User friendly computational tools for the analyses of large nucleic acid sequences

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We propose a user-friendly computational bench work for large sequence analysis.
Large scale sequencing is of great contribute to the amount of biological data concerning the structures and the functions of nucleic acid and protein macromolecules. This is the reason of the strong impact of this technique in Computational Biology. The interest for the development of computational tools for sequence characterisation, gives place to well representative examples of the necessity of efficient and exhaustive methods for the analyses. In particular, one of the most spreading computational challenges in the Biocomputing field is the search for biologically meaningful patterns and motifs, for instance the search for coding regions. The wide development of computational tools for coding regions analyses available on the net, while offering varied analytical approaches, often gives place to confusion about the reliability of the methods and to drawbacks caused by unapproachable software. Moreover, sequence dimensions, usually hundred thousands of nucleotides, can be a limit according to the computational power usually available in a laboratory and to the methods employed. These troubles may be complicated by the fact that often the software runs in remote sites.To overcome all these limits, trying to enhance the reliability and exhaustivity of the results searched for, we developed a set of computational tools, written in C language. By the methods available in the set, a user-driven manipulation of the sequence under analysis allows to overcome dimensional problems. The integration and the comparison of results obtained with software available on several remote sites in Internet seems to guarantee a certain accuracy in the analysis. The implementation of a graphical interface allows a direct interpretation of the displayed results that can be easily manipulated for further studies.This bench work can be considered an advantageous collection of tools and helpful in a useful manipulation, description and interpretation of integrated comparative analyses of large nucleic acid sequences.