

RNA Viruses

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Where to find viral sequences?

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- NCBI
- Rfam
- ViPR

Where to find viral alignments?

OOPSY! A FATAL ERROR HAS OCCURED!

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Problems:

- Number of sequences

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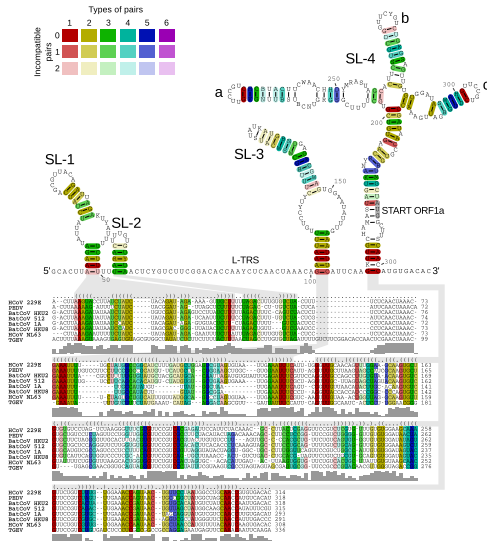
Problems:

- Number of sequences
- Iff subset: Which sequences? (ICTV)
- Mutational hotspots and insertion/deletions

Apply RNA Secondary Structures tools to RNA viruses?

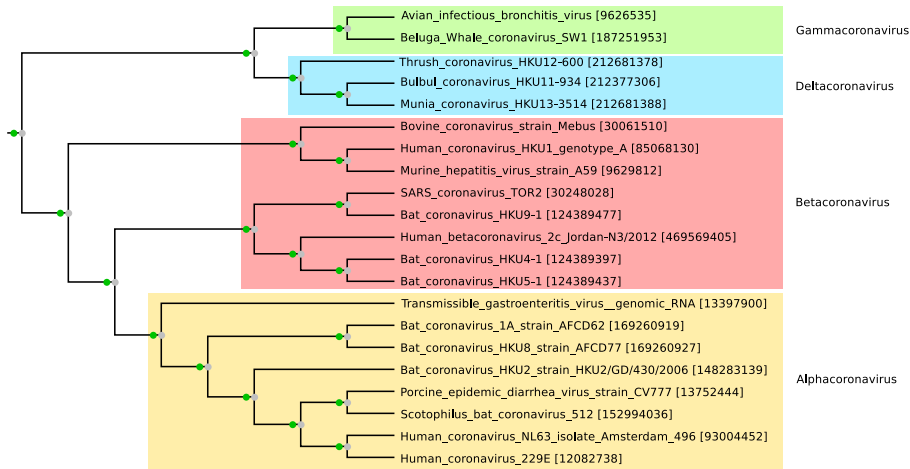
Apply RNA Secondary Structures tools to RNA viruses?

Example: Coronaviruses, 5' UTR

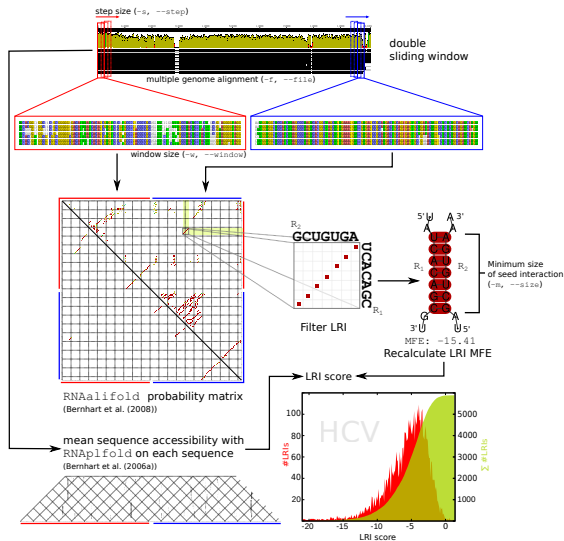


Clustering of secondary structures

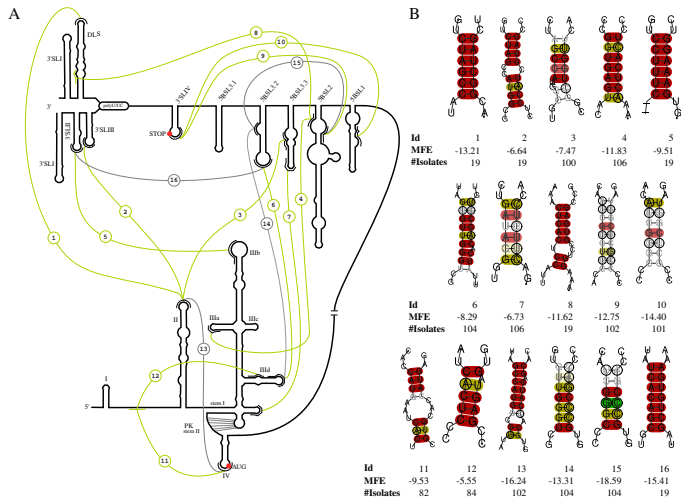
Clustering of secondary structures



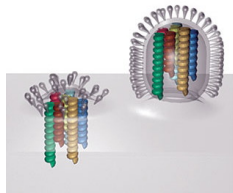
Secondary structures in RNA viruses: Long-range interactions



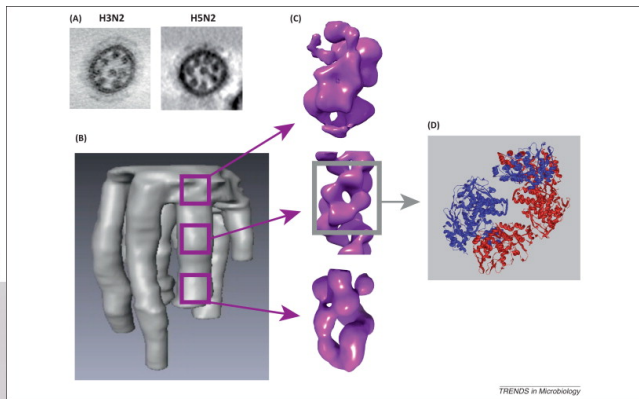
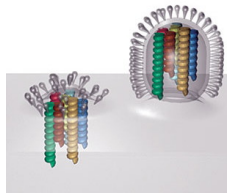
Impact of secondary structures in RNA viruses: Long-range interactions in HCV



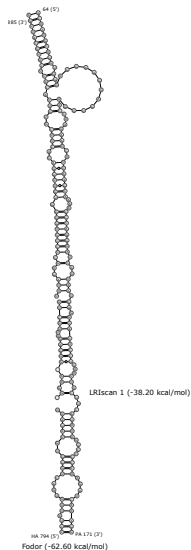
Packaging in Influenza



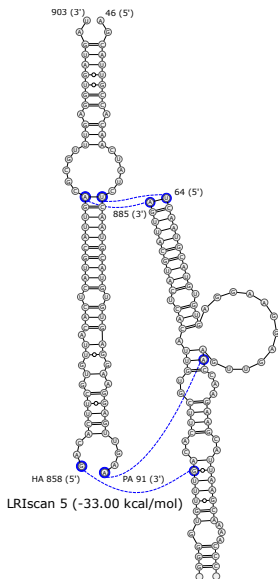
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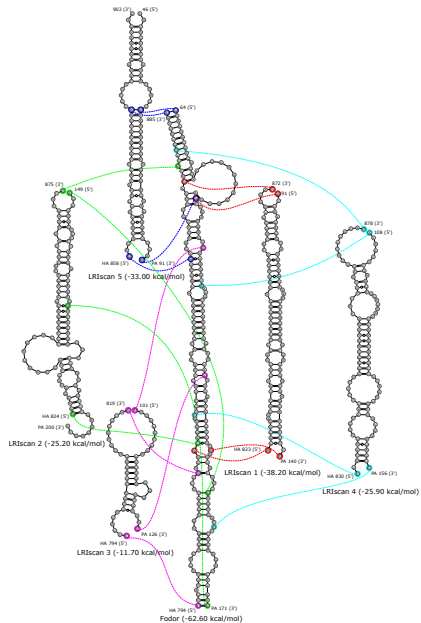
Packaging in Influenza HA:PA



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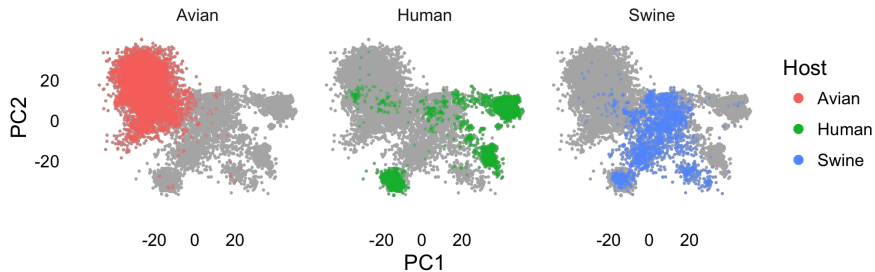


Packaging in Influenza HA:PA

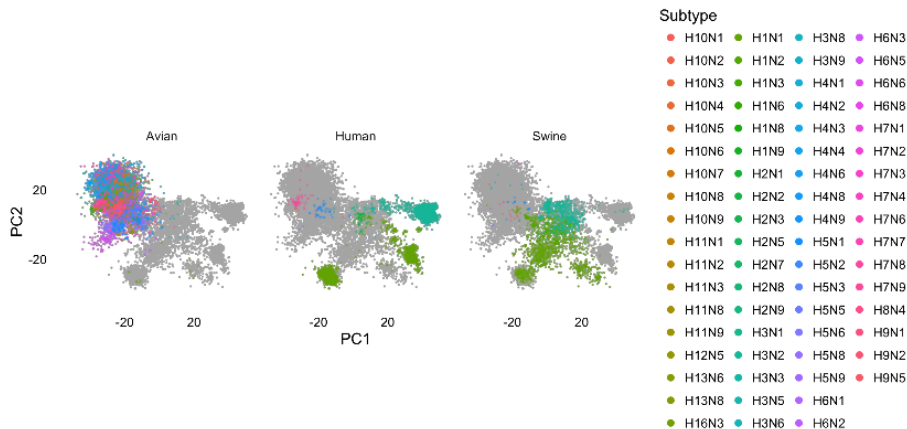


Give me your virus and I tell you the host

Give me your virus and I tell you the host



Give me your virus and I tell you the subtype



Give me your virus and I tell you the host

$y \setminus \hat{y}$	Avian	Human	Swine	All
Avian	3207	49	13	3269
Human	6	4470	82	4558
Swine	9	10	849	868
All	3222	4529	944	8695

metric \ host	Avian	Human	Swine	All
accuracy				0.95
recall	0.99	0.95	0.94	
precision	0.88	1.00	0.89	
F1-score	0.94	0.97	0.93	

Codon usage

$y \setminus \hat{y}$	Avian	Human	Swine	All
Avian	5524	227	576	6327
Human	168	11314	1251	12733
Swine	25	800	995	1820
All	5717	12341	2822	20880

Dinucleotides

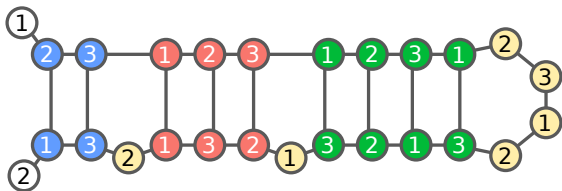
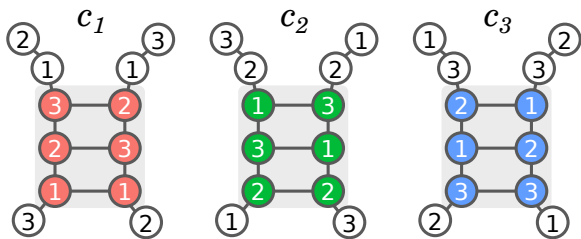
$y \setminus \hat{y}$	Avian	Human	Swine	All
Avian	4294	1048	985	6327
Human	173	8376	4184	12733
Swine	17	630	6342	1820
All	4484	10054	6342	20880

Sequence – Secondary structure – Proteins

Another layer?

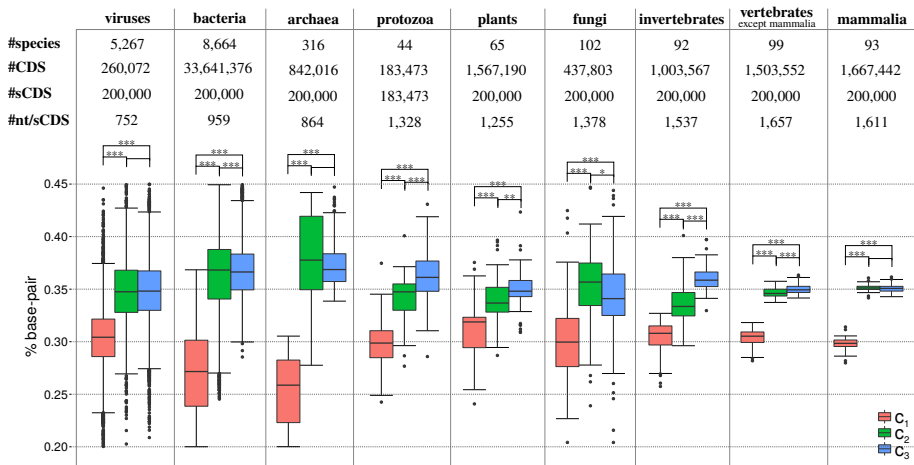
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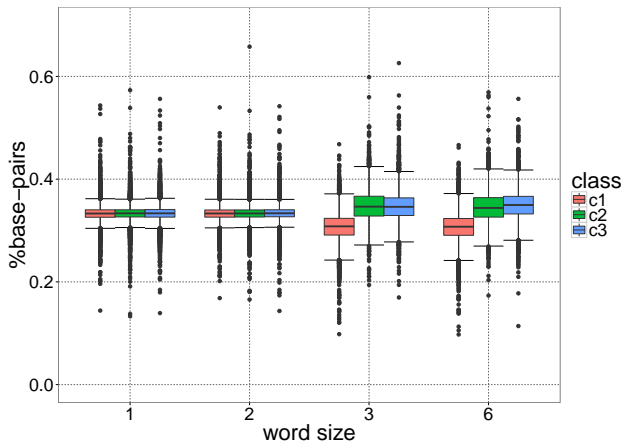
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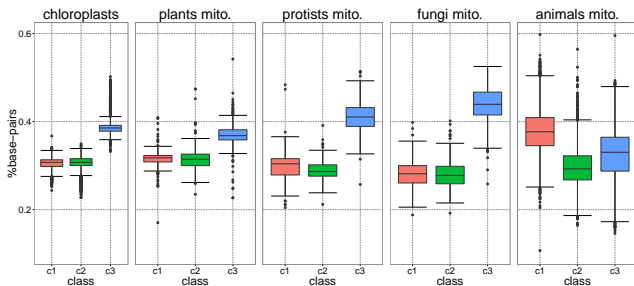
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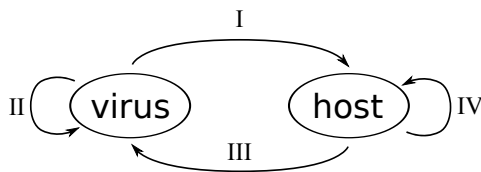
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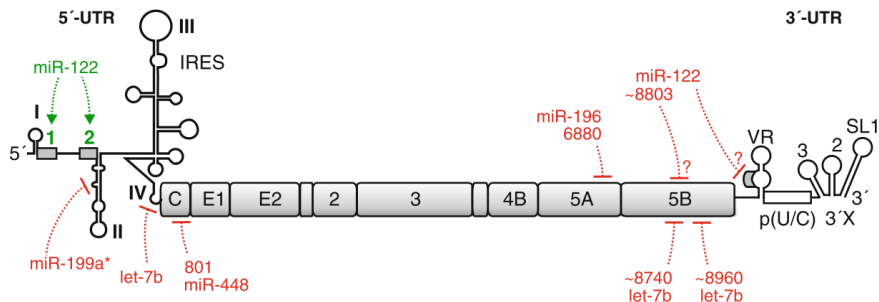
Specific non-coding RNAs during viral infection

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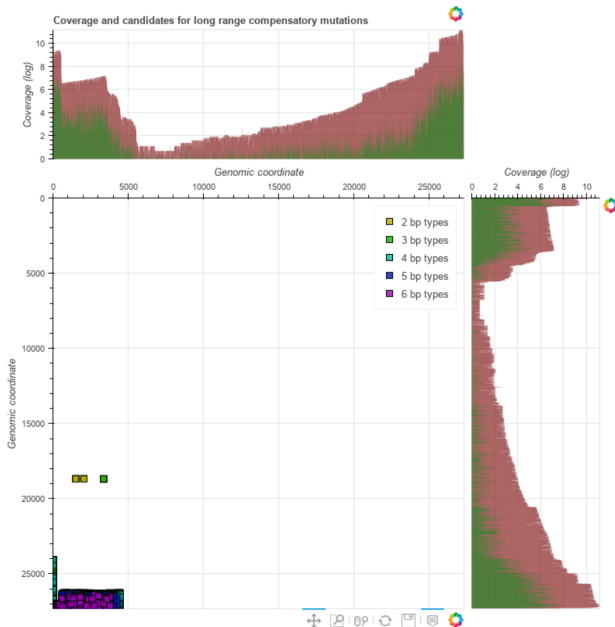


I:	WNV DENV BLV	KUN-miR-1 sfRNA BLV-miR-B4	mosquito human bovine
II:	EBV EBV hCMV	miR-BART1-5p BART16;17-59 miR-UL122-1	
III:	HCV EEEV HIV1 HPV	miR-122 miR-142-3p NEAT1 lncRNA MALAT1 lncRNA	human human human human
IV:	WNV EBV	Aae-miR-2940-5p miR-127	mosquito human

Impact of secondary structures in RNA viruses: miRNAs in HCV



Use Minion: Location



There is endless much to be done....

- RNA:protein
- dynamics
- RNA elements: shunt, leaky scanning, frameshifts, ribosomal skipping, pseudoknot termination
- Phylogeny
- Haplotypes/quasispecies

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