

Matrix Plot for predicting RNA structure using the principle of Mutual Information

URL: <http://www.cbs.dtu.dk/services/MatrixPlot/mutualNucl/>

MatrixPlot 1.2: Mutual information in RNA and DNA sequences

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[Mutual](#)

Compute mutual information of your sequence alignment. You can submit the data by [pasting](#) or [uploading a file](#). When the processing is done you can zoom around in your plot as much as you want. For more information, see [sequence-structure logos](#). For publication of results, please cite

MatrixPlot: visualizing sequence constraints. J. Gorodkin, H. H. Stærfeldt, O. Lund, and S. Brunak. *Nucleic Acids Res* 27:15:769-770, 1999. (<http://www.cbs.dtu.dk/services/MatrixPlot/>)

Submission by pasting the alignment:

Alignment: ([data format](#) description)

This approach **REQUIRES** a Multiple Sequence Alignment

Step 1: Paste in sequence alignment. These are aligned RNA sequences in Fasta format (test data).

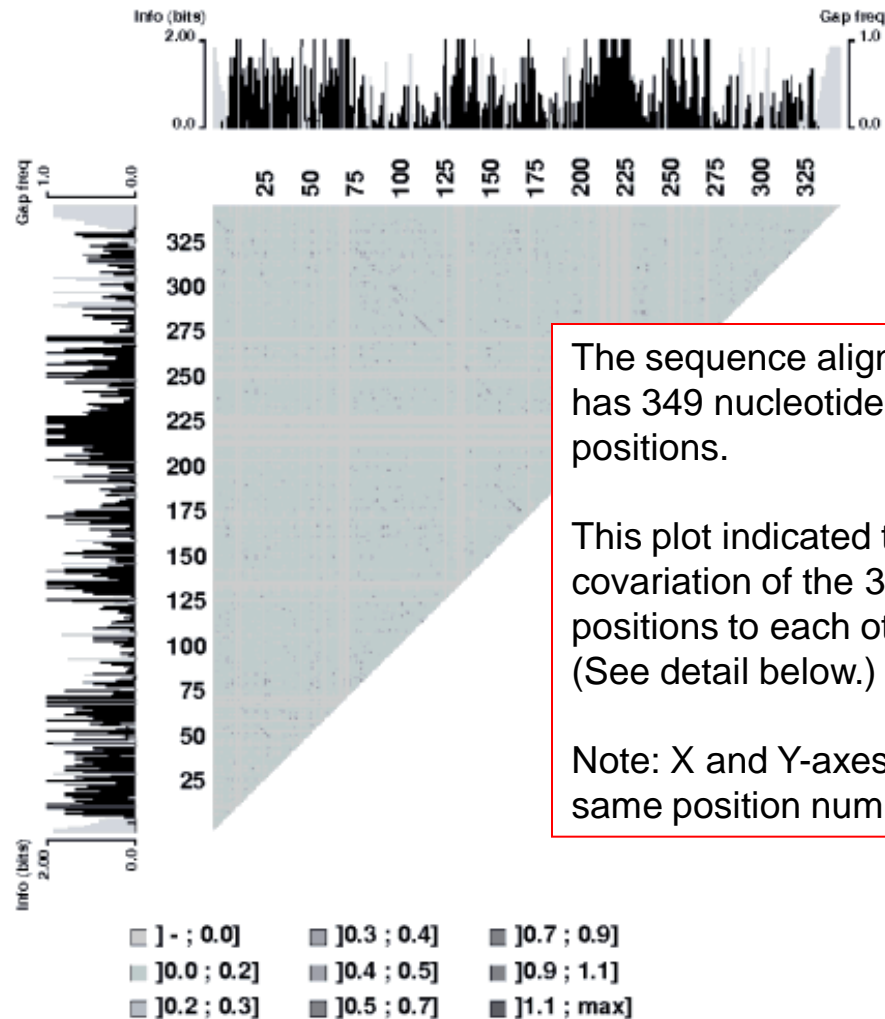
```
>METJAN
GGUGUGCAUGGcua-gGCCgGGGGGuuGGGCG-UCCCCuguaaCCCGa-a-auCGCCC
>METVOL
-----UGGcua-gGCUgGGAGGuuAGGCG-UCUCCuguaaCUUGa-a-auCGCCU-
>METFER
-----AGGcua-gGCCgGGGGGuuAGGGG-UCCCCuguaaGCGCa-a-auCCCCUa
>METTHE
-----UGGGcua-gACCgGAGGGuuAGGGG-UCCUCuguaaGCGCa-a-auCCCCUa
>METACE
----UGAUGAGcua-gUCCgGGUAGccCGGCG-UUACCuguaaCCCGa-a-auCGCCGa
```

Make plot

Reset

Step 2: Click "Make plot"

Output Plot: This difficult to read plot shows which positions of your alignment have evidence of covariation (mutual information).

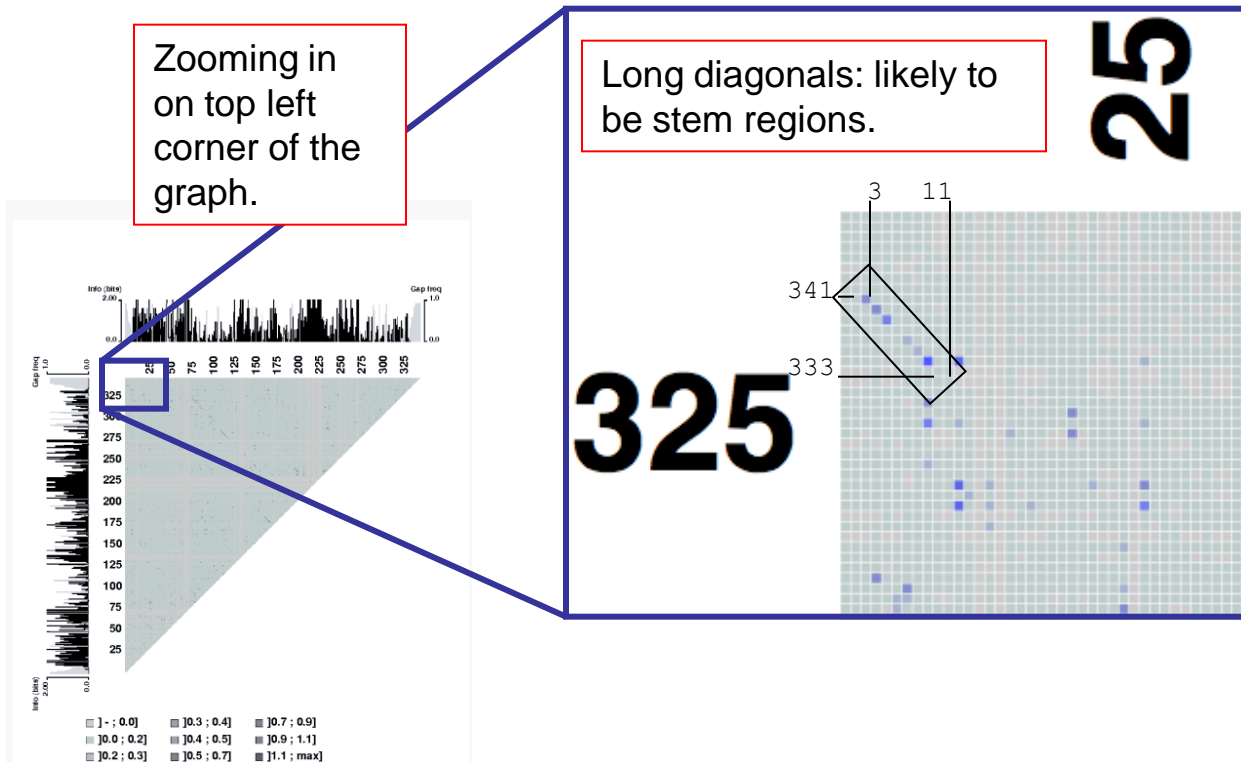


The sequence alignment has 349 nucleotide positions.

This plot indicated the covariation of the 349 positions to each other. (See detail below.)

Note: X and Y-axes have same position numbers.

Zoom In: You can download a postscript version and zoom in to see details (dots). Then you need to refer back to the sequence alignment.



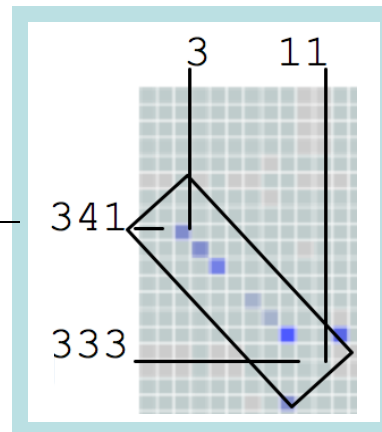
Interpretation: How do these results correspond to interactions of nucleotides within a sequence?

Let's determine how these results predict the RNA structure of the input sequences using a particular sequence from the Multiple Sequence Alignment (THECEL):

```
>THECEL
--GGCGGCGGGcua-gGCCgGGGGGuuCGGCG-UCCCCuguaaCCGG
a-a-acCGUCGauacgCCGGGGCc-g-aaGCCCGGGGggc-GGuuCC
Cg-aaGCCGUUCCcggaGCCGGGGCacaacggugauCCCUCGuCcC
ACGGgGCC-GGCG-guGGGc-gGGUCCGGCUggagGGCCGGGCUaa
cGCCC-uuu-gcCCGCCgaaccCCGucaggCCCggaaGGGagcagCG
GuaGGCGGgaCGuUCGGCgcUCGUGgGguagCGGGGGugagc-gaGC
CCCGGUggaa---GGGGA-CGGUgg---aGGGucCCcacCCCCGGGC
gcgCCCGCGCC-----
```

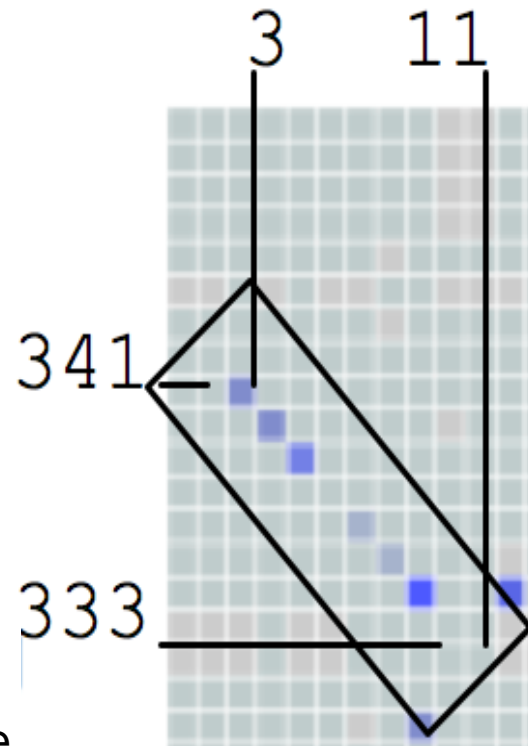
Positions 1-11
11
12345678901
--GGCGGCGGG

Positions 333-349
33333333333333333333
3333333444444444444
34567890123456789
CCCGCGCC-----



Structure Interaction: How do the positions interact?
 Diagonals indicate a region of complementary pairing,
 usually a stem.

Are they complementary? Perfectly!			
3	G	- C	341
4	G	- C	340
5	C	- G	339
6	G	- C	338
7	G	- C	337
8	C	- G	336
9	G	- C	335
10	G	- C	334
11	G	- C	333
11	G	- C	333



The positions colored **blue** have evidence of covariation. The others are likely base-paired in the stem, but do not co-vary in the sequence alignment.