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A pipeline for ncRNA sequence reconstruction and structure characterization of potential homologs from BLAST output

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The BLAST algorithm is used by many researchers as an exploratory RNA sequence search tool. It is extremely useful, but its output includes basically sequence information only, which is not sufficient namely for characterization of sequence fragments. Thus we have developed a pipeline to identify complete sequences of the fragments, predict secondary structures of the subject sequences and infer their homology to the query RNA. The pipeline includes several stages: 1) reconstitution of BLAST hits with anchored Locarna algorithm, 2) inference of homology to the query RNA with RSEARCH algorithm, 3) prediction of a secondary structure with Centroid-homfold algorithm. Our pipeline can be used for characterization of ncRNAs in general by extending information included in the BLAST output. Also, it can be extremely useful when homologs of uncharacterized, e.g. newly identified ncRNAs need to be found and for which more sophisticated methods of homology search cannot be used as they require more information of the RNA in their input that is not available.

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