

MERGE: a software package for generating a single data-base starting from EMBL and GenBank collections

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MERGE is a software package which has been developed to compare EMBL and GenBank collections generating a new collection containing the GenBank entries along with EMBL entries not contained in the GenBank.

As shown in figure 1a, the following categories of sequences are identified:

- a) EMBL-entries already present in GenBank collection, but updated in the latest EMBL release;
- b) EMBL-entries not present in GenBank collection;
- c) EMBL-entries containing partial GenBank sequences;
- d) EMBL-entries which are part of GenBank entries.

Sequences of categories a), b) and c) are then transformed, using the program TRANSF, in GenBank data-format and inserted into our ACNUC database. The major problem was encountered during the transformation of the EMBL features table into the GenBank features and sites table, owing to the different syntax used

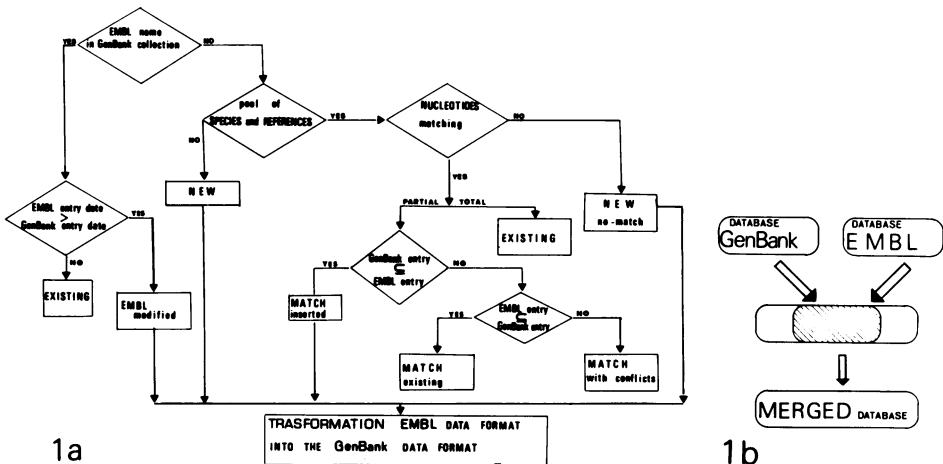


Fig. 1 - a) Flow chart of MERGE software
 b) Merged collection obtained from the EMBL and the GenBank collections by removing the overlapping region.

in the two collections as well as to the incongruency encountered within each collection.

This software package has been developed in order to improve usage of two of our existing packages: ACNUC (1), for retrieval and extraction of the nucleic acid sequences; and GLORIA (submitted for publication) for analysis of extracted sequences. In fact, application of ACNUC and GLORIA on the merged database has proven to be extremely advantageous. In our opinion this work will be a great help to projects devoted to automatization of collection updating as well as in generation of specialized databases.

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