

GeneRfold Package

A. Lucas, C. Thermes & Y. d'Aubenton-Carafa

April 22, 2010

Contents

1	Overview	1
2	Main functions	1
2.1	Fold routine	1
2.2	Plot routine	1

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 energy in 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 postscript 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
```

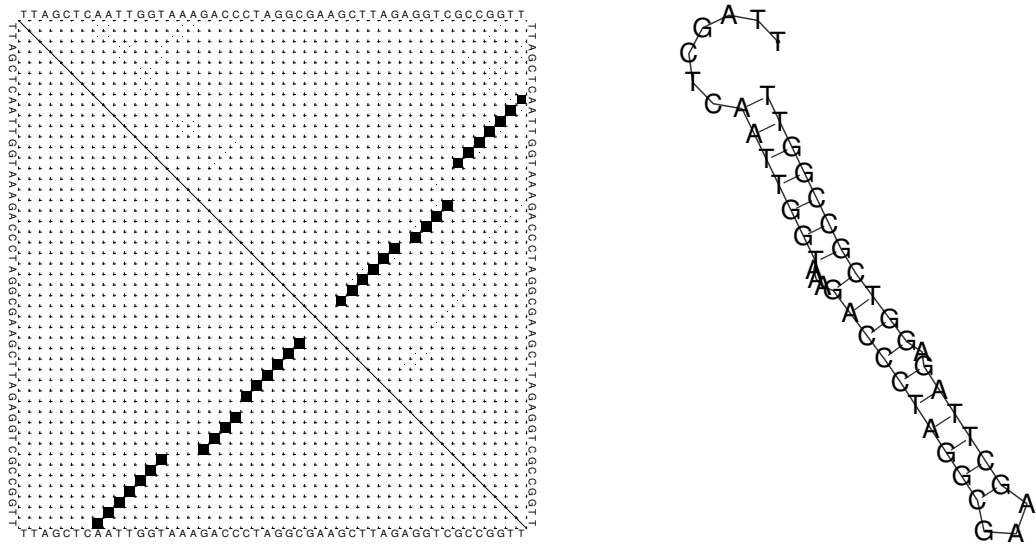


Figure 1: Plot routine