<SEQ2SEP>

    SEQ2SEP collects together separate SEQ files and converts them to SEP.
    The number of SEQ files which can be collected together at one time is 16.
    The SEQs in a SEP are given an ID number starting from 0.

    Execution Method:

        SEQ2SEP -o <foo.sep> <seq1> <seq2> <seq3> ....

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