Due to novel experimental methods on the genomic scale, biologists are struggling with ever increasing magnitudes of data that can, in many cases, only be harnessed by previous bioinformatics analyses. Currently many tools are either only accessible on the command line and web servers tend to lack easy usability. The Freiburg RNA Tools webserver attemping at supplying an easy to use and comprehensive web resource for RNA analysis, also for non-adept users. We designed a webserver framework that simplifies the access to our RNA analysis tools. The tools are accompanied by extensive help pages and direct help requests are rapidly answered. All tools incorporate individual post processing steps that aid result interpretation. The results can be viewed in the browser and/or downloaded for further local analysis or archiving. Individual job descriptions can be entered by the user, thus alleviating parallel online archiving. Furthermore, results are stored for 30 days. The Freiburg RNA tools webserver currently integrates eight tools for RNA analysis. It includes CopraRNA [1] (siRNA target prediction), LocARNAn (alignment and design) [2], CARNA (ensemble alignment) [3], MARNA (structure alignment) [4], ExpaRNA (exact matching) [5], INFORNA (RNA secondary structure) [6], IntaRNA (RNA-RNA interaction) [7] and CRISPRmap (CRISPR conservation) [8]. The addition of several further tools is under construction. The tools are available at: http://rna.informatik.uni-freiburg.de.

**Overview**

CopraRNA & IntaRNA

Searching for functionally enriched terms within the top predictions, regularly yields insight into the correct in vivo function of an investigated siRNA. This facilitates construction of functional networks. See the examples below (GcvB, Muf, RflB).

CRISPRmap

Employing an extensive dataset of 18 enterobacterial siRNAs and 152 experimentally verified interactions, we compared CopraRNA to other state of the art siRNA target prediction approaches. CopraRNA yields considerably superior results with respect to sensitivity. Furthermore CopraRNA appears to be at least as reliable as pulse expression microarray experiments.

**ExpaRNA**

ExpaRNA [2] is a tool for very fast comparison of RNAs by exact local matches. Instead of computing a full sequence-structure alignment, ExpaRNA efficiently computes the best alignments of sequence-structure motifs common to two RNAs. Finding identical motifs is not directly addressed by sequence-structure alignment tools and they may remain hidden. In addition, the predicted set of motifs can be used as anchor constraints to speed up and guide Sankoff-style alignment methods like LocARNAn [2].

**LocARNAn & MARNA**

LocARNAn [2] requires several alignment of RNA molecules. LocARNAn requires only RNA sequences as input and will simultaneously build and align the input sequences. LocARNAn submits a multiple alignment together with a consensus structure. For the folding it makes use of a very realistic energy model for RNAs which is also employed by RNAalid of the Vienna RNA package (or mirNA). For the alignment it features RIBOSUM-like similarity scoring and realistic gap cost. MARNA [4] is also offered, yet LocARNAn superseded it.

**CARNA**

In contrast to LocARNAn [2], CARNA [3] does not plot the most likely consensus structure, but computes the alignment that is best to all likely structures simultaneously. Hence, CARNA is particularly useful when aligning RNAs like riboswitches, which have more than one stable structure. Also, CARNA is not limited to rooted structures, but is able to align arbitrary pseudoknots.

**INFORNA**

INFORNA [6] is a server for the design of RNA sequences that fold into a given pseudo-knot free RNA secondary structure.