GeneRfold Package

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1 Overview

GeneRfold allows the use of Vienna RNA library within R.

The Vienna RNA library propose some tools for the prediction and comparison of RNA secondary structures.

2 Main functions

2.1 Fold routine

Folds the sequence and returns the minimum free energyin kcal/mol; the mfe structure in bracket notation is returned.

```
> library(GeneRfold)
> s <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGGTT"
> fold(s)

[[1]]
[1] ".......(((((((...(((((((((((...))))))).)))))))))))"

[[2]]
[1] -17.3
```

2.2 Plot routine

Plot (to a postcript file) a structure (rnaPlot) made by fold or the dot plot.

```
> s <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGGTT"
> dotPlot(s, file = "dot.ps")

[1] 1

> rnaPlot(s, file = "rna.ps")

[1] 1
```
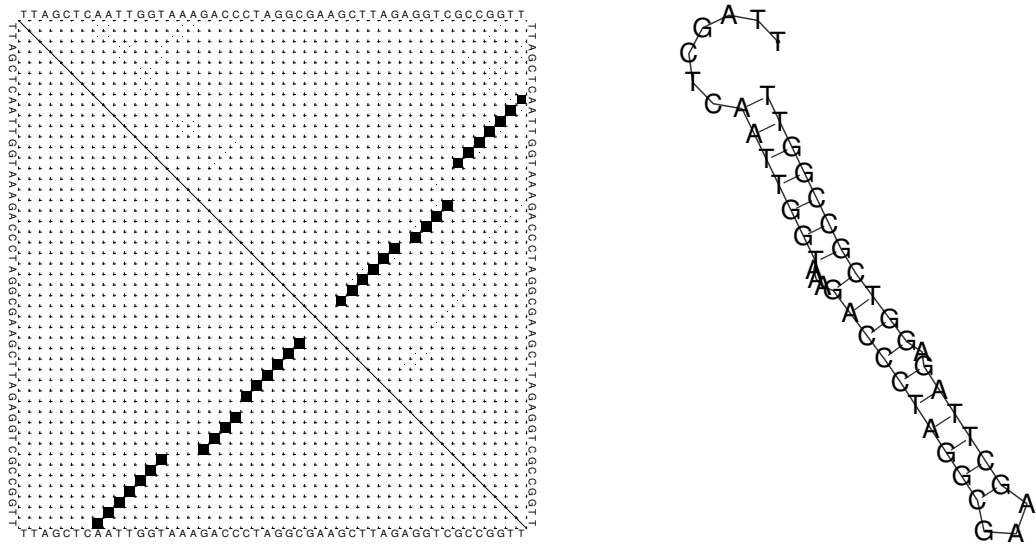
Figure 1: Plot routine