

# Kinetic Folder Update

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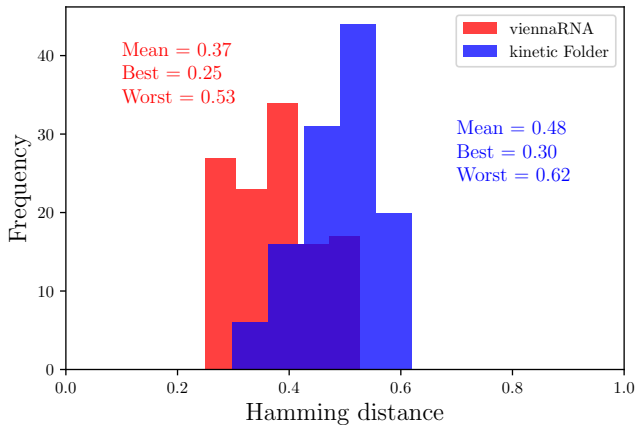
# "Bad Seq" Dataset

- ▶ 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 structures<sup>1</sup>
- ▶ Mean length: 29 ntds

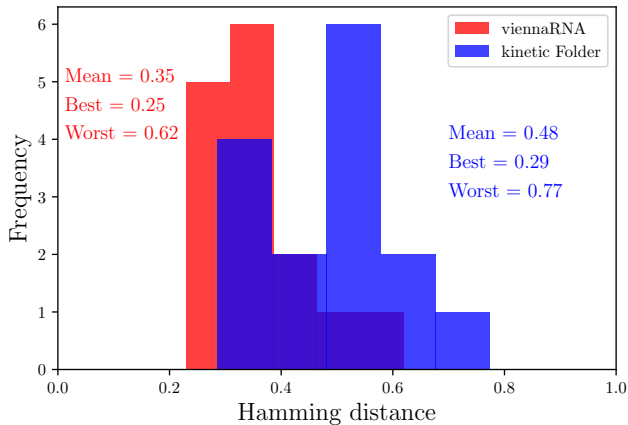
Stats	Kinetic Folder	viennaRNA
Mean	0.48	0.35
Best	0.29	0.25
Worst	0.77	0.62

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<sup>1</sup>Sequences from Pseudobase++

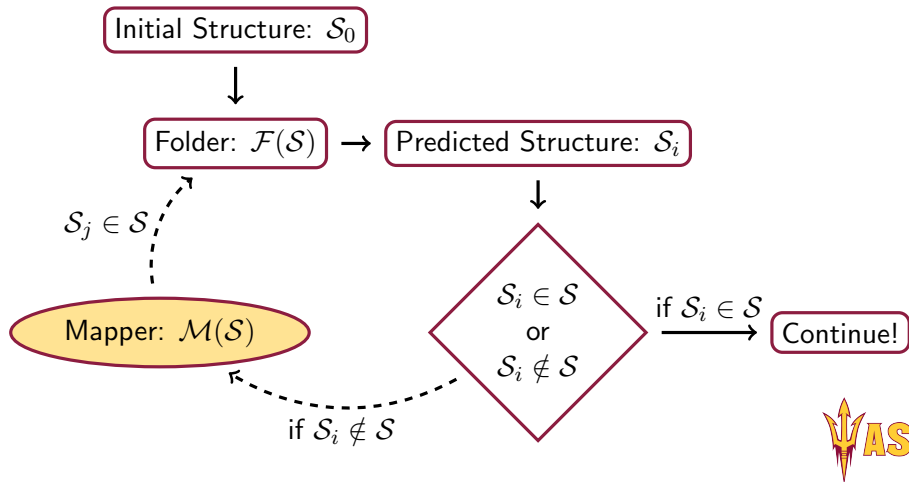


# Results



# Mapping function

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



# Mapping function

Example from Folder

## Output of Kinetic Folder

```
+: [[3,17],[4,16],[5,15]]...(((.....))).....  
+: [[10,21],[11,20],[12,19]]...(((...[[[.)))).]]].....  
-: [[3,17],[4,16],[5,15]]...(((.....))).....  
+: [[3,17],[4,16],[5,15],[6,14]]...(((...[[[.)))).]]]...
```

