rnaspace.org

a web application for noncoding RNA identification

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The increasing number of non-protein-coding RNA (ncRNA) discovered since 2000 and the lack of user friendly tools for finding and annotating them, have made necessary to propose to biologist an in silico environment allowing structural and functional annotations of these molecules. For the purpose, RNAspace is developed as a collaborative and open software allowing to:

- run a variety of ncRNA gene finders in an integrated environment,
- explore computed results with dedicated tools for comparison, combination, visualization, alignment and edition of putative ncRNAs, and
- export them in various formats (FASTA, GFF, CSV, RNAML).

The platform is a web application available for use on the web site rnaspace.org (with limitations on analyzed sequence size and execution time), and for local installation. It is written in Python language using CherryPy web framework (see cherrypy.org) and Cheeta template engine (see cheetahtemplate.org).

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General workflow

1. Load genomic sequence
   - RNAspace.org

2. Choose and launch gene finders
   - RNAspace.org

3. Explore ncRNA predictions
   - RNAspace.org

Dynamic exploration (sorting and filtering) of putative ncRNAs found on the genomic sequence. Additional information can be computed and/or visualized [12, 13, 14] on line (e.g., secondary structure [15,16], alignment of predictions[15]) and saved. It is also possible to edit and to delete any putative ncRNA.

References