

October 16, 1964

## CTSS BULLETIN #58

Subject: COMBIN COMMAND - a new version

Purpose

The COMBIN command combines several files of the same secondary name into a new file, also of the same secondary name.

Implementation

The new version of COMBIN is now available in the public file as COMBIN SAVED. It will become the standard version in the near future.

Modifications

1. Line-marked files and/or files without line-marks may now be combined.
2. The major field in the sequence field may be alphabetic.

Usage

COPY P COMBIN SAVED

RESUME COMBIN SEQ NAM1 NAM2 FIL<sub>1</sub> . . . . FIL<sub>n</sub>

COMBIN will combine files FIL<sub>1</sub> through FIL<sub>n</sub> of secondary name NAM2 into one file NAM1 NAM2 within the current file directory. If any FIL cannot be found, the NEED-USE convention will be followed. Within the USE process, an \* for a corresponding FIL means that FIL should be ignored. The combining will not begin until all FIL's are accounted for. FIL's are not deleted.

SEQ is a decimal number of 1-4 digits. The numeric sequence field begins with SEQ x 10 with leading zeros to complete the numeric field or with the most significant digits lost if SEQ x 10 exceeds the numeric field width. Sequencing is done by incrementing the numeric field by 10. If SEQ = '\*' or if NAME2 is 'SAVED', 'BSS' or 'CRUNCH', no sequencing will take place.

The entire sequence field (characters 73-80) may be composed of 2-5 numeric characters and 3-6 alphabetic characters. The numeric field width is determined by a scan of the first line of FIL<sub>1</sub> from right to left beginning with character 78 looking for the

first non-numeric character (blanks are treated as numeric zeros). The numeric field width and the alphabetic field width will remain fixed through the remainder of the command. The alphabetic information is obtained from each line of the FIL's. Note that the numeric field width will be at least 2 and not more than 5 characters wide.

**EXAMPLES:**

If characters 73-80 of the first line of FIL<sub>1</sub> are ABC123GH and SEQ = 1, the new sequence for NAM1 NAM2 will begin with ABC00010.

If line one contains Abbbbbbb and SEQ = 1, the new sequence will begin with Abb00010.

If the numeric field overflows, a message will be printed, "SEQUENCE FIELD OVERFLOW", and sequencing will continue from 0.

Line-marked files composed of 14-word lines may be sequenced. If a line of more or less than 14 words is encountered, sequencing is stopped and not resumed during execution of the rest of the command. A message is printed, "SEQUENCING STOPPED AT xxxxx".