Part 1

Note:

- If running procedure on OFF sequence →
  - seq = GGGCGACCCUGAUGAGCUUGAGUUUAGCUCGUCACUGUCCAGGUUCAUCAGGCGAAACGGUGAAAGCCGUAGGUUGCCC
- If running procedure on ON sequence →
  - seq = GGGCGACCCUGAUGAGCUUGAGUUUAUCAGGCGAAACGGUGAAAGCCGUAGGUUGCCC

1. Predicted MFE structure:

   We run the following code to get statistics calculated:
   - $ RNAfold <seq>

   This yields an rna.ps file that can be converted to a PDF for viewing — which can be done on a Linux machine using the command:
   - $ convert rna.ps rna.pdf

2. Base-pairing probability plot

   Now, we run the plotting tool, where <structure> is the structural data from the terminal output of RNAfold <seq>:
   - $ RNAplot <seq> <structure>

   This returns a probability of nucleotides, which is returned as dot.ps. We convert again to PDF format for viewing using the command (on Linux):
   - $ convert dot.ps dot.pdf

3. Status of stems I, II and III from the hammerhead structure, and accessibility of the cleavage site

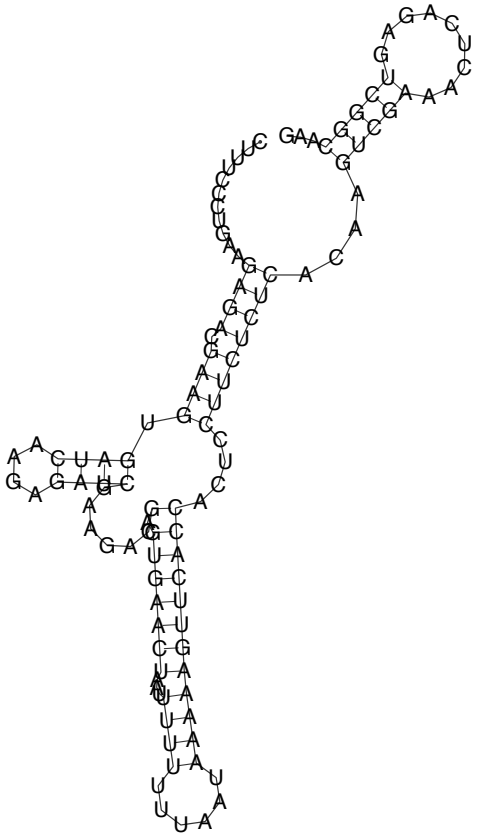
   Using the PDF output from the last step, we just look for the 3 diagonal "lines" of boxes on the probability dot-plot — if *line IV* shows up, we know it's in the OFF conformation, and if *line II* shows up, we know it's in the ON conformation. In the OFF conformation, we know the ribozyme's cleaving site can't be accessed.

Part 2

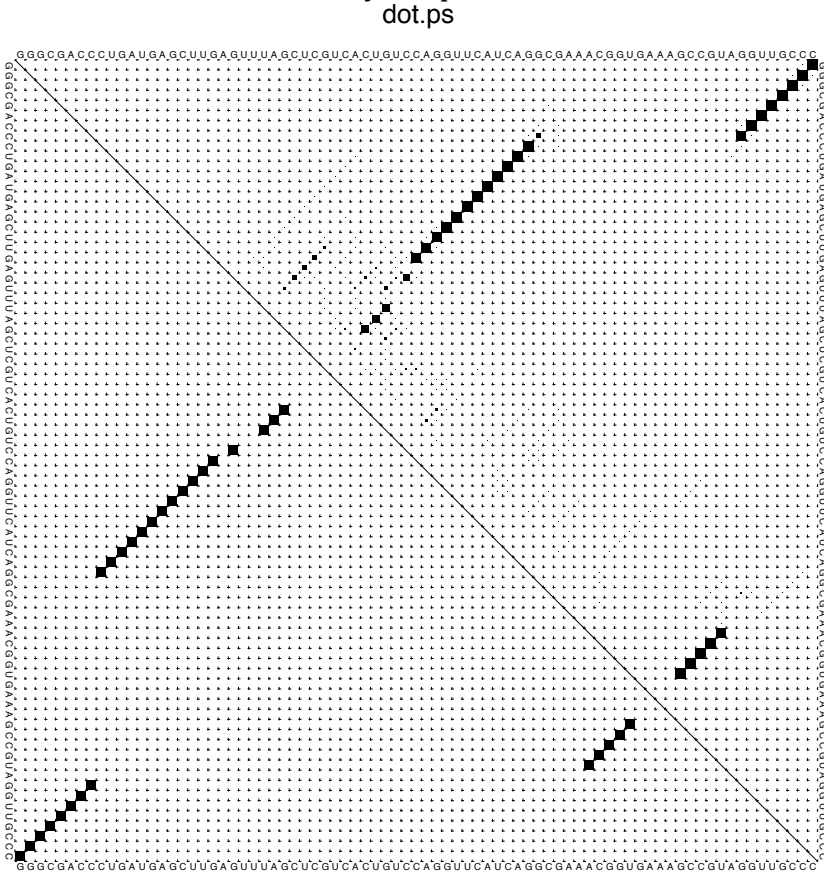
See pseudo-code Included in python file

Part 3

My rna.pdf:

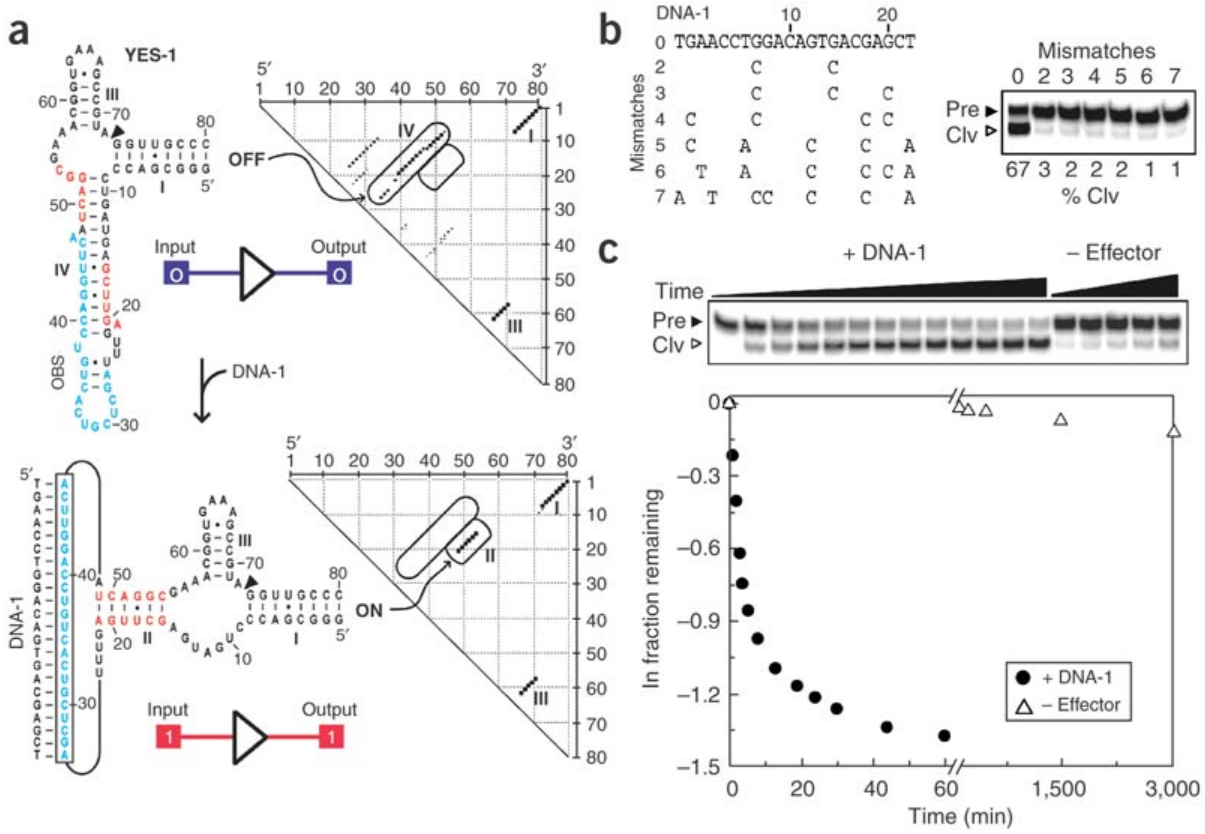


My dot.pdf:



Comparison with actual file:

- First of all, since the 5' and 3' ends are in Stem I, we know that this structure is a type 1 hammerhead ribozyme.
- Our output matches the structure and dot-plot of the paper's OFF conformation, as shown in the figure below — the dot plot tells us that our input sequence has stem IV present and our structure show us 3 stems branching from a central node, which are both characteristic of the OFF conformation.


a
YES-1
OFF
Input
Output
DNA-1
ON
b
DNA-1
Mismatches
Pre
Clv
% Clv
c
+ DNA-1
– Effector
Time
In fraction remaining
Time (min)