

Comparing forward/reverse strand exonic and intronic RNA secondary structures, for PHO1-2 *Oryza sativa* transcript orthologs

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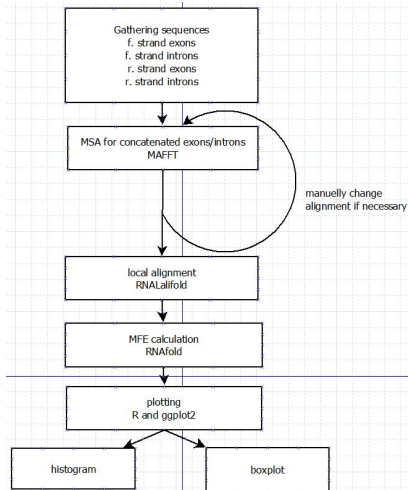
Introduction

water stress in *O.sativa*:

- ▶ normal levels of PHO1-2 mRNA
- ▶ high levels of antisense mRNA, and PHO1-2 protein

Question: translation regulation via secondary structures, binding of antisense to the mRNA transcript?

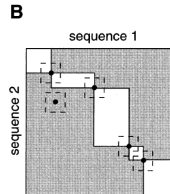
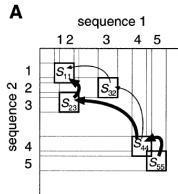
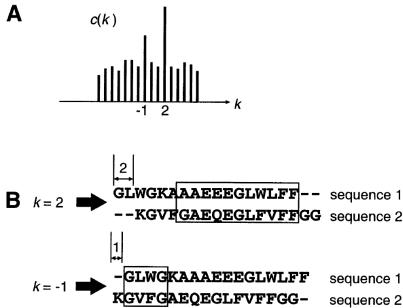
Workflow



MAFFT

- ▶ multiple sequence alignment with fast fourier transform
- ▶ works with vectores:
 - AA: $v(a)$ volume and $p(a)$ polarity
 - nucleotide: frequency of bases at each column
- ▶ peaks for homologous regions

MAFFT



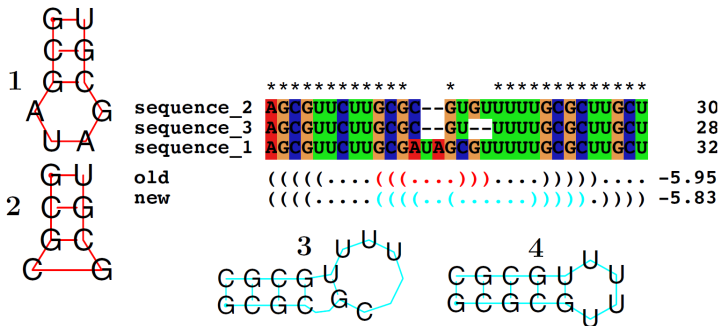
- ▶ CPU time from n^2 to $n \cdot \log n$
- ▶ faster than T-coffee and ClustalW, same accuracy

Nucleic Acids Res. 2002 Jul 15; 30(14): 30593066.

RNAalifold

- ▶ prediction of consensus structure for given alignment
- ▶ computation of MFE structures via RNAfold (recursive algorithm)
- ▶ thermodynamic energy minimization + simple scoring model (conservation score, gap elimination, structure constraints)

RNAalifold

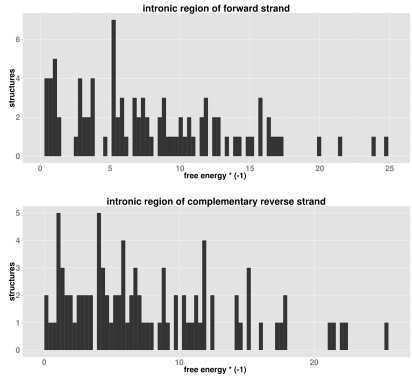
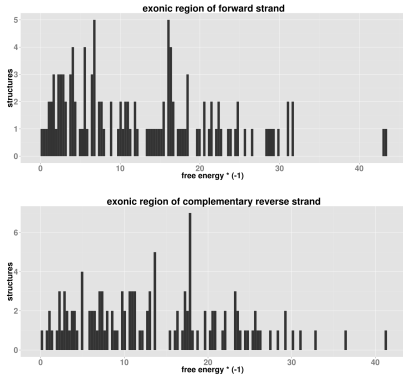


doi:10.1186/1471-2105-9-474

Predictions

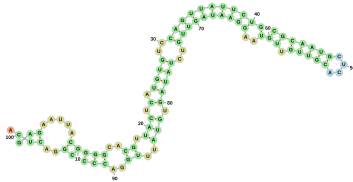
- ▶ exons should be evolutionary conserved and could also have compensatory mutations
- ▶ exonic secondary structures should be unstable
- ▶ introns experience less selective pressure, prone to accumulation of mutations
- ▶ intronic secondary structures should be stable, interaction with ribosome

Results

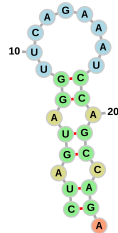


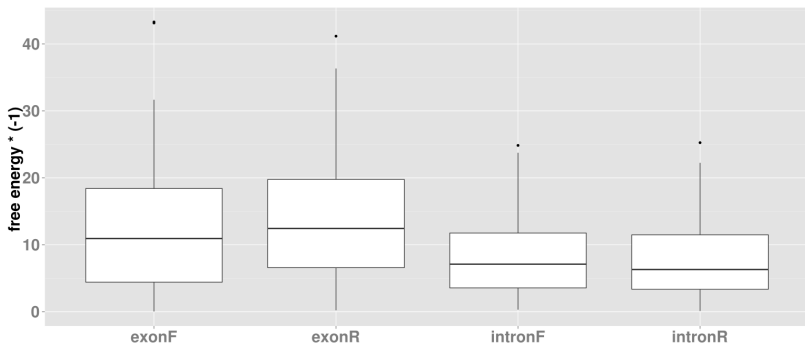
Secondary structure visualization

exonR MFE -40kcal/mol



exonR MFE -1kcal/mol





Discussion

