A Simple Protocol for the Inference of RNA Global Pairwise Alignments

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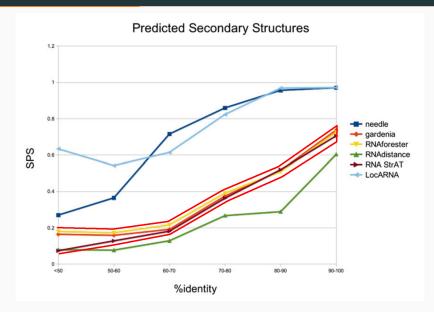


Content

Tree-Based

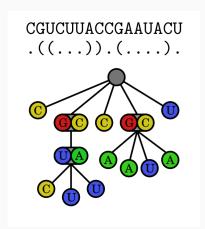
Content

Tree-Based

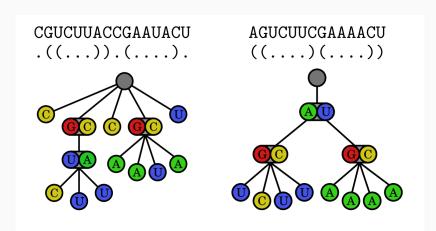


Using the secondary structure:

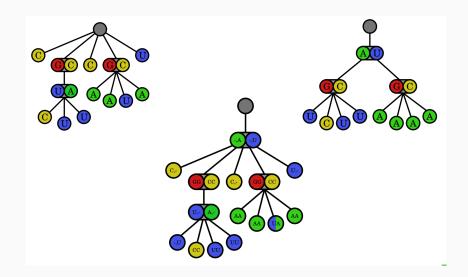
Using the secondary structure:



Using the secondary structure:



Tree-Alignment



• This is not always possible.

- This is not always possible.
- There's structures that cannot be represented in trees.

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- There's structures that cannot be represented in trees.

Example: (.[.).]

Tree-Editing

Edit operations on Trees ...

Tree-Editing

Edit operations on Trees are edit operations on arc-annotated sequences!

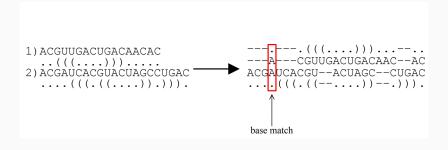
Tree-Editing

```
Edit operations on Trees ... ... are edit operations on arc-annotated sequences! (.((..(..)..)))
```

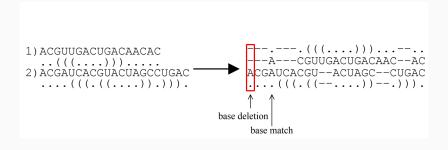
```
1) ACGUUGACUGACAACAC
..(((...)))....
2) ACGAUCACGUACUAGCCUGAC
...(((.((...)))))).

-------(((...)))...-..

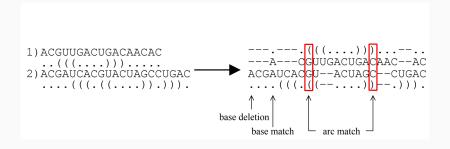
ACGAUCACGU-ACUAGC-CUGAC
...(((.((--...))--.))).
```



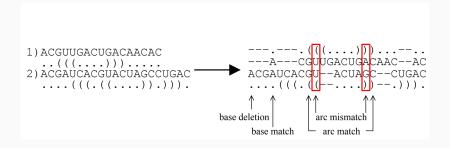
base match



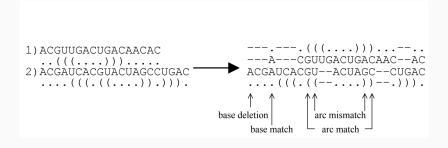
- base match
- base indel



- base match
- base indel
- arc match

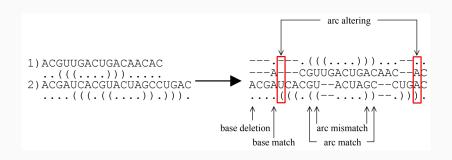


- base match
- base indel
- arc match
- arc mismatch



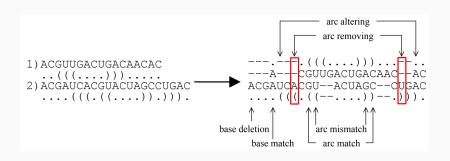
- base match
- base indel
- arc match
- arc mismatch

arc breaking (missing)



- base match
- base indel
- arc match
- arc mismatch

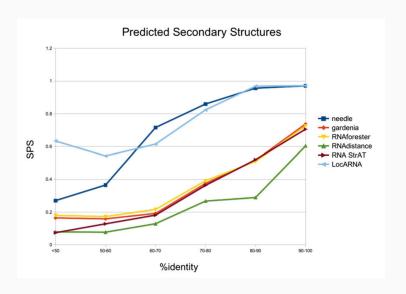
- arc breaking (missing)
- arc altering



- base match
- base indel
- arc match
- arc mismatch

- arc breaking (missing)
- arc altering
- arc removing

Performance comparison



Performance comparison

