Kinetic Folder Update

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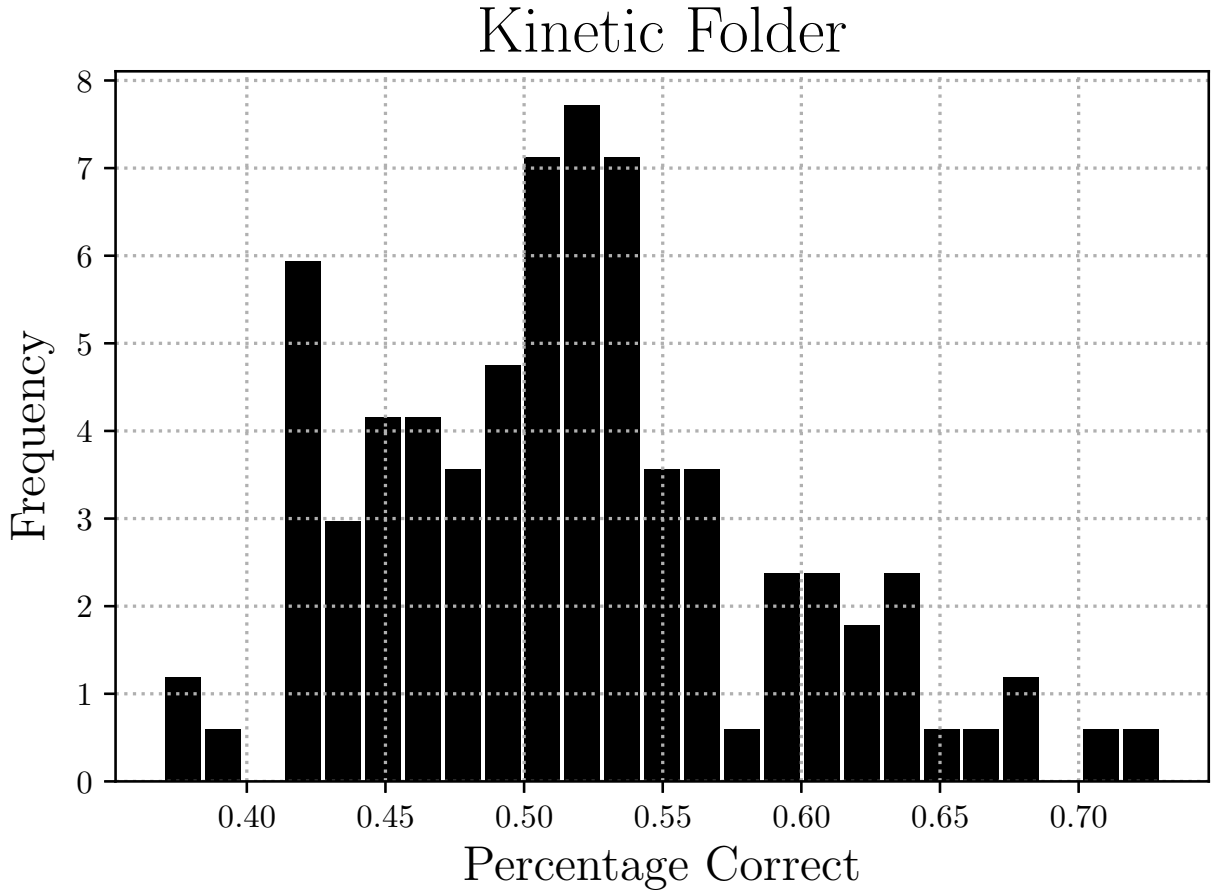
"Bad Seq" Dataset

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

Stats	Kinetic Folder	viennaRNA
Mean	0.52	0.63
Best	0.73	0.75
Worst	0.37	0.47

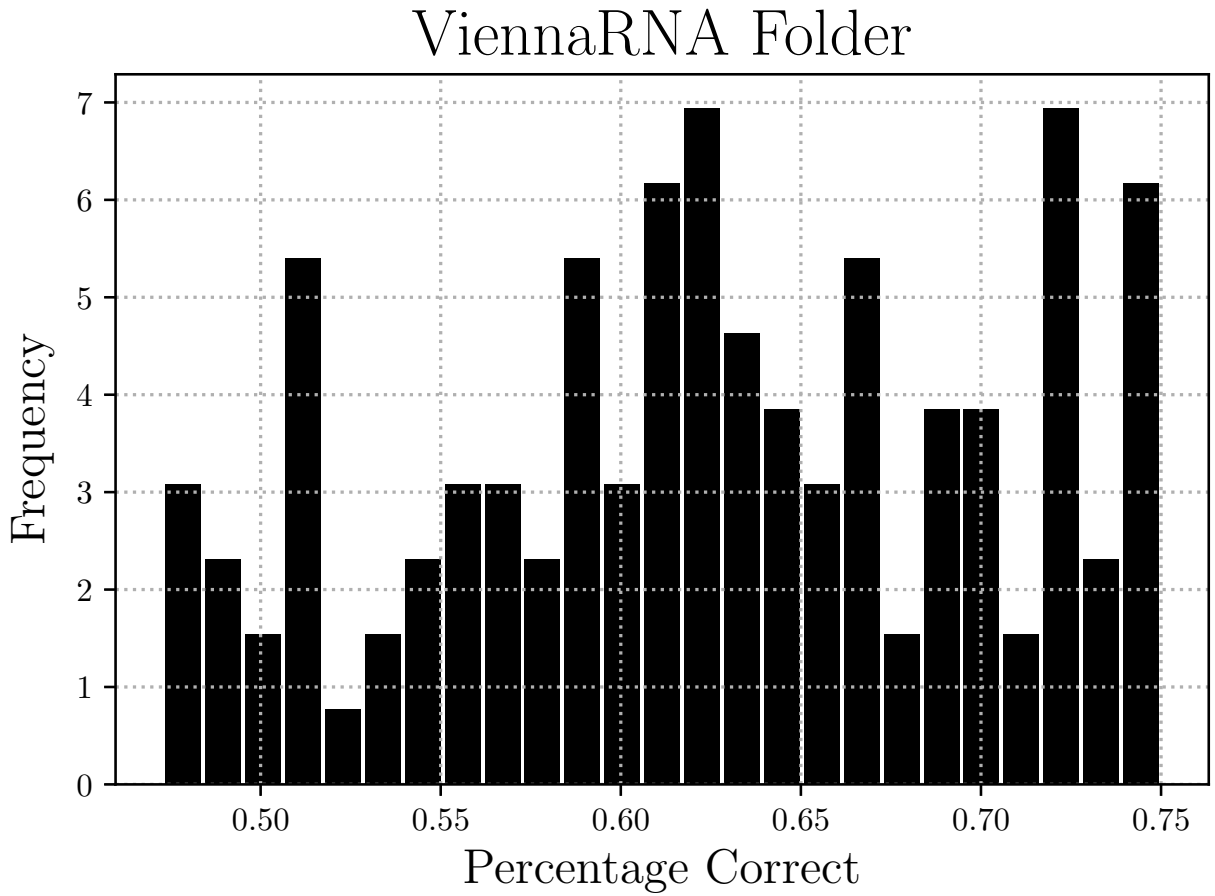
Results - kinetic folder

Mean	Best	Worst
0.52	0.73	0.37



Results - viennaRNA folder

Mean	Best	Worst
0.63	0.75	0.47



pseudoknotted

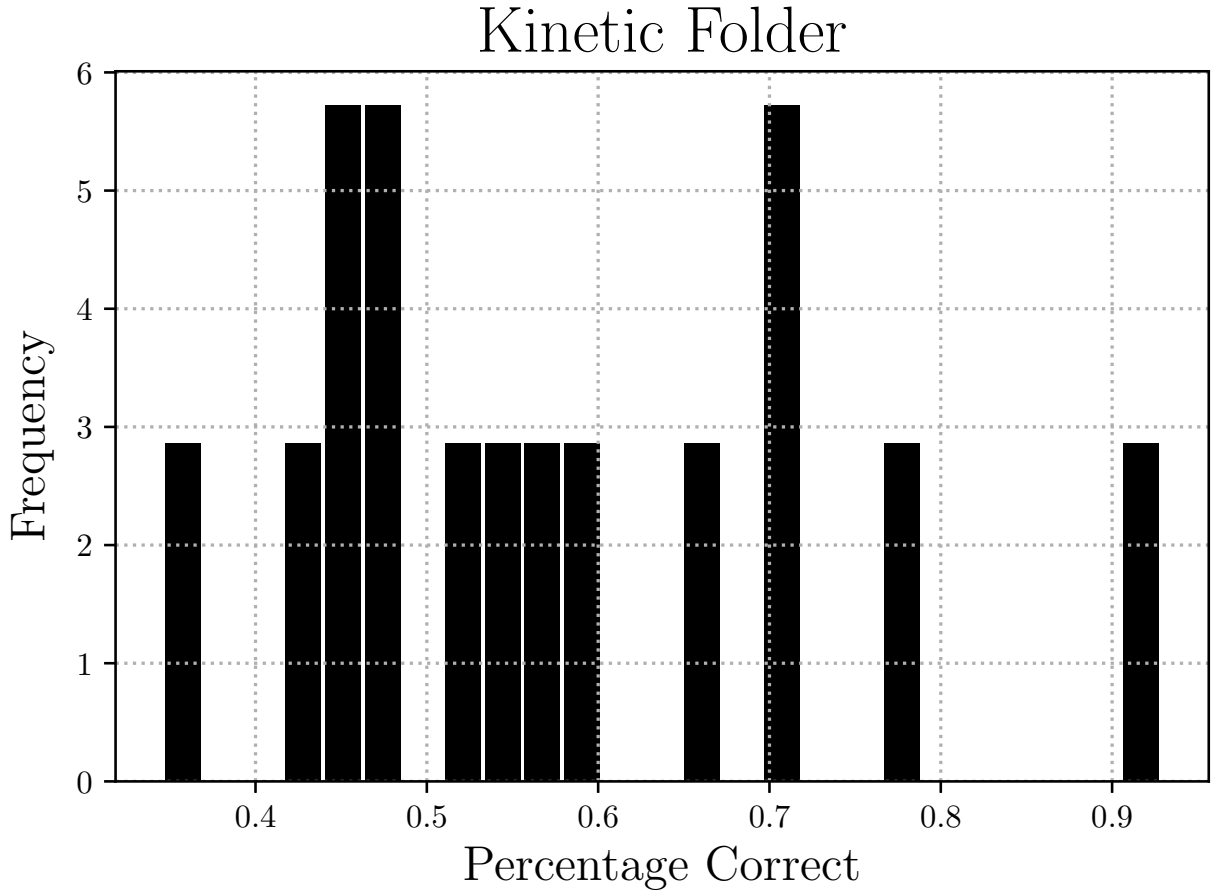
- 15 sequences with pseudoknotted secondary structures[1]
- Mean length: 29 ntds

Stats	Kinetic Folder	viennaRNA
Mean	0.58	0.65
Best	0.93	0.77
Worst	0.35	0.38

[1] Sequences from Pseudobase++

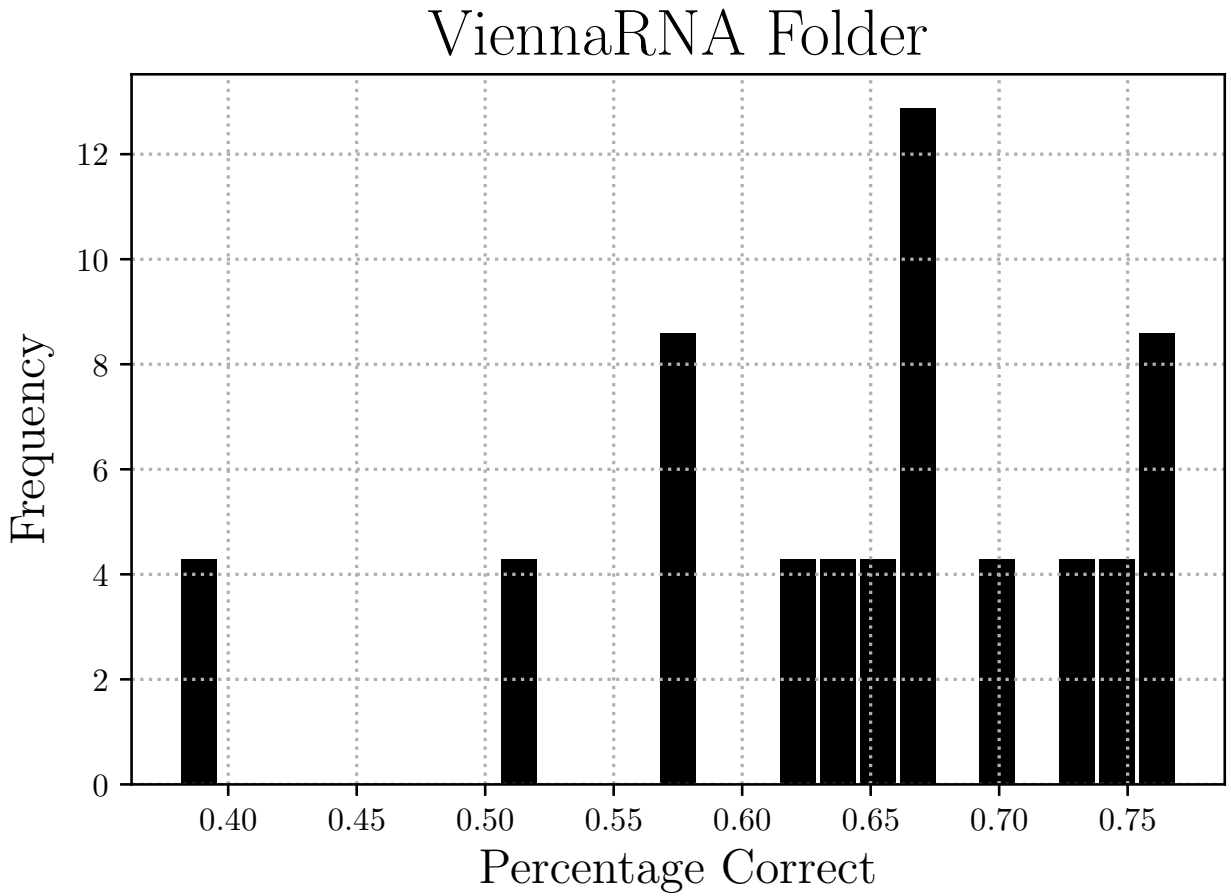
Results - kinetic folder

Mean	Best	Worst
0.58	0.93	0.35



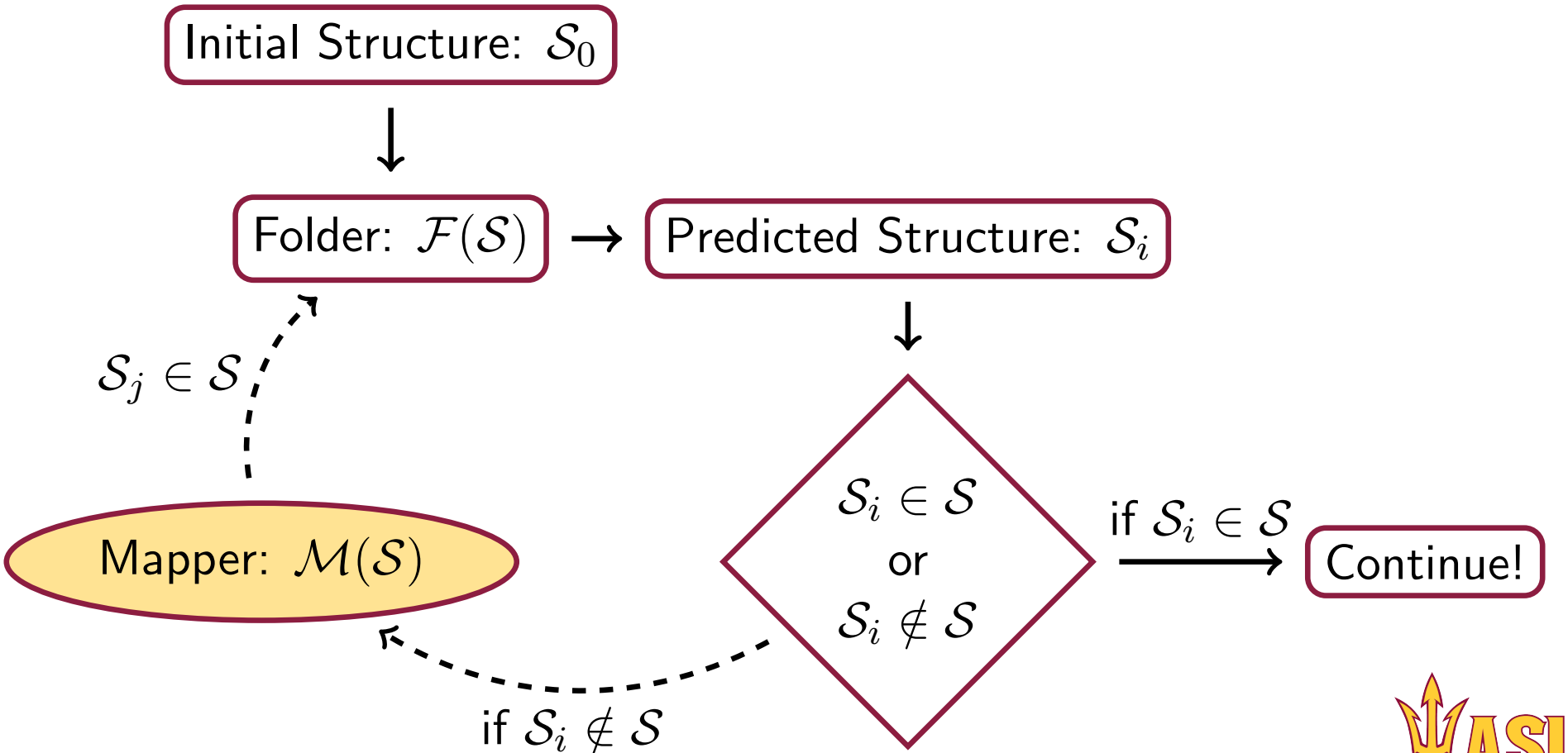
Results - viennaRNA folder

Mean	Best	Worst
0.65	0.77	0.38



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]]...((((...[[[.)))).]]]...
```