

R-scape User's Guide

RNA Significant Covariation Above Phylogenetic Expectation

<http://eddylab.org/R-scape/>
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1 Introduction

R-scape (RNA Significant Covariation Above Phylogenetic Expectation) is a program that given a multiple sequence alignment (MSA) of RNA sequences, finds the pairs of positions that show a pattern of significant covariation. Each covariation score has an E-value associated to it. E-values are determined using a null model of covariation due to phylogeny but independent of any structural constraints.

How to avoid reading this manual

- Follow the quick installation instructions on page 5.
- Go to the tutorial section on page 7, which walks you through some examples of using R-scape on real data.

Everything else, you can read later.

How do I cite R-scape?

Rivas, E. *et al.*, “A statistical test for conserved RNA structure shows lack of evidence for structure in lncRNAs”, *Nature Methods* 14, 4548 (2017).

2 Installation

Quick installation instructions

Download `R-scape.tar.gz` from <http://eddylab.org/>; unpack it, configure, and make:

```
> tar xf R-scape.tar.gz
> cd R-scape
> ./configure
> make
> make install
```

The newly compiled binary (`R-scape`) is in the `R-scape/bin` directory. You can run it from there, as in this example:

```
> bin/R-scape tutorial/updatedArisong.sto
```

That's it. You can keep reading if you want to know more about customizing a `R-scape` installation, or you can skip ahead to the next chapter, the tutorial.

System requirements

Operating system: `R-scape` is designed to run on POSIX-compatible platforms, including UNIX, Linux and MacOS/X. The POSIX standard essentially includes all operating systems except Microsoft Windows. We have tested most extensively on Linux and MacOS/X because these are the machines we develop on.

Compiler: The source code is C conforming to POSIX and ANSI C99 standards. It should compile with any ANSI C99 compliant compiler, including the GNU C compiler `gcc`, and the C++ compiler `g++`. We test the code using the `gcc` and `g++` compilers.

Libraries and other installation requirements: `R-scape` includes two software libraries:

- the Easel library package (<http://bioeasel.org/>),
- the HMMER library package (<http://hmmer.org/>),

and three independent programs:

- FastTree (Price et al., 2010) (for building phylogenetic trees),
- R2R (Weinberg and Breaker, 2011) (for drawing consensus RNA structures),
- RNAVIEW (Yang et al., 2003) (for identifying different types of basepairs in nucleic acid alignments).

All libraries and independent programs will automatically compile during `R-scape`'s installation process. By default, `R-scape` does not require any additional libraries to be installed by you, other than standard ANSI C99 libraries that should already be present on a system that can compile C code.

Executables for the three independent programs will appear in the `R-scape/bin` directory.

Makefile targets

all Builds everything. Same as just saying `make`.

install Installs the binaries (`R-scape`, `FastTree`, `r2r`).

By default, programs are installed in `R-scape_version/bin`. You can customize the location of the binaries by replacing

```
> ./configure
```

with

```
> ./configure --prefix=/the/directory/you/want
```

The newly compiled binaries are now in the `/the/directory/you/want/bin` directory.

clean Removes all files generated by compilation (by `make`). Configuration (files generated by `./configure`) is preserved.

distclean Removes all files generated by configuration (by `./configure`) and by compilation (by `make`).

Why is the output of 'make' so clean?

Because we're hiding what's really going on with the compilation with a wrapper. If you want to see what the command lines really look like, pass a `V=1` option (V for "verbose") to `make`, as in:

```
> make V=1
```

What gets installed by 'make install', and where?

The top-level configure file has a variable `RSCAPE_HOME` that specifies the directory where `make install` will install things: `RSCAPE_HOME/bin`.

By default `RSCAPE_HOME` is assigned to the current directory `R-scape`.

The best way to change this default is when you use `./configure`, and the most important variable to consider changing is `--prefix`. For example, if you want to install `R-scape` in a directory hierarchy all of its own, you might want to do something like:

```
> ./configure --prefix=/usr/local/rscape
```

That would keep `R-scape` out of your system-wide directories like `/usr/local/bin`, which might be desirable. Of course, if you do it that way, you'd also want to add `/usr/local/rscape/bin` to your `$PATH`.

3 Tutorial

Here's a tutorial walk-through of how to use R-scape. This should suffice to get you started.

Modes of R-scape

MSA input *with* annotated consensus secondary structure:

Reports all pairs that have covariation scores with E-values smaller than a target E-value (where E-values are calculated relative to the *given structure*).
Draws the given consensus structure annotated with the significantly covarying base pairs.

MSA input *without* an annotated secondary structure:

Reports all pairs that have covariation scores with E-values smaller than a target E-value. (where E-values are calculated assuming *no structure*).
Builds the best consensus structure that includes all significantly covarying pairs, *the maximum-covariation optimal consensus structure*.
Reports all pairs that have covariation scores with E-values smaller than a target E-value. (with E-values calculated relative the *maximum-covariation structure*)
Draws the *maximum-covariation optimal consensus structure* annotated with the significantly covarying base pairs.

I'll show examples of running each mode, using examples in the `tutorial/` subdirectory of the distribution.

Files used in the tutorial

The subdirectory `/tutorial` in the R-scape distribution contains the files used in the tutorial.

The tutorial provides several examples of RNA structural alignments, all in Stockholm format:

updated_Arisong.sto Structural alignment of the ciliate Arisong RNA. This alignment is an updated version of the one published in (Jung et al., 2011).

ar14.sto Structural alignment of the α -proteobacteria ncRNA ar14. This alignment is an updated version of the one published in (del Val et al., 2012).

RF00005.sto Rfam v12.0 (Nawrocki et al., 2015) seed alignment of tRNA.

RF00001-noss.sto Rfam v12.0 seed alignment of 5S rRNA, after removing the consensus secondary structure.

Running R-scape on one alignment file

To run R-scape with default parameters on alignment file `tutorial/updated_Arisong.sto` use:

```
> bin/R-scape tutorial/updated_Arisong.sto
```

The output is a list of the significantly covarying positions

```
# R-scape :: RNA Structural Covariation Above Phylogenetic Expectation
# R-scape 0.6.1 (Jul 2017)
# Copyright (C) 2016 Howard Hughes Medical Institute.
# Freely distributed under the GNU General Public License (GPLv3).
# -----
# MSA updated_Arisong_1 nseq 95 (95) alen 65 (150) avgid 66.35 (64.97) nbpairs 20 (20)
# Method Target_E-val [cov_min,cov_max] [FP | TP True Found | Sen PPV F]
# GTP 0.05 [-9.64,121.98] [0 | 11 20 11 | 55.00 100.00 70.97]
```


#	left_pos	right_pos	score	E-value
*	98	106	121.98	3.71083e-07
*	122	137	95.92	1.81573e-05
*	96	108	89.19	4.97828e-05
*	120	139	77.12	0.000300864
*	119	140	59.65	0.00394406
*	121	138	59.15	0.00437784
*	124	134	58.40	0.00485901
*	123	135	58.24	0.00485901
*	94	110	56.89	0.00598452
*	99	105	55.36	0.00776149
*	97	107	52.27	0.0117527

A star “*” in the first column indicates that the pair is part of the annotated structure in the `updated_Arisong.sto` file. A blank indicates a pair that is not compatible with the structure. A “~” indicates an interaction not in the annotated structure but compatible with it (none in this example).

Default parameters

Default parameters are:

- Target E-value:** default is 0.05. R-scape reports pairs which covariation score has E-value smaller or equal to the target value. The target E-value can be changed with option `-E <x>`, $x \geq 0$.
- Sequence weighting:** Sequences are weighted according to the Gerstein/Sonnhammer/Chothia (GSC) algorithm (Gerstein et al., 1994). This algorithm is time consuming. For alignments with more than 1000 sequences, we use the faster position-based weighting algorithm (Henikoff and Henikoff, 1994). Both weighting algorithms are implemented as part of the easel library.
- Gaps in columns:** Columns with more than 50% gaps are removed. The gap threshold for removing columns can be modified using option `--gapthresh <x>`, $0 < x \leq 1$.
- Covariation statistic:** The default covariation statistic is the average product corrected G-Test (equivalent to option `--GTp`).
- Covariation Class:** R-scape uses the 16 component covariation statistic (C16), unless the number of sequences in the alignment is ≤ 8 or the length of the alignment is ≤ 50 , in which case it uses the two-class covariation statistic (C2). A particular covariation class can be selected using either `--C16` or `--C2`.
The threshold for the minimum number of sequences can be changed with option `--nseqthresh <n>`. The threshold for the minimum alignment length can be changed with option `--alenthresh <n>`.
- Null alignments:** In order to estimate E-values, R-scape produces 20 null alignments, unless the product of the number of sequences by the length of the alignment $< 10,000$ in which case the number of null alignments is 50; or $< 1,000$ in which case it is 100. The number of null alignments can be controlled with option `--nshuffle <n>`.

A full list of the R-scape options is found by using

```
> R-scape -h
```

4 Outputs

For each alignment file `rnafile.sto`, R-scape produces the following output files:

`rnafile.out` Tabular output with the significant pairs, with their score and E-value.

`rnafile.sorted.out` Tabular output sorted from highest to lowest E-value.

`rnafile.sum` Tabular output with a line summary statistics per alignment in the file.

Tabular output per input file

The distribution includes in the directory `tutorials/` examples of output files. If you run R-scape, the outputs will go into your current working directory (not necessarily `tutorials/`).

The output file `tutorial/updated.Arisong.out` looks like this: [> more tutorial/updated.Arisong.out](#)

```
# MSA updated_Arisong_1 nseq 95 (95) alen 65 (150) avgid 66.35 (64.97) nbpairs 20 (20)
# GammaFIT: pmass 0.050024 mu 19.840474 lambda 0.152973 tau 1.281689
# Method Target_E-val [cov_min,cov_max] [FP | TP True Found | Sen PPV F]
# GTp 0.05 [-9.64,121.98] [0 | 11 20 11 | 55.00 100.00 70.97]
# left_pos right_pos score E-value
#-----
* 94 110 56.89 0.00598452
* 96 108 89.19 4.97828e-05
* 97 107 52.27 0.0117527
...
```

The output file is a tabular list of significant pairs sorted by sequence positions:

`First column` indicates whether the significant pair is part of the given structure (*), or not. If the pair is not in the structure, we distinguish whether the pair is compatible with the given structure (~) or not (blank).

In addition, if the structure is provided by a PDB file (using the option `--pdbfile`), a non Watson-Crick/Watson-Crick base pair is designated by "***". A contact that is not a basepair is designated by: "`c ~`" if compatible with all the basepairs, or by "`c`" otherwise.

`Second and third columns` are the two positions of the pair, $i \leq j$ respectively. Positions are relative to the input alignment.

`Fourth column` is the covariation score.

`Fifth column` is the E-value. Significant positions have E-values $\ll 1$.

The output file also includes two comment lines per alignment in the file:

`First comment line` describes properties of the alignment: number of sequence (nseq), alignment length (alen), average percentage identity (avgid), and number of base pairs (nbpairs). Values in parentheses correspond to the alignment as given. Values not in parentheses correspond to the analyzed alignment after the filters (for redundant sequences and gapped columns) have been applied.

`Second comment line` describes properties of the R-scape search: the covariation method (GTp), the E-value threshold (0.05), the range of scores for all pairs in the alignments (from -9.7 to 89.1), the number of covarying non base pairs (0), the number of covarying base pairs (11), the number of base pairs (20), and the total number of covarying pairs (11). Lastly we provide the sensitivity (SEN=55.00=11/20), positive predictive value (PPV=100.00=11/11), and F-measure (F=70.97 = 2 * SEN * PPV / (SEN+PPV)).

Other tabular outputs

R-scape produces two more tabular outputs per input file that are more relevant for benchmarking purposes, those are:

File `tutorial/updated_Arisong.sum` looks like:

```
> more tutorial/updated_Arisong.sum
```

```
#target_E-val  MSA          nseq  alen  avgid  method  TP    True  Found  SEN    PPV
0.05           updated_Arisong_1  95    65    66.35  GTp     11    20    11    55.00 100.00
```

This file produces a one line output per alignment in the file.

Column 1 Target E-value.

Column 2 Alignment name.

Column 3 Number of sequence in the analyzed alignment.

Column 4 Number of columns analyzed.

Column 5 Average percentage identity in the analyzed alignment.

Column 6 Covariation statistic.

Column 7 Number of significant base pairs, TP (true positives).

Column 8 Number of base pairs, T (True).

Column 9 Number of significant pairs, F (Found).

Column 10 Sensitivity = TP/T.

Column 11 Positive predictive value = TP/F.

Outputs per alignment

A Stockholm alignment file can include several different multiple sequence alignments (MSAs). R-scape produces the following output files, one for each individual alignment in the input Stockholm file:

Alignment with consensus secondary structure

If the given alignment has a consensus secondary structure (`#=GF SS_cons` markup), the following files are produced

`rnafile.msaname.R2R.sto` Stockholm file annotated by a modified version of the R2R program. This file includes the information necessary to draw the consensus structure, and to annotate the significantly covarying base pairs.

`rnafile.msaname.R2R.sto.pdf,svg` Drawing of the R-scape-annotated consensus secondary structure.

`rnafile.msaname.surv` A two column file with the survival functions (`surv`) for the covariation scores.

`rnafile.msaname.surv.ps` Plot of the score's survival function $P(X > \text{score})$. Drawing this file requires that program `gnuplot` is installed somewhere in the `$(PATH)`, or that the environmental variable `GNUPLOT` pointing to a `gnuplot` executable is defined.

`rnafilename.msaname.dplot.{ps,svg}` Dot plot of the consensus secondary structure annotated according to co-variation. Drawing of this file requires that program `gnuplot` is installed somewhere in the `$(PATH)`, or that the environmental variable `GNUPLOT` pointing to a `gnuplot` executable is defined.

For each alignment, `msaname` is given by `<ACC>_<ID>`, the combination of the accession `#=GF AC <ACC>` and name `#=GF ID <ID>` in the Stockholm-format markups (or one of two if the other is not defined). If none of those fields are defined, `msaname` is a number describing the order in the file of the given alignment.

Alignment without consensus secondary structure

Alternatively, if the alignment does not have a consensus secondary structure (or if it does and the option `R-scape --cyk` is used) `R-scape` produces the following files describing the maximal-covariation optimal secondary structure:

```
rnafilename.msaname.cyk.R2R.sto
rnafilename.msaname.cyk.R2R.sto.{pdf,svg}
rnafilename.msaname.cyk.surv
rnafilename.msaname.cyk.surv.{ps,svg}
rnafilename.msaname.cyk.dplot.{ps,svg}
```

These files are formatted identically to those for describing the given consensus structure.

Details about outputs per alignment

Two files are produced per alignment in the input file:

File `tutorial/updated_Arisong_1.R2R.sto` is a Stockholm formatted alignment that includes the input alignment annotated with the consensus structure. This Stockholm file also includes the additional annotation required to use the drawing program `R2R`.

It is possible that the resulting drawing will show parts of the secondary structure occluded from each other (especially for long RNAs). Using this file, one can customize a different drawing of the structure using the `R2R` documentation, provided in `lib/R2R/R2R-manual.pdf`.

File `tutorial/updated_Arisong_1.surv` looks like this:

```
> more tutorial/updated_Arisong_1.surv
121.795428      0.05
95.862635      0.1
89.113004      0.15
...
&
63.890698      0.000485437
58.917286      0.000970874
47.904730      0.00145631
...
&
81.652885      2.40385e-06
77.745204      4.80769e-06
77.034717      7.21154e-06
...
&
256.788050     2.64342e-17
256.432807     2.7899e-17
256.077563     2.94449e-17
...
&
```

The first column is a covariation score (x). The second column is the survival function $P(X > x)$, that is the frequency of pairs having score larger than x . The file includes four survival functions separated by a “&” line. The three survival functions correspond to:

First functions: the given alignment, proposed base pairs. (This section is empty if no secondary structure is proposed.)

Second functions: the given alignment, not proposed pairs.

Third function: the aggregation of all null alignments, all possible pairs.

Fourth function: the expected null survival function according to the tail Gamma fit.

Graphical outputs per alignment

Three plots are produced per alignment in the input file:

updated_Arisong_1

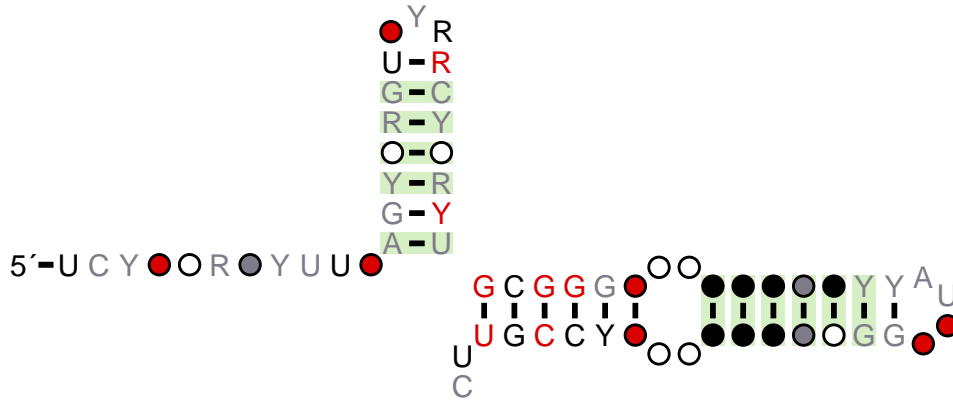


Figure 1: `tutorial/updated_Arisong_1.R2R.sto`. {pdf, svg}: annotated consensus secondary structure. Base pairs with covariation scores equal or below the target E-value (0.05 as default) are depicted in green. By default only positions in the alignment with more than 50% occupancy are depicted (unless they form a base pair). Option `--r2rall` forces the depiction of all positions in the alignment.

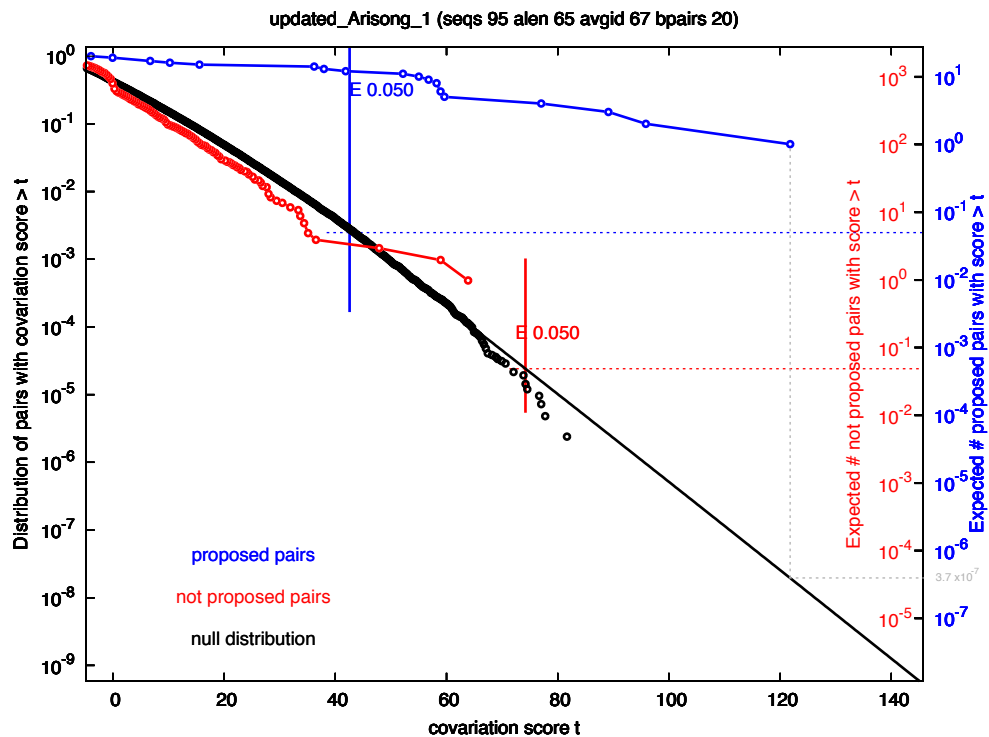


Figure 2: `tutorial/updated_Arisong_1.surv.{ps,svg}`: covariation scores survival function $P(X > x)$. The survival function of scores for all pairs in the given alignment is depicted in blue. The survival function for the null alignments is depicted in black. A black line indicates to fit to a truncated Gamma distribution of the tail of the null distribution. In red, we plot the survival function of scores for the pairs in the given alignment excluding those proposed as base pairs. For a particular pair, as an example the highest scoring one from the distribution of proposed pairs (blue), we obtain its E-value by drawing a vertical (gray) line from the point to the null distribution (black). The corresponding value in the blue scale gives us the E-value for that pair (in this example, $3.7 \cdot 10^{-7}$).

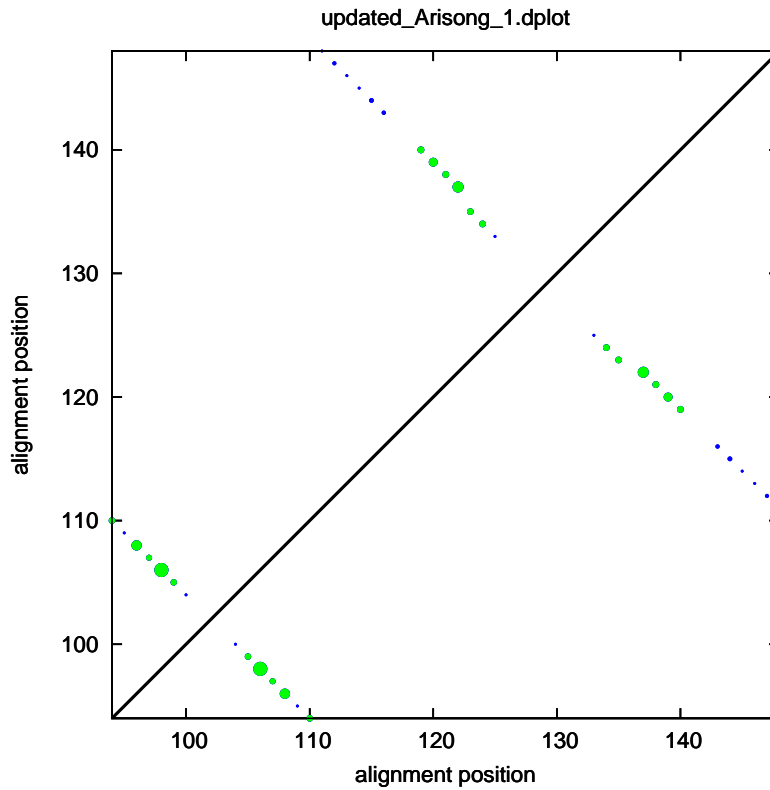


Figure 3: `tutorial/updated_Arisong_1.dplot`. `{ps,svg}`: `dotplot`. Dot size is proportional to the covariation score. In blue we depict the consensus base pairs; in green, the consensus base pairs that show significant covariation; in orange (none shown in this plot), we depict other pairs that have significant covariation, are not part of the consensus secondary structure but are compatible with it; in black we depict other significant pairs. Position are relative to the original input alignment (before any gapped column is removed).

5 Options

The whole list of options can be found using

```
> R-scape -h
```

Some important options are:

Covariation statistic options

-E <x>

Target E-value is $x \geq 0$.

--GT, --MI, --MIr, --MIg, --CHI, --OMES, --RAF, --RAFS,

We favor the G-test covariation statistic, but a total of eight covariation statistics are currently implemented in R-scape. For each covariation statistic (GT, for instance), R-scape can also calculate its average product correction (GTP) and its average sum corrections (GTa). For each option above, appending “p” or “a” chooses one of the corrections. For example, --GT does the G-test statistic, --GTP does the APC-corrected G-test statistic, --GTa does the ASC-corrected G-test statistic.

The R-scape default is --GTP.

Details of the definition and provenance of the different covariation statistics can be found in the R-scape manuscript: Rivas, E. & Eddy S. E., “A statistical test for conserved RNA structure shows lack of evidence for structure in *lncRNAs*”.

In a nutshell, given two alignment columns i, j ,

G-test:(Woolf, 1957)	$GT(i, j) = 2 \sum_{a,b} \text{Obs}_{ij}^{ab} \log \frac{\text{Obs}_{ij}^{ab}}{\text{Exp}_{ij}^{ab}},$
Pearson’s chi-square:	$CHI(i, j) = \sum_{a,b} \frac{(\text{Obs}_{ij}^{ab} - \text{Exp}_{ij}^{ab})^2}{\text{Exp}_{ij}^{ab}},$
Mutual information:(Shannon, 1948; Gutell et al., 1994)	$MI(i, j) = \sum_{a,b} P_{ij}^{ab} \log \frac{P_{ij}^{ab}}{p_i^a p_j^b},$
MI normalized:(Martin et al., 2005)	$MIr(i, j) = \frac{MI(i, j)}{H(i, j)} = \frac{MI(i, j)}{-\sum_{a,b} P_{ij}^{ab} \log P_{ij}^{ab}},$
MI with gap penalty:(Lindgreen et al., 2006)	$MIg(i, j) = MI(i, j) - \frac{N_{ij}^G}{N},$
Obs-Minus-Exp-Squared:(Fodor and Aldrich, 2004)	$OMES(i, j) = \sum_{a,b} \frac{(\text{Obs}_{ij}^{ab} - \text{Exp}_{ij}^{ab})^2}{N_{ij}},$
RNAalifold (RAF):(Hofacker et al., 2002)	$RAF(i, j) = B_{i,j},$
RNAalifold Stacking (RAFS):(Lindgreen et al., 2006)	$RAFS(i, j) = \frac{1}{4} (B_{i-1,j+1} + 2 B_{i,j} + B_{i+1,j-1}).$

where a, b are (non-gap) residues; N is the total number of aligned sequences; Obs_{ij}^{ab} is the observed count of $a : b$ pairs in columns i, j (only counting when both a,b are residues); N_{ij} is the total number of residue pairs in columns i, j (only counting when both a,b are residues); P_{ij}^{ab} is the observed frequency of pair $a : b$ in columns i, j ($P_{ij}^{ab} = \frac{\text{Obs}_{ij}^{ab}}{N_{ij}}$); $\text{Exp}_{ij}^{ab} = N_{ij} p_i^a p_j^b$ is the expected frequency of pair $a : b$ assuming i, j are independent, where p_i^a are the marginal frequencies of a residues in column i (averaged to all other positions) ($p_i^a = \frac{1}{L-1} \sum_{j \neq i} \sum_b P_{ij}^{ab}$); $N_{ij}^G = N - N_{ij}$ is the number of pairs involving at least one gap symbol; the definition of $B_{i,j}$ used in the RAF and RAFS statistics is involved, a concise definition can be found elsewhere (Lindgreen et al., 2006).

The background corrections (Dunn et al., 2007) for a given covariation statistic above $\text{COV}(i, j)$ are,

$$\begin{aligned} \text{Average product correction} \quad \text{COVp}(i, j) &= \text{COV}(i, j) - \frac{\text{COV}(i)\text{COV}(j)}{\text{COV}}, \\ \text{Average sum correction} \quad \text{COVa}(i, j) &= \text{COV}(i, j) - (\text{COV}(i) + \text{COV}(j) - \text{COV}). \end{aligned}$$

--C2, --C16

For all the covariation statistics (except RAF and RAFS), one can do a 16-component (C16) or a two-component (C2) calculation, depending on whether it uses the 16 possible pair combinations, or those are group in two classes depending on whether they form a Watson-Crick pair (6 cases, including U:G and G:U), or whether they do not (10 cases).

R-scape's default is the 16 component covariation statistic, unless the number of sequences in the alignment is ≤ 8 or the length of the alignment is ≤ 50 , in which case it uses the two-class covariation statistic.

Search options

--cyk

An optimal secondary structure is computed that includes all significant base pairs. The files for this maximum-covariation optimal structure all include the suffix `.cyk`.

When option `--cyk` is used, a file with the original alignment annotated with the R-scape structure in Stockholm format is produced. This alignment has the suffix `.cyk.sto`.

--naive

Reports the laundry list of all covariation scores, without any statistical significance (E-value) associated to them. No null alignments are created.

--tstart <n>

Analyze starting from position $n \geq 1$ in the alignment.

--tend <n>

Analyze ending at position $n \leq L$ in the alignment.

--window <n>

R-scape can be run in a window scanning version for long alignments. The window size is $n > 0$.

--slide <n>

In scanning mode, this options sets the number of positions to move from window to window, $n > 0$.

Input alignment options

-I <x>

Only sequences with less than $0 < x \leq 1$ pairwise similarity are considered in the analysis. Pairwise % identity is defined as the ratio of identical positions divided by the minimum length of the two sequences. If this option is not used all (weighted) sequences are used in the analysis.

--gapthresh <x>

Only columns with less than $0 < x \leq 1$ fraction of gaps are considered in the analysis.

--consensus

If the alignment has a GC "seq_cons" field, only consensus positions will be analyzed.

--submsa <n>

Analyzes a random subset of the input alignment.

--treefile <f>

A phylogenetic tree in Newick format can be given (by default a tree is created from the alignment using the program FastTree (Price et al., 2010)). R-scape checks that the number of taxa and the names of the taxa matches for all alignments analyzed.

Options for importing a structure

R-scape does not require to input a structure (either a RNA structure or a protein contact map).¹

There are two ways to provide a contact map (or structure):

- By providing the alignment in Stockholm format with a “ss_cons” field including the consensus structure for the alignment. (For RNA alignments only.)
- By analyzing a 3D structure provided in a PDB file. (For either RNA or peptide alignments.)

These two options are incompatible with each other. If both a consensus structure is provided, and a PDB file, the consensus structure will be ignored, and a structure will be calculated from the PDB file using the program `rnaview` (Yang et al., 2003).

If the sequence in the PDB file is found not to be a homolog of those in the input alignment (using the program `nhmmer`), no contact map is produced.

The contacts are extracted using two methods:

- The distance between any two residues is calculated (as the minimal Euclidean distance between any two atoms, except for H atoms). Any two pairs at a distance not larger than a maximum value (`contmaxD`) are called a “contact”.
- In addition if a nucleic acid alignment, R-scape runs the program `rnaview` (Yang et al., 2003) (<http://ndbserver.rutgers.edu/ndbmodule/services/download/rnaview.html>) in order to identify RNA base pairs within the contacts.

The options that control the input of a structure or contact map are:

--pdbfile <s>

Reads a `pdbfile` associated to the alignment, and extracts the contacts from it.

Option `--pdbfile` is incompatible with `--cyk`.

--cntmaxD <x>

Maximum distance (in Angstroms) allowed between two residues to define a “contact” is $\langle x \rangle$.

¹For RNA alignments alone, if no structure is provided, R-scape computes the best secondary structure that includes the maximum number of significantly covarying basepairs.

--cntmind <n>

Minimum distance (in residue positions) in the backbone between two residues required to define a “contact” is $\langle n \rangle$.

Example of reading a structure from a PDB file for the FMN riboswitch:

```
> bin/R-scape --cntmaxD 4 --cntmind 3 --pdbfile tutorial/3f2q.pdb tutorial/RF00050.sto
```

This command line extracts contacts from the pdb file that are at a Euclidian distance $\leq 4\text{\AA}$ in the PDB structure, and such that they are at least 3 residues apart in the backbone.

The output is

```
# R-scape :: RNA Structural Covariation Above Phylogenetic Expectation
# R-scape 0.6.1 (July 2017)
# Copyright (C) 2016 Howard Hughes Medical Institute.
# Freely distributed under the GNU General Public License (GPLv3).
# -----
# 6 215 | bptype WWc
# 6 216 | bptype CONTACT
# 7 214 | bptype WWc
# 7 215 | bptype CONTACT
# 8 213 | bptype WWc
# 8 214 | bptype CONTACT
# 9 212 | bptype WWc
# 9 213 | bptype WWc
#
#
#
# 193 201 | bptype WWc
# 193 202 | bptype CONTACT
# 195 198 | bptype WHt
# 198 201 | bptype CONTACT
# contacts 153 (46 bpairs 32 wc bpairs)
# maxD 4.00
# mind 3
# L 139
# alen 221
# MSA RF00050_FMN.3f2q_nseq 144 (144) alen 139 (221) avgid 69.18 (68.15) nbpairs 46 (0)
# Method Target_E-val [cov_min,conv_max] [FP | TP True Found | Sen PPV F]
# GTp 0.05 [-9.58,216.11] [3 | 14 46 17 | 30.43 82.35 44.44]
# left_pos right_pos score E-value
#-----
* 171 183 216.11 4.41458e-11
* 170 184 211.69 8.02215e-11
* 192 202 168.72 1.91884e-08
* 8 213 149.72 2.19077e-07
* 172 182 138.67 8.92814e-07
* 169 185 137.23 1.10807e-06
** 16 30 133.45 1.70655e-06
* 84 186 125.61 4.75589e-06
* 17 29 112.05 2.66491e-05
* 7 214 111.13 2.96758e-05
* 6 215 96.44 0.000194387
* 36 87 96.33 0.000194387
~ 5 216 131.03 0.000489499
* 94 163 78.82 0.00183574
* 7 213 107.69 0.0094673
* 7 8 98.52 0.0308494
* 37 86 53.10 0.0438743
```

All coordinates are relative to the input alignment. The annotation of all types of RNA basepairs (WWc, WWt, WHc,...) is produced by the program `rnaview` (Yang et al., 2003).

Options for type of pairs tested

--sampleall

The statistical test includes all possible pairs in the alignment. This is the default option (both for nucleic acid or amino acid alignments) when no list of contacts is identified.

--samplecontacts

The statistical test includes all the contacts identified in a PDB or/and as a RNA secondary structure included with a input alignment in Stockholm format. This is the default option for amino acid alignments if a PDB file is provided. If no contacts are found, it reverts to option `--sampleall`.

--samplebp

For RNA alignments with only. The statistical test includes basepairs of all 12 possible types. This is the default option for RNA/DNA alignments if a PDB file is provided. If no consensus structure is found, it reverts to option `--sampleall`.

--samplewc

For RNA alignments only. The statistical test includes only the canonical (Watson-Crick/Watson-Crick type) basepairs (A:U, G:C, G:U). This is the default option for RNA/DNA alignments if a consensus secondary structure is provided. If no canonical basepairs are found, it reverts to option `--sampleall`.

Output options

--roc

Produces a tabular output that provides statistics for each score value.

File `tutorial/updated_Arison.g.roc` looks like:

```
> more tutorial/updated_Arison.g.roc
# MSA nseq 95 alen 65 avgid 66.352419 nbpairs 20 (20)
# Method: GTP
#cov_score FP TP Found True Negatives Sen PPV F E-value
121.79543 0 2 2 20 2060 10.00 100.00 18.18 4.07104e-05
121.44018 0 2 2 20 2060 10.00 100.00 18.18 4.29443e-05
121.08494 0 2 2 20 2060 10.00 100.00 18.18 4.53006e-05
120.72970 0 2 2 20 2060 10.00 100.00 18.18 4.53006e-05
...
```

This file produces a tabular output for each alignment as a function of the covariation score, for plotting ROC curves. The values in the file are described by the comment line. Notice that the number of Trues (column 5) and Negatives (column 6) are fixed for a given secondary structure and do not change.

--outmsa <f>

The actual alignment analyzed can be saved in Stockholm format to file `<f>`.

Plotting options

--nofigures

None of the graphical outputs are produced using this option.

--r2rall

Forces R2R to draw all positions in the alignment. By default only those that are more than 50% occupied or are base paired are depicted.

Other options

`--seed <n>`

Sets the seed of the random number generator to <n>. Use n = 0 for a random seed.

6 Some other topics

How do I cite R-scape?

Pending a publication, the appropriate citation is to the web server, github.com/EddyRivasLab/R-scape.

You should also cite what version of the software you used. We archive all old versions, so anyone should be able to obtain the version you used, when exact reproducibility of an analysis is an issue.

The version number is in the header of most output files. To see it quickly, do something like `R-scape -h` to get a help page, and the header will say:

```
# R-scape :: RNA Structural Covariation Above Phylogenetic Expectation
# R-scape 0.2 (June 2016)
# Copyright (C) 2016 Howard Hughes Medical Institute.
# Freely distributed under the GNU General Public License (GPLv3).
# -----
```

So (from the second line there) this is from R-scape v0.1.

How do I report a bug?

Email us, at elenarivas@fas.harvard.edu.

Before we can see what needs fixing, we almost always need to reproduce a bug on one of our machines. This means we want to have a small, reproducible test case that shows us the failure you're seeing. So if you're reporting a bug, please send us:

- A brief description of what went wrong.
- The command line(s) that reproduce the problem.
- Copies of any files we need to run those command lines.
- Information about what kind of hardware you're on, what operating system, and what compiler and version you used, with what configuration arguments.

7 Acknowledgments

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