NAME

MASE internal variables; ways to affect *MASE* behavior

SYNOPSIS

MASE provides a common interface to change several internal variables. These variables affect several of the *MASE* intrinsic functions. All these variables are modified through two interfaces: *SET-VARIABLE,* which is described further in *INTRINSIC FUNCTIONS* for interactive use, and via *TAKE* files (including startup files) which is described in *STARTUP* and in the discussion of *TAKE* in *INTRINSIC FUNCTIONS.*

This list of variable names is alphabetical order; functional groups of variables are noted in other help files.

Note also that current variable values may be stored in a *TAKE*-able format via *STORE-VARIABLES* (see *INTRINSIC FUNCTIONS STORE-VARIABLES* for more information).

There are three types of variables. *INTEGER* variables may contain any integer value. *FLOAT* variables may contain any floating point value. *BOOLEAN* variables may be set to either ‘‘*YES*’’ or ‘‘*NO*’’ to reflect whether that property should be enabled.

DESCRIPTION

@NONE

Null operation - to abort *SET-VARIABLE.*

COLUMN-CORRELATION-FIXED-P

Float
For *COLUMN-CORRELATION.*
The ‘‘p’’ value will be fixed (to the specified value) rather than calculated from per-case data. Set to ‘‘-1.0’’ to re-enable case-by-case calculation of ‘‘p’’.

COLUMN-CORRELATION-MODEL-SEQ

Integer
For *COLUMN-CORRELATION.*
Use the sequence specified by this variable rather than neighbors for counting changes. Set to ‘‘0’’ to count changes from the *CONSENSUS-SEQUENCE.* Set to ‘‘-1’’ to change back to neighbors method.

COLUMN-CORRELATION-THRESHOLD

Float
For *COLUMN-CORRELATION.*
Correlation scores above this threshold will be discarded.

COLUMN-HIGHLIGHT

Integer
For interactive editing mode.
Provide highlighted columns to serve as rule marks; a rule will be placed every *COLUMN-HIGHLIGHT*’th column.
Set to ‘‘0’’ for higher speed screen updating if rulers are not desired.

CONSENSUS-THRESHOLD

Float
For *CONSENSUS.*
Minimum fraction of sequences that must contain a letter before that letter might be placed into the consensus.
Defaults to 0.0

CONSENSUS-USE-GAP

Boolean
For *CONSENSUS.*
If set, gaps will be treated as any other sequence element. If unset, gaps will be ignored

unless there are no other sequence elements down that column.

CONSENSUS-USE-STAR

Boolean
For *CONSENSUS.*
If set, stars (asterisks ("*")) will be treated as any other sequence element. If unset, stars will be ignored unless there are no other sequence elements down that column.

DISPLAY-ALTERNATE-CHARACTER-MAP

Boolean
Affects the interactive display.
When *ON,* characters will be displayed according to the status of the *CHARACTER-SET.*
When *OFF,* characters will be displayed as themselves, regardless of the loaded *CHARACTER-SET.*
This variable does not affect the function of *HIGHLIGHT-DIFFERENCES.* Thus, it may be useful to load an alternate *CHARACTER-SET,* generate a *CONSENSUS,* turn on *HIGHLIGHT-DIFFERENCES,* then turn off *DISPLAY-ALTERNATE-CHARACTER-SET.* The actual characters will be displayed, but ‘‘conservative’’ differences from a ‘‘conservative’’ consensus would not be highlighted.

DISPLAY-POSITION

Boolean
For interactive editing mode.
Display the current cursor position in real and effective positions (ignoring gaps) at the bottom of the screen.

NOTE: the editor will be more ‘‘responsive’’ if this feature is disabled.

HIGHLIGHT-DIFFERENCES

Boolean
For interactive editing mode.
Highlight letters that differ from a specific sequence. The ‘‘model’’ sequence is defined by this variable. If this variable is set to ‘‘0’’, letters differing from the *CONSENSUS* sequence will be highlighted. These highlights can be printed via *OUTPUT-ALIGNED.*

HIGHLIGHT-MERGE-METHOD

String
Referenced when setting highlights from various methods.
Can be one of: *SET, AND, OR,* or *ADD.* Defines how to merge the existing highlight with the new highlight.

INCREMENTAL-COMPLETE

Boolean
For interactive editing mode.
Incremental completion of command names and variable names. When enabled, incremental completion will partially fill in the response as far as no ambiguity results, i.e. typing in **SHO** will give **SHOW- .**

LOCK-WINDOWS

Boolean
For interactive editing mode.
Treat both windows as one continuous window.

OUTPUT-CHARACTERS-BETWEEN-VERTICAL-BREAKS

Integer
For aligned *OUTPUT.*
Number of sequence positions between vertical breaks.
Set to ‘‘0’’ to disable vertical breaks.

OUTPUT-CHARACTERS-PER-LINE
Integer
For aligned *OUTPUT.*
Number of SEQUENCE POSITIONS horizontally fitting on a page.
NOTE: this is *NOT* the total number of **COLUMNS** per page, but of **SEQUENCE POSITIONS** per page.

OUTPUT-LABEL-EACH-PAGE
Boolean
For aligned *OUTPUT.*
Put the locus names in the left border of each page of the output.

OUTPUT-LINES-BETWEEN-HORIZONTAL-BREAKS
Integer
For aligned *OUTPUT.*
Number of sequences between horizontal breaks (makes it skip a line). If ‘‘0’’, no lines will be skipped.

OUTPUT-LINES-PER-PAGE
Integer
For aligned *OUTPUT.*
Number of SEQUENCE lines to occur on each page.
The minimum page length is 5.
NOTE: this is the number of **SEQUENCE** lines **not including headers** that will fit on each page.

OUTPUT-POSITION
Boolean
For aligned *OUTPUT.*
Print the effective position at the end of each output line (ignoring gaps).

OUTPUT-SUPRESS-LOCUS-NAMES
Boolean +
For aligned *OUTPUT.* +
Supress printing each locus's number at the beginning of the line. +
Allows more space on each line for sequence data. +

OUTPUT-USE-FORMFEED
Boolean
For aligned *OUTPUT.*
Put a ‘‘form feed’’ between pages. Disabling will make the output more compact, but perhaps less readable.

PATTERN-ASK-CLEAR
Boolean
For *PATTERN-HIGHLIGHT.*
If *‘‘ON’’* - ask whether old patterns should be cleared at each call of *PATTERN-HIGHLIGHT.*
If *‘‘OFF’’* - use *PATTERN-DEFAULT-CLEAR to determine whether or not* the old highlights.

PATTERN-DEFAULT-CLEAR
Boolean
For *PATTERN-HIGHLIGHT.*
When *PATTERN-ASK-CLEAR* is *‘‘FALSE’’*, this variable provides the default response when the user is asked if he wants to clear the old patterns. When *PATTERN-ASK-CLEAR* is *‘‘OFF’’*, this variable DETERMINES whether old patterns will be cleared.

PATTERN-IGNORE-CASE
Boolean
For *SEARCH, SEARCH-AGAIN,* and *PATTERN-HIGHLIGHT.*

Ignore case for regular expression searches and highlighting.

SYNONYM for SEARCH-IGNORE-CASE

PATTERN-IGNORE-GAPS

Boolean
For *SEARCH, SEARCH-AGAIN,* and *PATTERN-HIGHLIGHT.*
Ignore case for gaps for regular expression searches and highlighting.

SYNONYM for SEARCH-IGNORE-GAPS

PROTECT

Boolean
For interactive editing.
When set, one will not be able to delete ‘‘non-gap’’ letters. Unset this variable if you want to delete actual sequence positions.
This variable is treated specially within *DELETE-COLUMNS.* See *INTRINSIC FUNCTIONS* for more information.

PROTECT-ASK-OVERRIDE

When both *PROTECT-ASK-OVERRIDE* and *PROTECT* are set, one will be prompted as to +
whether or not ‘‘non-gap’’ letters should be actually deleted. On a case by case basis, you +
can override or observe the protection. +

SEARCH-IGNORE-CASE

Boolean
For *SEARCH, SEARCH-AGAIN,* and *PATTERN-HIGHLIGHT.*
Ignore case for regular expression searches and highlighting.

SYNONYM for PATTERN-IGNORE-CASE

SEARCH-IGNORE-GAPS

Boolean
For *SEARCH, SEARCH-AGAIN,* and *PATTERN-HIGHLIGHT.*
Ignore case for gaps for regular expression searches and highlighting.

SYNONYM for PATTERN-IGNORE-GAPS

SEQUENCE-LINE-LENGTH

Integer
For *SAVE.*
How many bases should be written per line.
Defaults to 70.

SILENT

Boolean
For *LOAD.*
Inhibits display of length and name information as each sequence is read.

SIMILARITY-DISCARD-GAPS

Boolean +
For *SIMILARITY.* +
When *ON*, positions containing gaps in both sequences will be discared from the *SIMILARITY* +
score computation. +

SIMILARITY-IGNORE-SELVES

Boolean
For *SIMILARITY.*
Ignore similarity comparisons of sequences against themselves.

STOP-AT-BORDERS

Boolean

For *MV-LEFT* and *MV-RIGHT*

If set, horizontal cursor motion will pause at window borders. (the next *MV-* will go past the window border.)

TRANSLATE-IGNORE-GAPS

Boolean +

For *CREATE-LOCUS.* +

Strip gaps and anchor points from sequences before translating, then synchronize the peptide sequence to the original nucleic acid sequence. +

VERIFY-PAUSE

Boolean +

For *VERIFY.* +

If set, and *VERIFY* fails, user will be prompted to hit <CR> before continuing. +

EXAMPLES

FILES

SEE ALSO

INTRINSIC FUNCTIONS - TAKE
INTRINSIC FUNCTIONS - SET-VARIABLE
STARTUP

BUGS

Since most variables are interpreted by the intrinsic functions rather than *MASE* proper, this document is likely to be out of date. Where there is a discrepancy, the information provided with the intrinsic function should be considered more current.