

### A database and a web resource for studying recurrent interaction networks in RNA structures

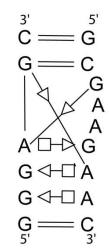
http://carnaval.lri.fr

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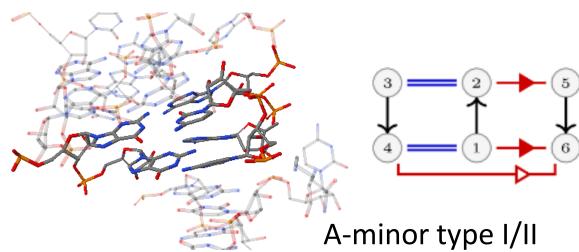
#### **RNA tertiary motifs**

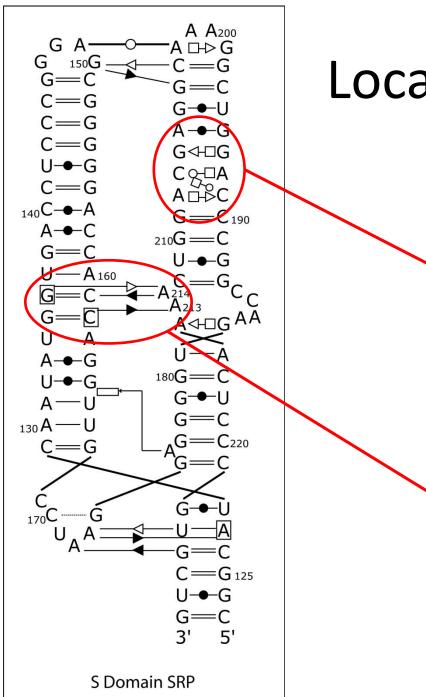
They are mostly composed of noncanonical interactions C A96 A95 G97 G79 G79 G94 A80 A98 G78 A99 C100 G92 C82 A99 C100



Kink-turn

They can mediate the 3D folding of the molecule, they can also be sites for chemical synthesis.





### Local and distant motifs

**Local**: within a secondary structure element.

**Distant**: connects 2 distinct secondary structure elements.

#### Databases for RNA structural motifs

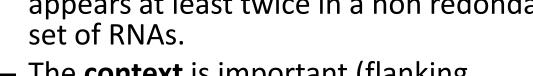
- RNA 3D Motif Atlas (Petrov et al. 2013)
- RNA Bricks (Chojnowski et al. 2014)

 But neither automatic detection nor comprehensive database for distant motifs until recently.

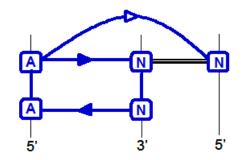


#### **Recurrent Interaction Networks (RINs)**

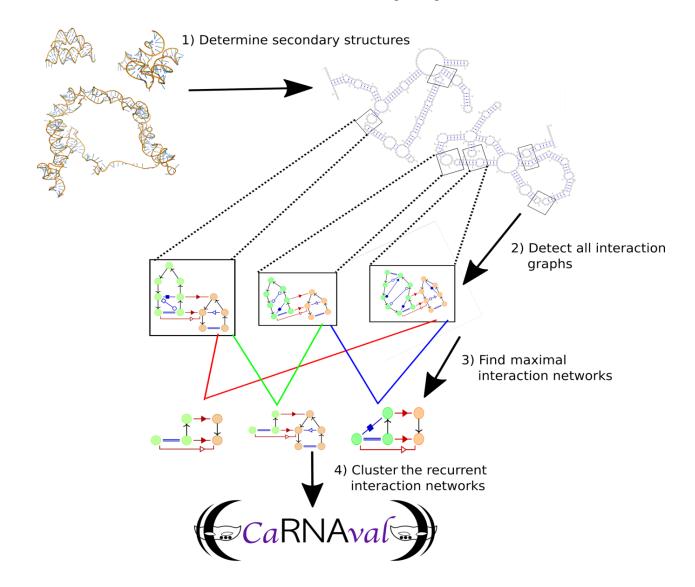
- Definition: remember Benasque 2015 <sup>(C)</sup> ... or read the paper (NAR 2018)
- Main properties:
  - An interaction network connects two secondary structure elements (SSEs)
  - An interaction network is recurrent if it appears at least twice in a non redondant set of RNAs.



- The context is important (flanking) interactions and nucleotides)
- An interaction network can be **modular**, *i.e.* it can contain smaller interaction networks.



# Automated extraction and classification pipeline



### Data and statistics

- All non-redondant structures in RNA3DHub (<u>http://rna.bgsu.edu/rna3dhub</u>) version 2.92, September 2016, at 3.0 Å resolution.
- Some statistics:
  - 845 structures extracted from the PDB, containing
     912 RNA chains identified as non-redundant
  - 1426 pairs of SSEs connected by long range interactions
  - 337 recurrent interaction networks (RINs) found; from 2 to 257 occurrences of each.

### Home page



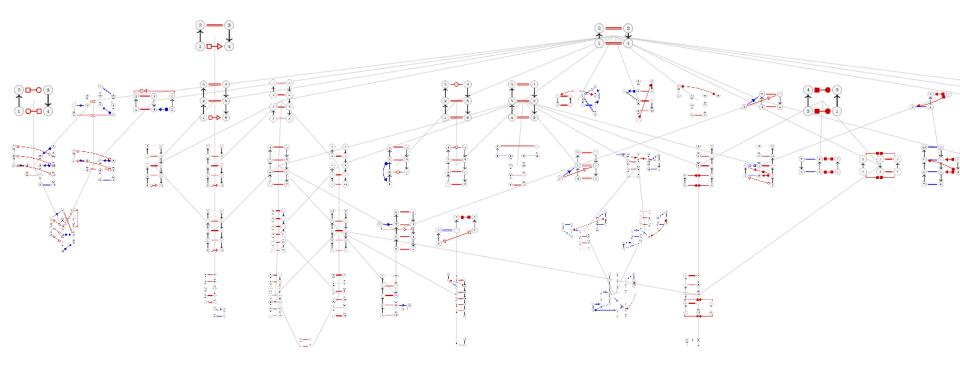
Organized collection of Recurrent Interaction Networks (RIN) in all experimentally determined RNA structures with proper display tools

#### carnaval.lri.fr

Info	All RINs
Adjacent SSEs RINs	Distant SSEs RINs
Catalogs	Upload
Filter by interactions	Filter by PDBs
Download dataset	Benefactors

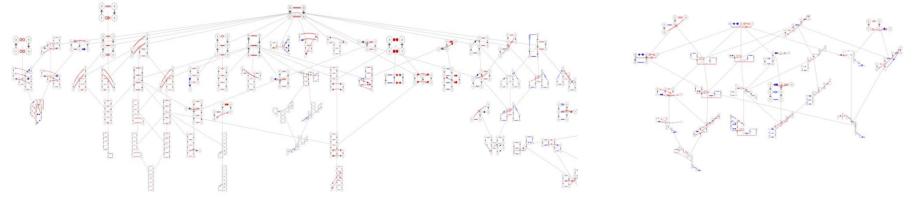


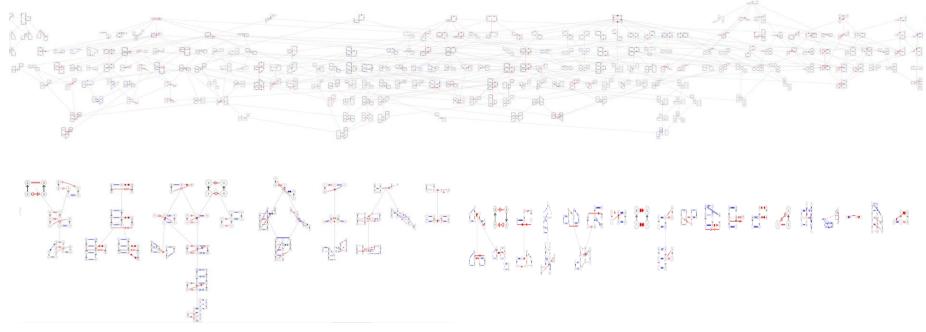




All RINs

#### All RINs with their inclusion relations



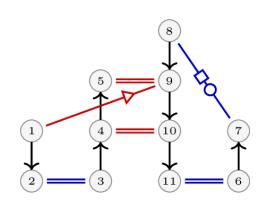


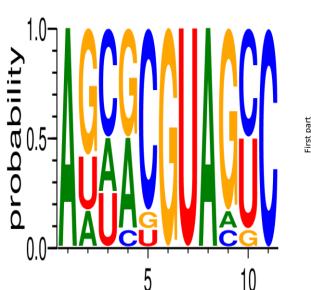
10

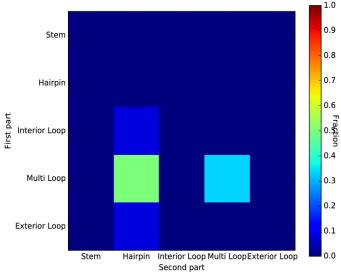
	Catalogs	All RINs ( Distant SSEs R Adjacent SSEs	RINs (press s)	CaRNA	val
#1 25		#2 194	#3 177	#4 176	#5 166
	0 <u>-0</u> 3				
		#7 142	#8 139	#9 139 ○ () → () () → ()	#10 135
i —i #1 13 2→0 1 → 0		#12 132	#13 118	#14 117 0,0,_0	#15 107
		#17 102 0,-0,-0	v — ∞ #18 101 v — ∞ → ∞	#19 100 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	#20 99
() () () () () () () () () () () () () (		#22 87	#23 82	#24 80 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	#25 79

### RIN #78 : general information

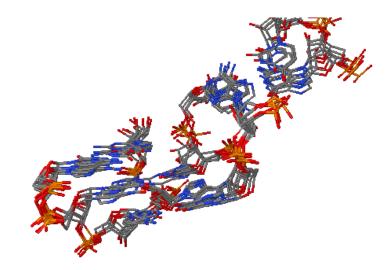
#### 12 occurrences







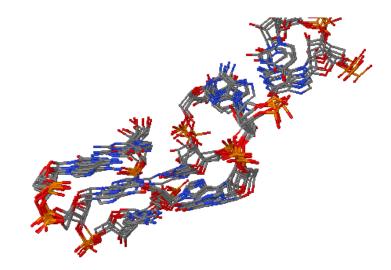
#### RIN #78 : locations and 3D alignment



<ul> <li>SFDU_1A_0 AGCCCGUAGGC</li> </ul>	Crystal structure of the metalnikow	vin i antimicrobial peptide bound to the therm
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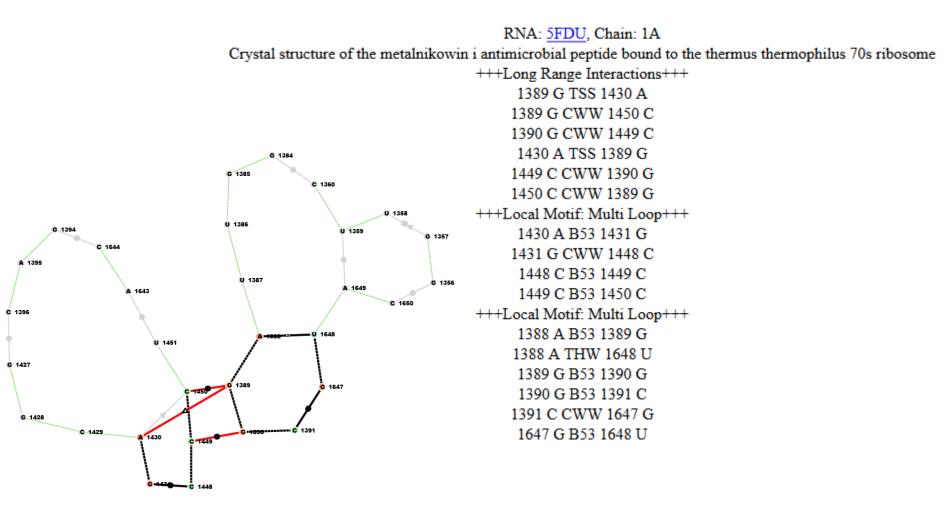
- 🗹 5J7L\_DA\_1 AGCGCGUAGCC Structure of the 70s e coli ribosome with the u1052g mutation in the 16s rrna bo
- 🗹 4RGE B 2 AUAGCGUAGCC Crystal structure of the in-line aligned env22 twister ribozyme
- 🗹 4V9F 0 3 AGCGUGUAACC The re-refined crystal structure of the haloarcula marismortui large ribosomal s
- 🗹 3F2Q X 4 AUAACGUAGUC Crystal structure of the fmn riboswitch bound to fmn
- 🔲 4V9F 0 5 AGUACGUAGUC The re-refined crystal structure of the haloarcula marismortui large ribosomal s
- 🔲 5FDU 1A 6 AGCGCGUAGCC Crystal structure of the metalnikowin i antimicrobial peptide bound to the therm
- 🗌 4V88 A5 7 AUAACGUAGUC The structure of the eukaryotic ribosome at 3.0 a resolution.
- 🔲 5DM6 X 8 AGCACGUAGUC Crystal structure of the 50s ribosomal subunit from deinococcus radiodurans
- 🔲 4V9F 0 9 AAUGCGUAGCC The re-refined crystal structure of the haloarcula marismortui large ribosomal s
- 🔲 4FRG\_B\_10 AGCAGGUACUC Crystal structure of the cobalamin riboswitch aptamer domain
- 🗏 40JI A 11 🛛 AAUGCGUAGCC Crystal structure of twister ribozyme

#### RIN #78 : locations and 3D alignment



• 🗹 5FDU_1A_0	AGCCCGUAGGC	Crystal structure of the metalnikowin i antimicrobial peptide boun	nd to the therm
• 🗹 5J7L_DA_1	AGCGCGUAGCC	Structure of the 70s e coli ribosome with the u1052g mutation in t	he 16s rrna bc:
• 🛛 4RGE_B_2	AUAGCGUAGCC	Crystal structure of the in-line aligned env22 twister ribozyme	
• 🗹 4V9F_0_3	AGCGUGUAACC	The re-refined crystal structure of the haloarcula marismortui lar	ge ribosomal s
• 🗷 3F2Q_X_4	<sup>.</sup> ● 8 in r	ibosomes,	
• 🔲 4V9F_0_5	<sup>⊾</sup> • 2 in t	wister ribozyme	ge ribosomal s
• 🔲 5FDU_1A_6	<sup>AG(</sup> • 2 in )	riboswitches (colabamin, FMN).	i to the therm
• 🔲 4V88_A5_7	AU		
• 🔲 5DM6_X_8	AGCACGUAGUC	Crystal structure of the 50s ribosomal subunit from deinococcus ra	diodurans
• 🔲 4V9F_0_9	AAUGCGUAGCC	The re-refined crystal structure of the haloarcula marismortui lar	ge ribosomal s
• 🔲 4FRG_B_10	AGCAGGUACUC	Crystal structure of the cobalamin riboswitch aptamer domain	
• 🔲 40JI_A_11	AAUGCGUAGCC	Crystal structure of twister ribozyme	1.4

#### Rin #78: all occurrences information



Info	All RINs	I want to see all RINs of the database which
Adjacent SSEs RINs	Distant SSEs RINs	have at least three distant cSS interactions
Catalogs	Upload	and one distant tSS interaction.
Filter by interactions	Filter by PDBs	
Download dataset	Benefactors	

Info	All RINs	I want to know whic RINS are present in 2GDI Y, 4P9R A pdb
Adjacent SSEs RINs	Distant SSEs RINs	
Catalogs	Upload	
Filter by interactions	Filter by PDBs 🖌	structures.
Download dataset	Benefactors	

Info	All RINs	I want to know which RINS are present in <b>my</b>
Adjacent SSEs RINs	Distant SSEs RINs	RNA structure (in CIF format).
Catalogs	Upload	ionnatj.
Filter by interactions	Filter by PDBs	
Download dataset	Benefactors	

	Info	All RINs
Ac	djacent SSEs RINs	Distant SSEs RINs
	Catalogs	Upload
Fil	ter by interactions	Filter by PDBs
D	ownload dataset	Benefactors

#### Mining for recurrent long-range interactions in RNA structures reveals embedded hierarchies in network families 3

Vladimir Reinharz, Antoine Soulé, Eric Westhof, Jérôme Waldispühl, Alain Denise 🐱

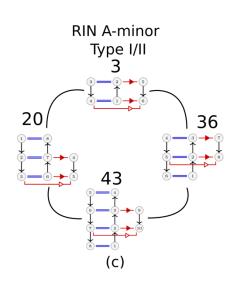
46

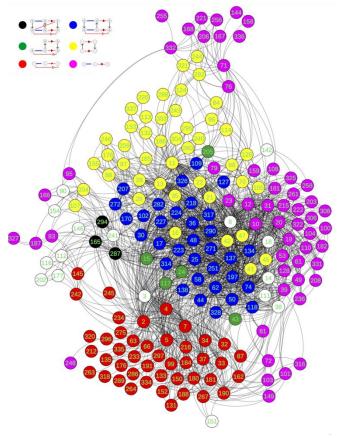
(d)

Nucleic Acids Research, Volume 46, Issue 8, 4 May 2018, Pages 3841–3851, https://doi.org/10.1093/nar/gky197

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- Pipeline / algorithms
- RINs' global analysis

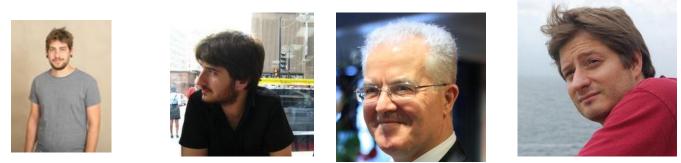




#### Perspectives

- CaRNAval 2 (hopefully before Benasque 2021)!
  - Local motifs, (classical) RINs, generalised RINs (more than two SSEs)
  - Much faster extraction algorithm.

• Structure prediction, structure design...



Vladimir Reinharz, Antoine Soulé, Eric Westhof, Jérôme Waldispühl, Alain Denise



#### Also thanks to : Yann Ponty, Anton Petrov, Neocles Leontis.







## Thanks !