SUPPLEMENTARY LISTING 1. ALIGN GENOMES SET

Input: non-reversed nodes chains
Output: list of aligned genomes

all_contigs ← get full contigs list from non-reversed chains
sort all_contigs by their length

aligned_contigs ← empty list

while all_contig is **not** empty **do**

        reference_contig ← longest (first) contig from all_contigs

        for each contig **in** all_contigs **do**
                if contig is reference_contig **do**
                    move contig from all_contig to aligned_contigs

                if reference_contig do not contains at least 50% of nodes from contig **do**
                    continue

                forward_count ← count of pair of sequently located gene contained in both reference_contig and contig
                reverse_count ← count of pair of sequently located gene contained in both reversed reference_contig and contig

                //forward_count and reversed_count calculated with multiplication by the length of the corresponding genes

                if reverese_count > forward_count **do**
                    move reversed contig from all_contigs to aligned_contigs

                else do
                    move contig from all_contigs to aligned_contig

list of aligned genomes ←sort aligned contigs by organisms
return list of aligned genomes