

ABSTRACT

A method in which a microorganism operational taxonomic unit (OTU) in a sample is defined based on a DNA sequence of a system generation information gene of microorganism in the sample. In the method, qualified sequence segments are obtained by means of processing and reading of an original sequence; the segments are sorted according to a relative abundance value of each segment; and only the qualified sequences with the high abundance values are used to obtain the temporary OTU. The qualified sequences with the low abundance values are reallocated; and the qualified sequence can be distributed to the proper temporary OTU respectively when a sequence similarity degree between the qualified sequence and an OTU sequence reaches at least 97%. The present invention also provides a sequence-assisted microorganism separation method.

Figure 1