

# GeneRfold Package

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

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## Contents

<b>1</b>	<b>Overview</b>	<b>1</b>
<b>2</b>	<b>Main functions</b>	<b>1</b>
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 <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTGCGCCGGTT"
> 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 <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTGCGCCGGTT"
> dotPlot(s, file = "dot.ps")
```

```
[1] 1
```

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

```
[1] 1
```

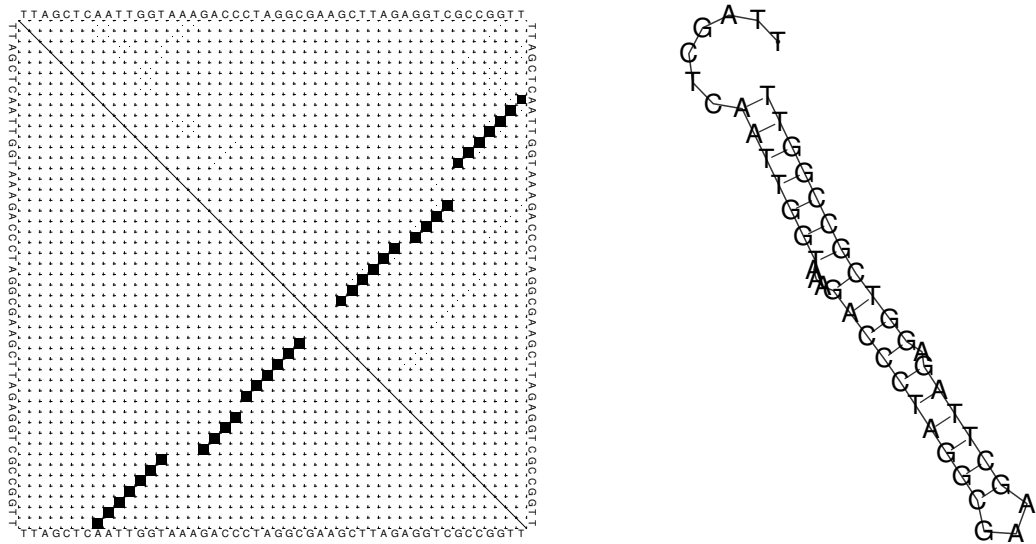


Figure 1: Plot routine