split α β b_1 s_1 ... b_{n-1} s_{n-1} b_n

Splits the file α, β into n new files b_1, β ... b_n, β, where the s_i specify where the splitting is to be performed. The identifier s_i is one of the following depending on the class name β.

   a. Sequence number if β signifies card images.
   b. Entry points if β signifies BSS card images.
   c. Physical record numbers if β signifies variable length
                                              BCD records.
   d. Physical word numbers if β signifies binary words.

In every case the splitting will be done after the card image, BSS subprogram, record, or word. All previous occurrences of files b_i, β will be deleted from the user's file directory.

The **split** command operates by scanning file α, β looking for the identifier s_i. If it is found, file b_i, β will be written from s_{i-1} (not included) to s_i (included). If identifier s_i cannot be found, the error message

              IDENTIFIER s_i NOT FOUND

The user may then type directly to the command program:

   u s_1' b_1' ... s_2' b_2' ... s_{n-1}' b_{n-1}' s_n'

The command program will then write out file b_i, β from s_{i-1} (not included) to s_i' (included) and proceed as if the user had typed all of the arguments to u in place of s_i. If no arguments are given, file b_i, β will not be written and previous copies will not be deleted. Instead file b_{i+1}, β will be written from s_{i-1} (not included) to s_{i+1} (included).

If file α, β cannot be found, the error message

FILE α β NØT FØUND

The user may then type directly to the command programs

u α' β'

The command will then split file α', β' as if it had been typed instead of α, β.

combin α β γ_1 ... γ_m

combines the files α_i, β into a single file α, β. This file is then added to the users file directory after all previous copies of file α, β have been deleted. No resequencing is performed during this process. CØMBIN processes each γ_i in order. If file γ_i is not found, CØMBIN will stop processing and print out

FILE γ_i NØT FØUND

The user may then type directly to the command program

u δ_1 ... δ_n
(u for use)

CØMBIN will use files δ_i in place of the missing file γ_i and will proceed with the combining. If any more files are found missing, the procedure outlined above will be repeated.

The following additional command is needed:

reseq α β a n i

resequences file α, β with a left justified alphabetic field of 1 to 6 characters, specified by a, and a numeric field of 1 to 5 digits starting with n. Each card will contain a BCD numeric field which is i greater than the previous one. If β is not one of the standard class names for BCD and BSS card image files, an error comment will be printed. If an overflow occurs in the numeric field, resequencing will continue modulo the numeric field. In addition the comment SEQUENCE FIELD ØVERFLØW will be printed.

Sequence Fields in Card-Image Files

The sequence field is composed of two subfields: an alphanumeric field consisting of from 3 to 6 alphanumeric characters, starting in column 73; and a numeric field of 2 to 5 digits ending in column 80. Blanks in the numeric field should be considered as zeroes.

The boundary between the subfields is determined by column 75 or the rightmost non-numeric, non-blank character occurring after column 75. For simplicity, all programs which generate sequence fields should generate trailing blanks in the alphanumeric field (to fill it out to 3 characters when necessary) and leading zeroes in the numeric field (to fill it out to a maximum of 5 digits); programs which examine the sequence field, however, should not expect this format but should allow for variations by treating blanks as zeroes in the numeric field.

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