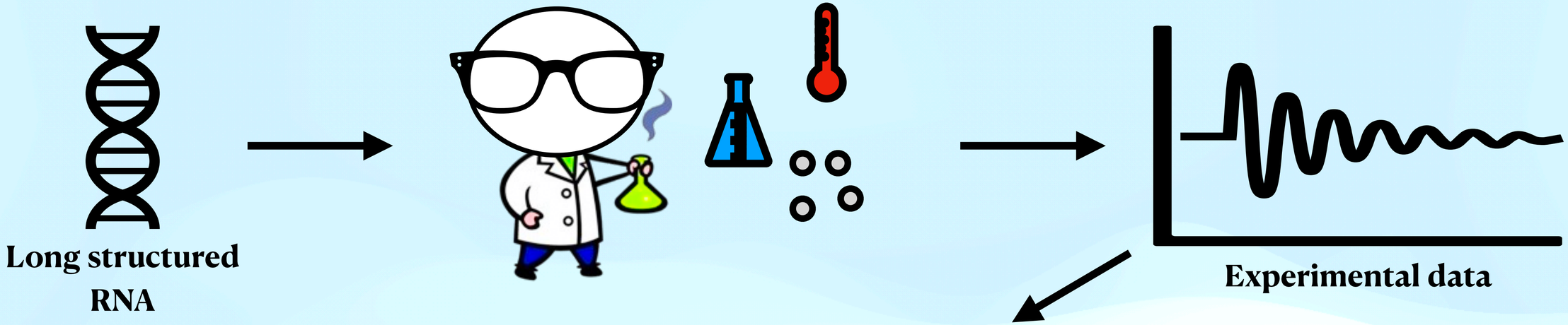
Structure modelling of RNA virus genomes

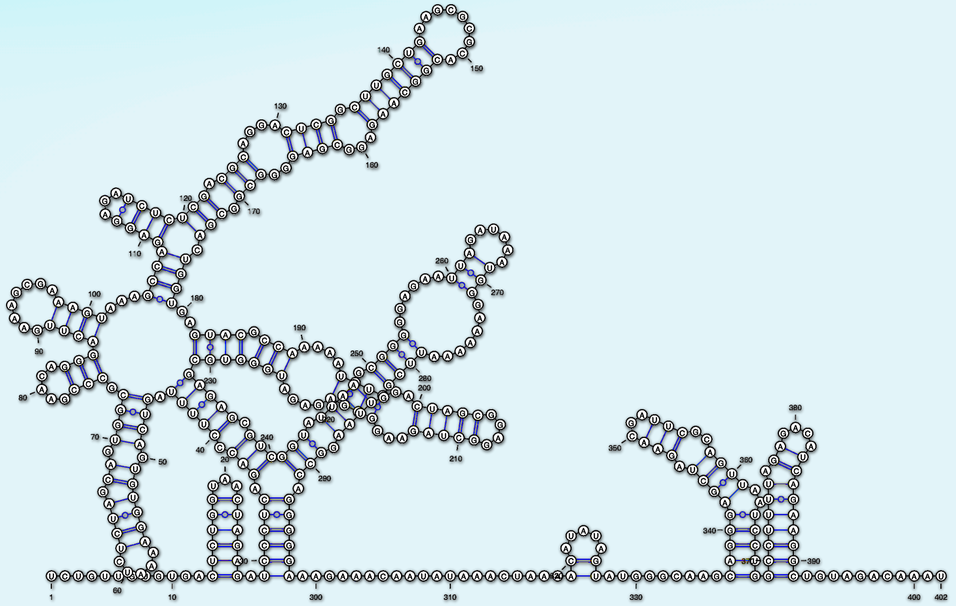
Nan PAN

The 39th TBI Winterseminar in Bled 2024
11-16 February 2024

Overall workflow



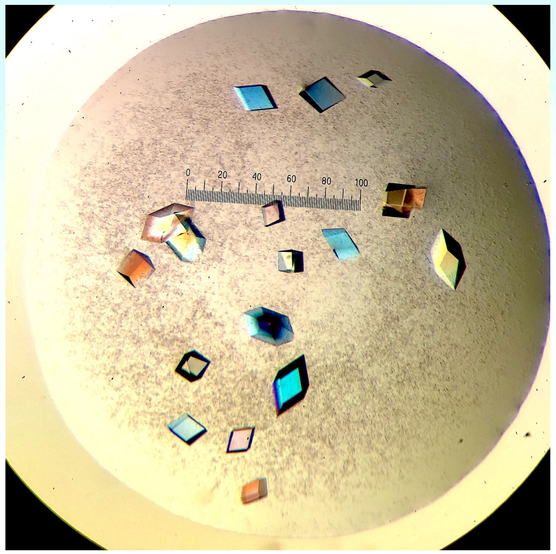
Automatic integrated analysis of RNA secondary structure prediction

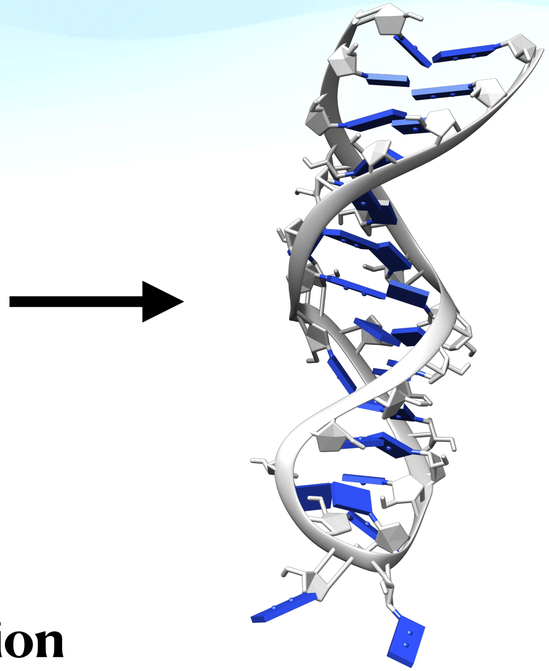


Challenge

RNA in PDB database : from tens to thousands of nucleotides.

X-ray diffraction, NMR and electron microscopy are the three main experiments used to study molecular structure.





Molecular crystals for X-ray diffraction

[1] J. Cui et al., 2014, An Allometric Relationship between the Genome Length and Virion Volume of Viruses.

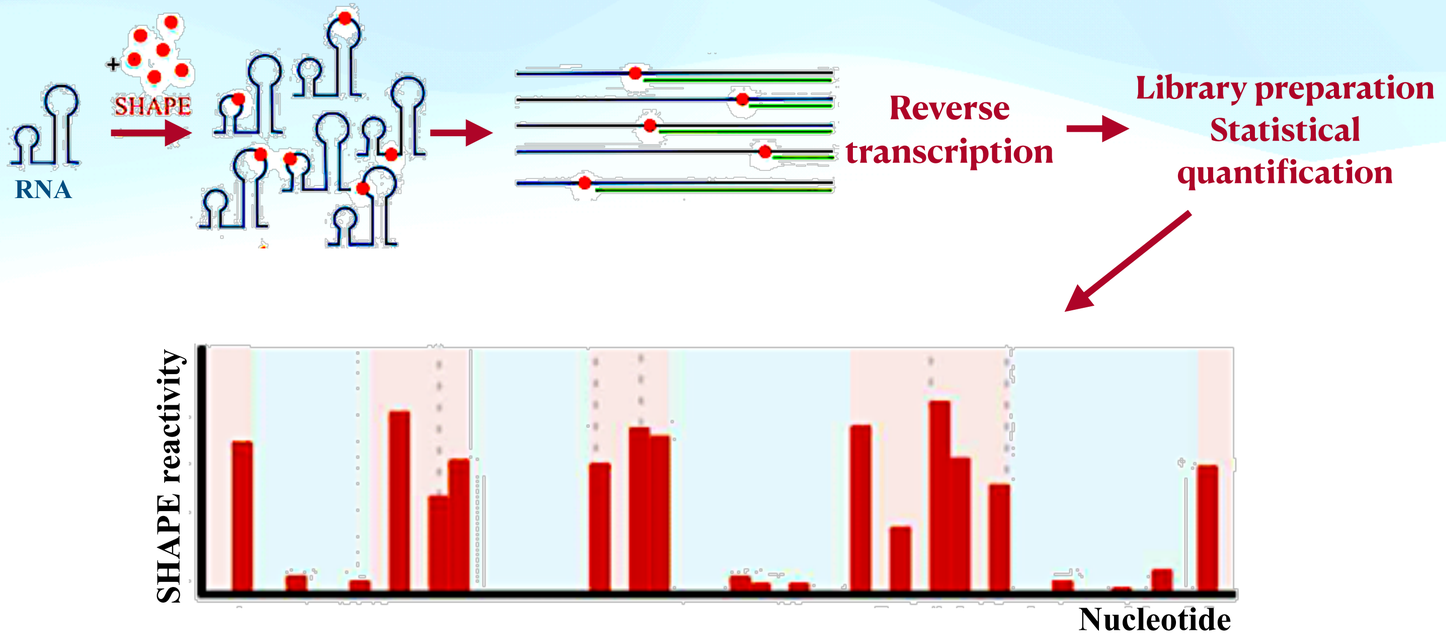
Challenge

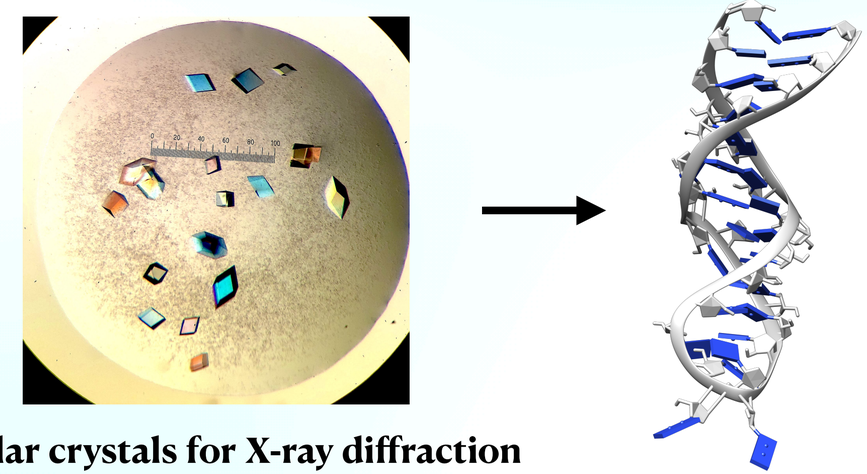
Size of RNA in PDB database : from tens to thousands.

X-ray diffraction, NMR and electron microscopy are the three main experiments used to study molecular structure.

The genome size of RNA viruses ranges approximately from 1.6k to 31 k nucleotides[1].

SHAPE Experiment





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Data

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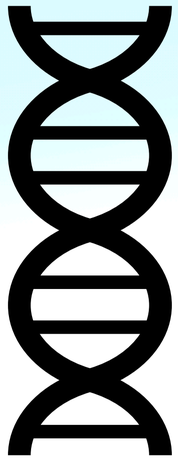
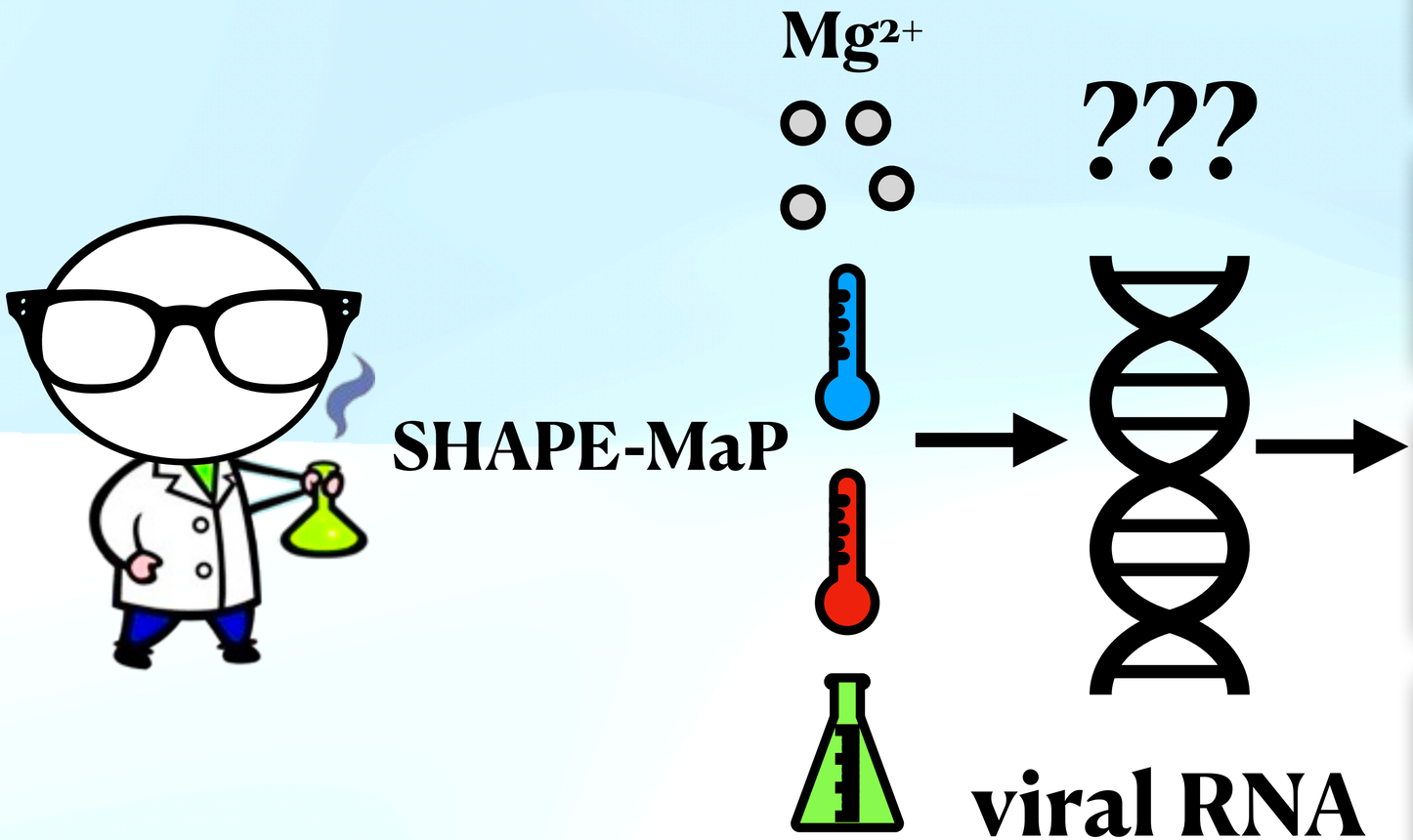
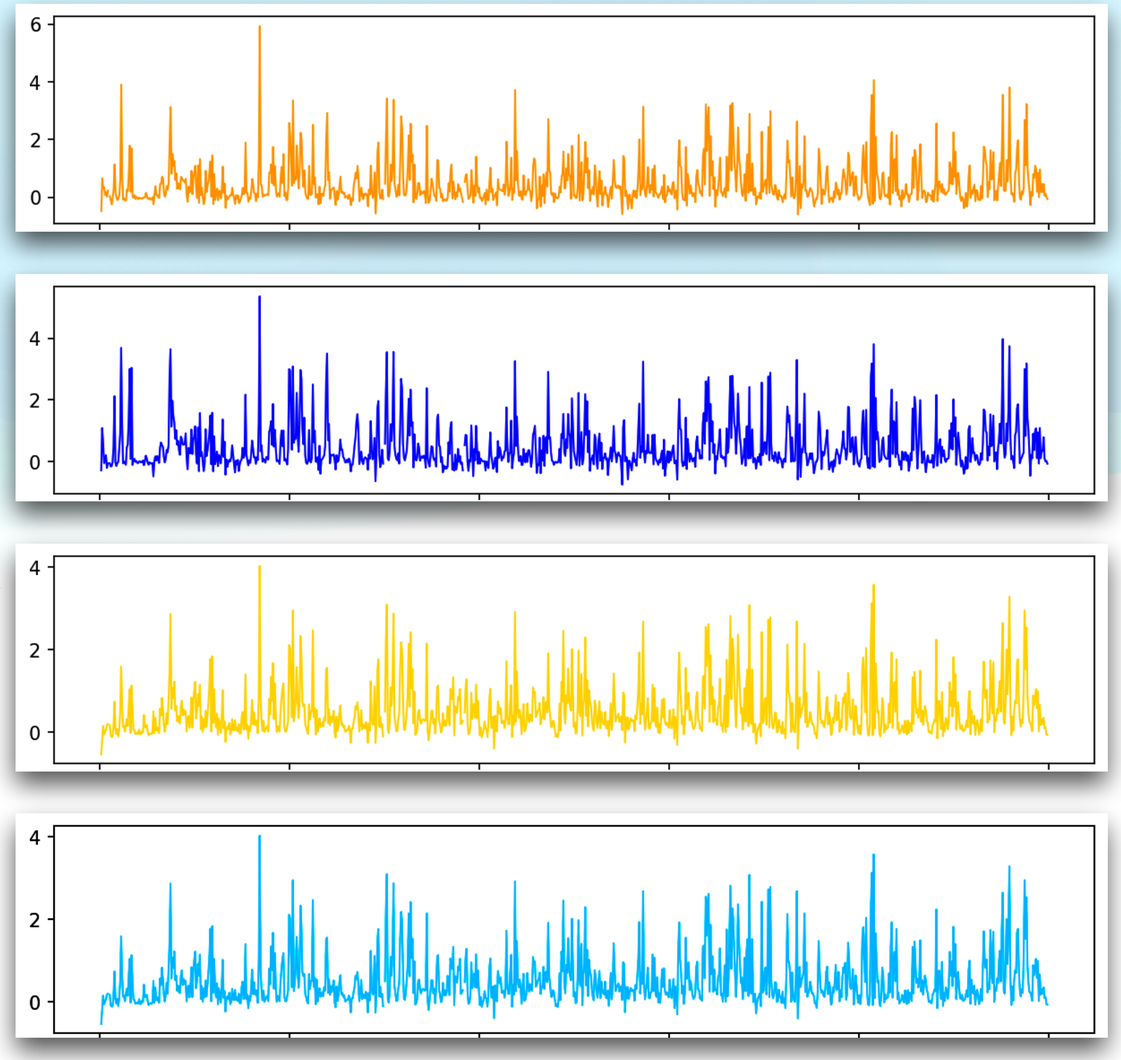


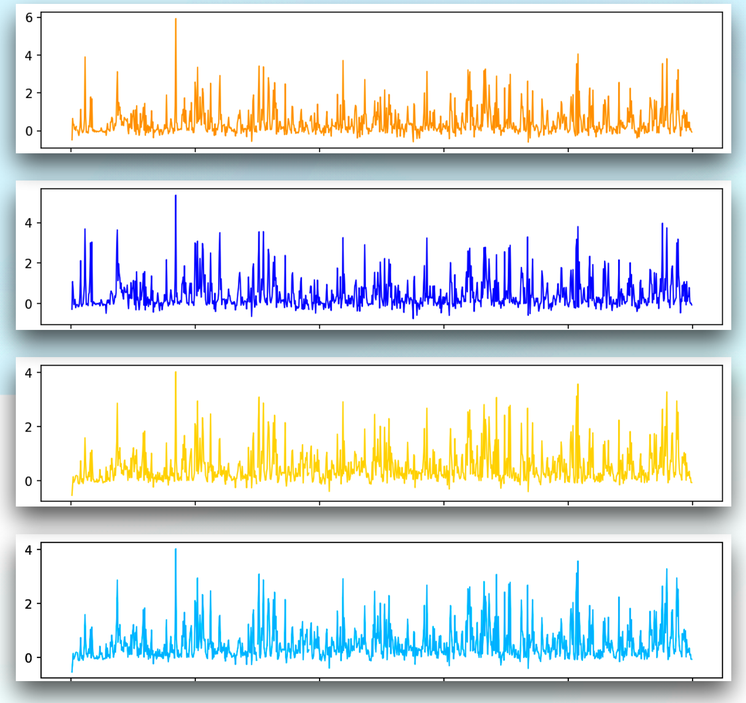
viral RNA

Data





Strategy



Statistical analysis

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Application of existing predictive tools

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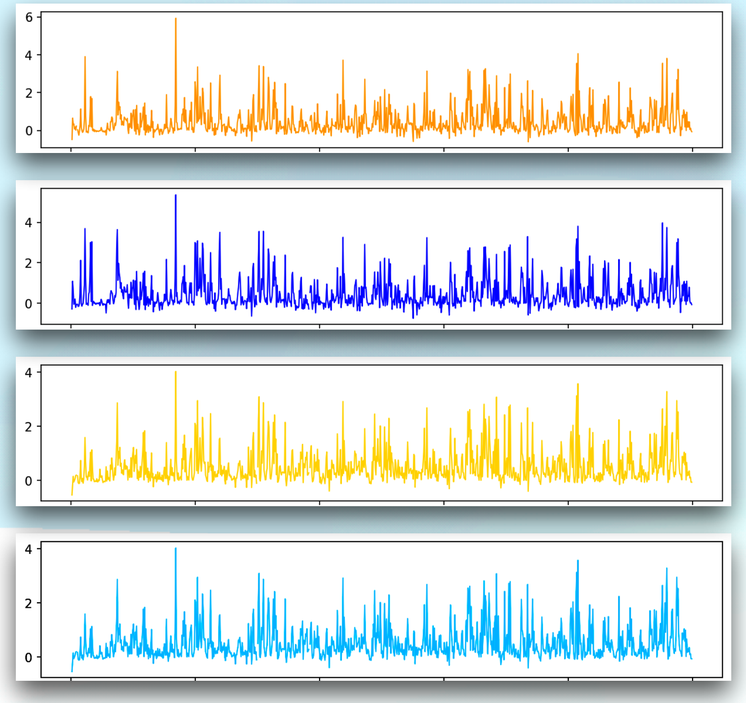
Comparison with literature models

- Integrating diverse experimental data.
- Designing efficient algorithms and data structures.
- Modelling and predicting viral RNA secondary structure.

Strategy



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Thanks for your attention !