RNAspace: non-coding RNA annotation web platform

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General presentation

The increasing number of ncRNA discovered since 2000 and the lack of user friendly tools for finding and annotating them, have made necessary to propose to biologists 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 non-protein-coding RNA (ncRNA) gene finders in an integrated environment**,
- **explore computed results** with dedicated tools for comparison, visualization, alignment and edition of putative ncRNAs
- and **export** them in various formats (FASTA, GFF, RNAML).

The platform is developed both as a web site **rnaspace.org** (with limitations on analyzed sequence size and execution time), and for local installation with user authentication. It is written in Python language using CherryPy web framework (see cherrypy.org) and Cheetah template engine (see cheetahtemplate.org).

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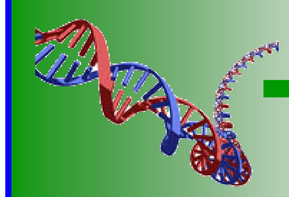
Main workflow

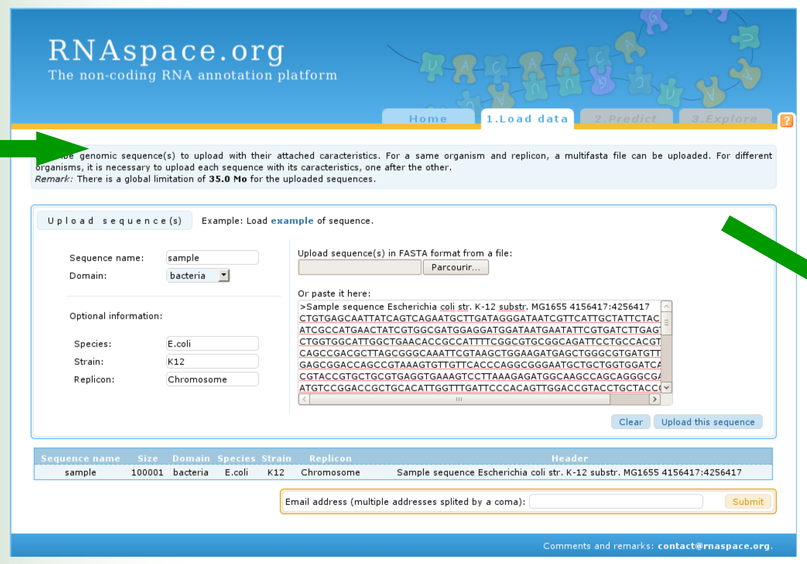
Gene finders are organized into 3 categories containing respectively:

- **known RNA based gene finders** including
  - (i) sequence homology search tools (BLAST[1], YASS[2]) on ncRNA databases (Rfam[3], fRNAdb[4]),
  - (ii) general purpose RNA motif search tools (darn![5], Erpin[6]),
  - (iii) specialized search tools (RNAmmer[7] for ribosomal RNAs, tRNAscan_SE[8] for transfer RNAs)
- **comparative analysis gene finders** (an *ad hoc* pipeline has been implemented based on BLAST or YASS for similarities search and caRNAc[9] or RNAz[10] for consensus structure inference),
- ***ab initio* gene finders** (just one based on detection of atypical GC% regions).

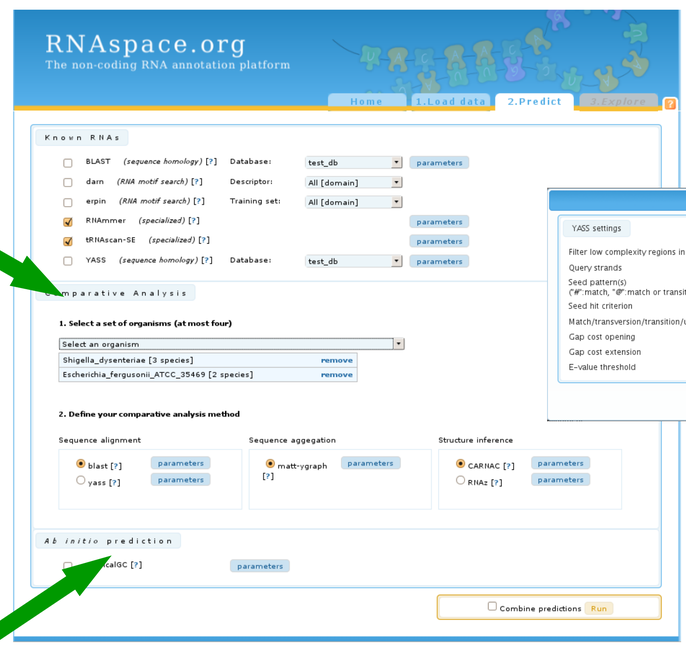
1. Enter genomic sequence(s)



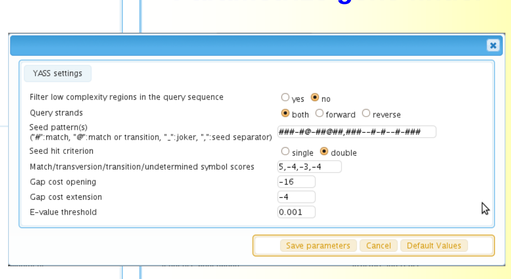
Genomic sequence

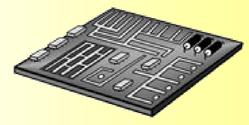


2. Predict ncRNAs



Parametrize gene finder

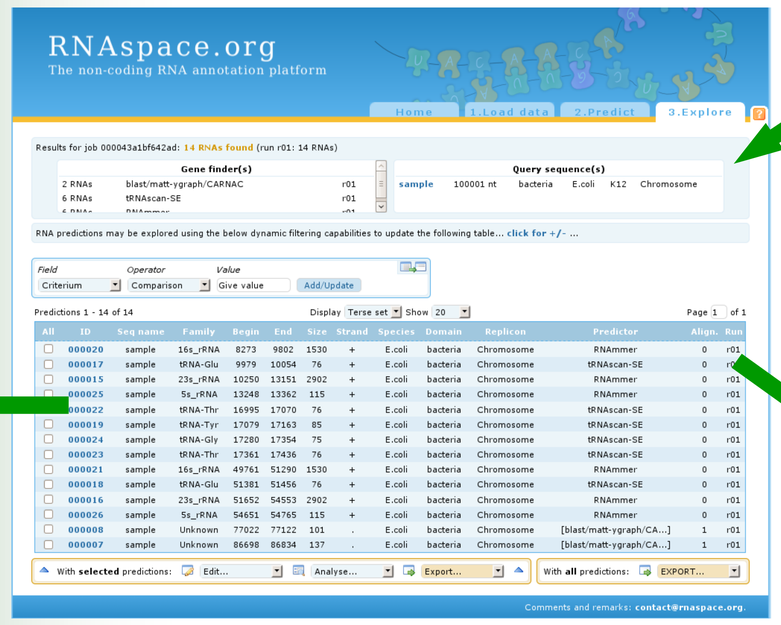


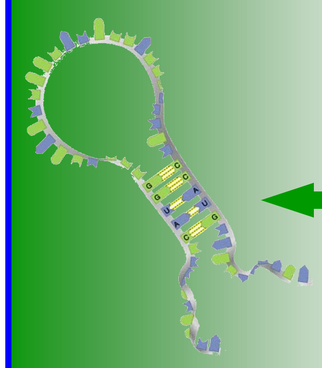


PC or cluster

BIOINFORMATIC'S PLATFORM

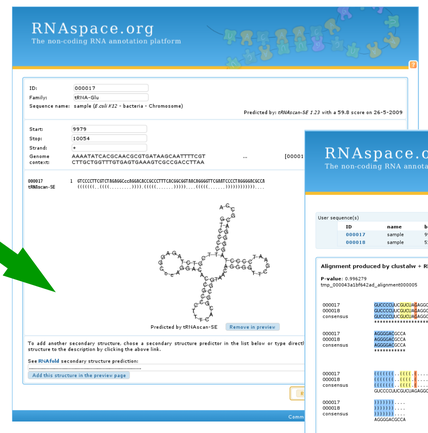
3. Explore and export putative ncRNAs



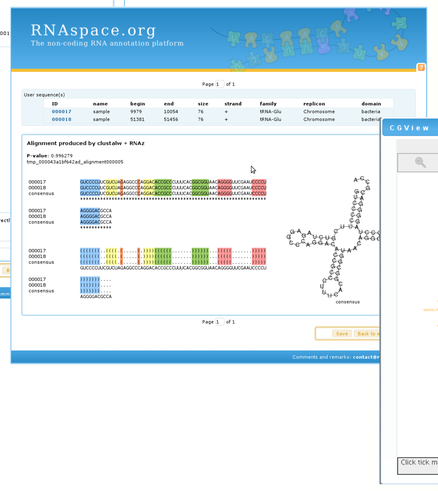


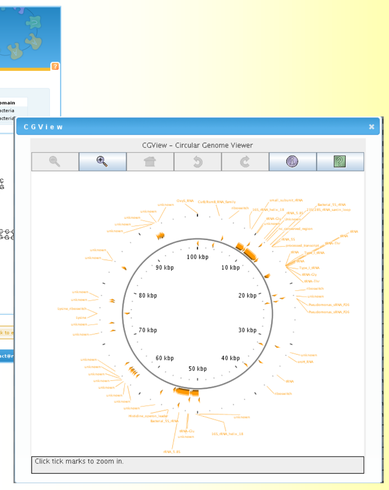
Putative ncRNA

Edit ncRNA



Generate and visualize ncRNAs alignment





Visualize ncRNAs on genomic sequence

(using CGview, see wishart.biology.ualberta.ca/cgview)

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

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