

Kinetic Folder Update

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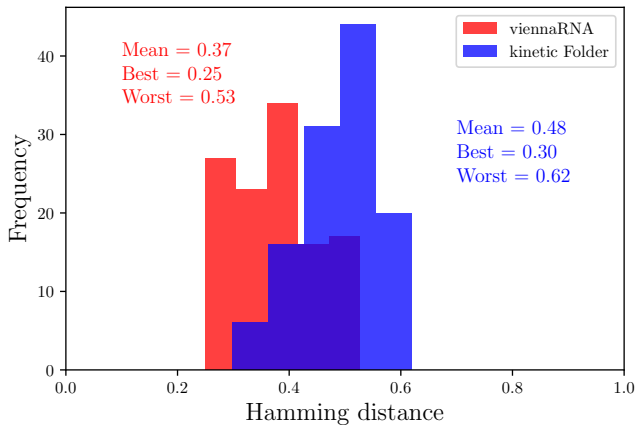
"Bad Seq" Dataset

- ▶ 117 sequences
- ▶ Variable length (max: 80 ntds)

Stats	Kinetic Folder	viennaRNA
Mean	0.48	0.37
Best	0.30	0.25
Worst	0.62	0.53



Results



pseudoknotted

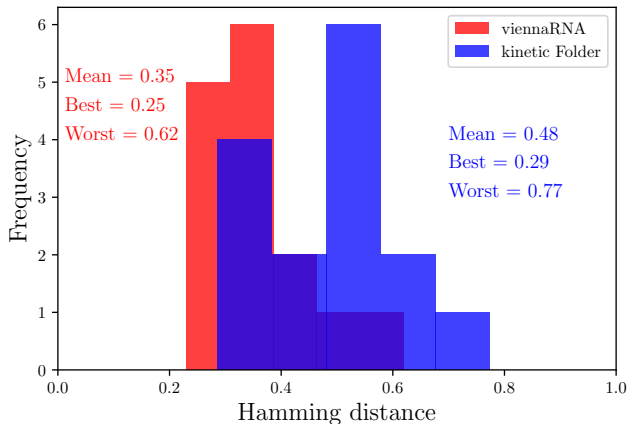
- ▶ 15 sequences with pseudoknotted secondary structures¹
- ▶ Mean length: 29 ntds

Stats	Kinetic Folder	viennaRNA
Mean	0.48	0.35
Best	0.29	0.25
Worst	0.77	0.62

¹Sequences from Pseudobase++

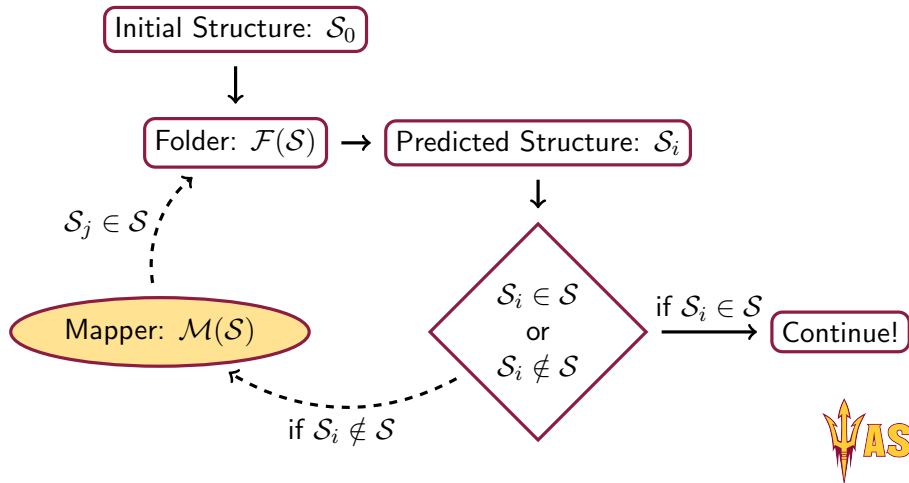


Results



Mapping function

A schematic of where the mapping function $\mathcal{M}(\mathcal{S})$ will be implemented in the roll-out algorithm.



Mapping function

Mapping function features:

- ▶ Checks that constraints are within the possible move space; if this condition is not met prints error.
- ▶ Two mapping features:
 1. Re-run algorithm until constraints are satisfied (Max iterations = 1000).
 2. Find the list of moves that satisfy the constraints enforce these moves to happen.

Note: By enforcing certain moves to exist the move space shrinks to essentially allow one move.



Mapping function

Examples from Folder

Constraints are $\mathcal{C} = [[0, (], [1, (]]$

Correct first try

All constraints are within the move space!

+ | `[[0, 12], [1, 11], [2, 10]] | (((.....))).....`

+ | `[[5, 26], [6, 25], [7, 24]] | (((..[[[.)).....]]]`

Structure meets constraints!



Mapping function

Examples from Folder

Constraints are $\mathcal{C} = [[0, (], [1, (]]$

Option 1

All constraints are within the move space!

Structure fails! Using option 1 to fix!

fixedStructure: (((((((.....)))))).....



Mapping function

Examples from Folder

Constraints are $\mathcal{C} = [[0, (], [1, (]]$

Option 2

All constraints are within the move space!

Structure fails! Using option 2 to fix!

ERROR: No structure found using option 2

