). Example:

    104,"disturbed ground"

Blanks may be used in text values to control matching of parts of words; for example, " tropical" will match 'tropical' and 'tropically' but not 'subtropical'.

A value consisting of a single blank is treated as a special case. It matches any text recorded in the data, even text without blanks.

Several strings separated by '/' may be specified for text characters. If MATCH is set to E or S, every string must be present to constitute a match; if MATCH is set to O, the presence of any of the strings is sufficient. Example:

    1,"poa/agrostis"

The MATCH U and I settings do not affect text characters, for which unknown and inapplicable attributes are never treated as matches.

See also SET MATCH, SET FIX, SET EXACT, Keywords.

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