

RNA fold analysis using MFOLD

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- The concept of RNA secondary structure began with the work of Doty and Fresco.
- The prediction of RNA secondary structure (folding) by energy minimization using nearest neighbor energy parameters began with Tinoco and colleagues and also with Delisi and Crothers.
- Efficient algorithms for RNA secondary structure prediction using dynamic programming methods borrowed from sequence alignment were developed independently by a number of people.

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- The 'mfold' software for RNA folding was developed in the late 1980s.
- The 'm' simply refers to 'multiple'.
- The core algorithm predicts a minimum free energy, ΔG , as well as minimum free energies for foldings that must contain any particular base pair.
- Any base pair, r_i-r_j , between the i th nucleotide and the j th nucleotide that is contained in a folding no more than $\delta\delta G$ from the minimum, is plotted in a triangular plot called the 'energy dot plot'.
- Base pairs within this free energy increment are chosen either automatically, or else by the user, and foldings that contain the chosen base pair are computed.
- They have minimum free energy conditional on containing the chosen base pair.
- The description and use of the mfold package has appeared in a number of articles.
- The closely related 'RNAstructure' program has also been described.

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Sequence

A sequence must be entered into the sequence text area box. All characters except for 'A-Z' and 'a-z' are removed. Lower case characters are converted to upper case. For RNA folding, 'T' or 't' are converted to 'U', while 'U' or 'u' are converted to 'T' in DNA folding. If, for example, you enter

```
> gi|26014111|ref|NW_044277.1|RnUn_1636 Rattus norvegicus WGS supercontig  
ATGTTCAATTTTATCTAATCCCTGTTACTCTGGAAAACAGGTTAAAAAAAAAAAAATCCTCCACAATCCATT  
TTCTGGAAAACAGCTTACTTCAAAGACCCACCCTTCCTGTAGGACTTTAGTACATCTTTCAGGTGCTTCT,
```

then the resulting sequence will be

```
          10          20          30          40          50  
GIREFNWRNU  NRAUUUSNOR  VEGICUSWGS  SUPERCONUI  GAUGUUCAAU  
          60          70          80          90          100  
UUUAUCUAAU  CCCUGUUACU  CUGGAAAACA  GGUUAAAAAA  AAAAAUCCUC  
          110         120         130         140         150  
CACAAUCCAU  UUUCUGGAAA  ACAGCUUACU  UCAAAGACCC  ACCCUUCCUG  
          160         170         180         190  
UAGGACUUUA  GUACAUCUUU  CAGGUGCUUC  U,
```

MFOLD is renamed as UNFOLD now which is mixture of mfold & DINAMelt

"UNAFold"

- "Unified Nucleic Acid Folding and hybridization package"

The UNAFold web server is currently an amalgamation of two existing web servers: mfold & DINAMelt. The aim of this web site is to integrate the existing servers and to expand by developing algorithms and software that will provide new services to the scientific community.

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