

(1) Vfold2D-result

You will receive three files by email:

jobname.base_pair.txt

jobname.2d_struct.eps

jobname.helix.txt

***.base_pair.txt looks like this,**

```
-----  
1 C-G 16 0.82  
2 G-C 15 0.90  
3 C-G 14 0.90  
3 C-G 17 0.04  
4 G-C 13 0.89  
4 G-G 16 0.10  
5 G-C 12 0.84  
5 G-C 15 0.10  
6 C-U 11 0.14  
6 C-G 14 0.10  
8 C-G 26 0.82  
9 C-G 25 0.83  
10 G-C 24 0.83  
11 U-A 23 0.82  
12 C-A 22 0.14  
-----
```

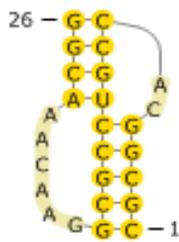
The file shows the probabilities [0, 1.0] of base pairs.

The first two columns are the position and the nucleotide type of residues i ; The fourth and fifth columns are the nucleotide type and position for residue j ; the last column is the probability of forming the i - j base pair.

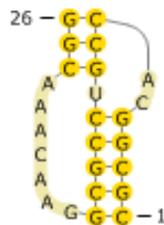
For example, residue 1 base paired with residue 16 with 0.82 probability. The base pair 2-15 has the probability of 0.90.

***.2d_struct.eps**

The file shows the predicted most probable 2D structure plotted by VARNA, given by all the base pairs with their probabilities > 0.5 :



Predicted



Native

***.helix.txt looks like this,**

helix 1 probability: 0.87

1 16
2 15
3 14
4 13
5 12

helix 2 probability: 0.825

8 26
9 25
10 24
11 23

helix 3 probability: 0.1

4 16
5 15
6 14

The file shows the predicted probabilities for the possible (including alternative) helices. It can help us to find out alternative structures, including the most probable structure shown in *.2d_struct.eps.

(2) VfoldThermal-result

You will receive two files by email:

jobname.ct.txt

jobname.ct.eps

***.ct.txt looks like this,**

0.5 0.0463899
1 0.0463899
1.5 0.0463899
2 0.00328919
2.5 0.0282802
3 0.0108527
3.5 0.0266198
4 0.0213973
4.5 0.0440978
5 0.0432021
5.5 0.0318608
6 0.0651456
6.5 0.0293057
7 0.037769
7.5 0.0317027
8 0.0350748
8.5 0.0394637
9 0.0323962
9.5 0.0514242
10 0.0293892
10.5 0.0531801

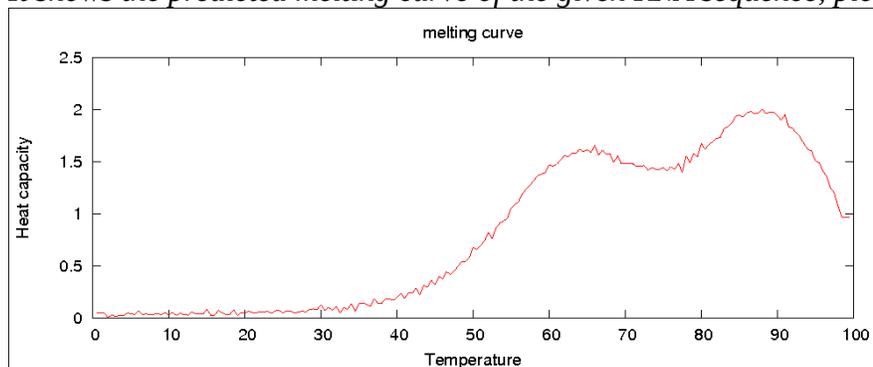
11 0.0214442

...

The first column is the temperature, the second one is the corresponding heat capacity.

***.ct.eps**

It shows the predicted melting curve of the given RNA sequence, plotted by Gnuplot.



(3) Vfold3D-result

You will receive one file by email:

jobname.3d_struct.pdb

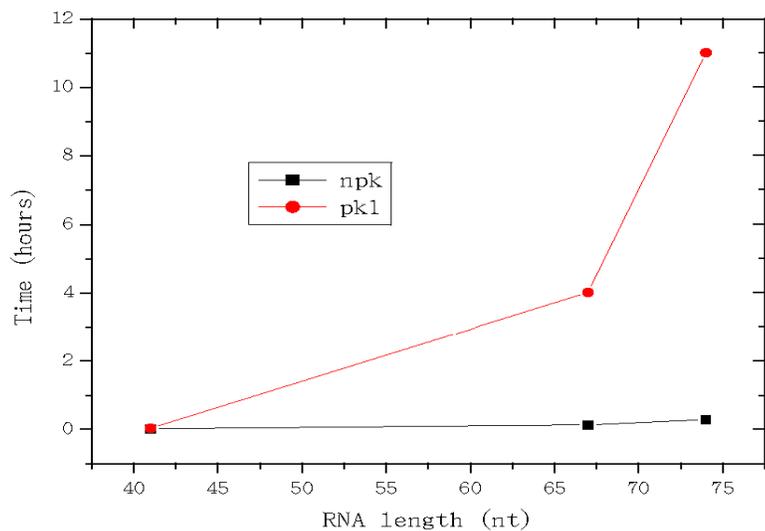
(a pdb file of the predicted structure in standard format)

OR

jobname.err.txt

(an error message file)

(4) Vfold computational time as a function of RNA sequence length



The computational time for the type of pk2 is much longer than that for types of pk1 and npk.