

Algorithms for RNA folding

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Abstract

Analysis of thermodynamically based algorithms for RNA structure prediction

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1 Introduction

1.1 Motivation

Ribonucleic acid (RNA) is at the core of many biological processes. Traditionally it has been described as the messenger molecule of DNA, faithfully carrying the code for protein from DNA to the site of protein synthesis. However, in a recent landmark paper, Amaral et al. [1] described our genome, and those of other eukaryotes, as being driven by an RNA machine. They noted that most of the eukaryote genome is transcribed into RNA, despite little of it coding for protein. It seems that much of our genome, originally called ‘junk DNA’, codes for functional RNA molecules. These RNAs can interact with DNA, affecting gene expression. This allows DNA to essentially regulate itself. For example, Makeyev & Maniati [6] reported that microRNAs affect the expression of genes by interfering with translation of protein. They also argued that microRNAs, and other regulatory RNAs, explain the vast differences between organisms with similar genomes. To put this idea into perspective, we share roughly 90% of our genes with the domestic Cat [12]. Mattick [9] has suggested that the process of development—from embryo to adult—is encoded in the interactions of such RNAs.

A widely held axiom is that chemical structure is tantamount to biological function. With increasingly important biological functions being associated with RNA, it is important to be able to predict its structure. The purpose of this paper is to provide a survey of some widely used RNA structure prediction algorithms. In the interest of keeping this report succinct, I review only algorithms based on a conventional thermodynamically based model. Other algorithms often use machine learned, statistical parameters; these shall not be explored here. In essence, all the algorithms I test take a single RNA primary sequence as input, and return a predicted secondary structure. I hypothesize that newer algorithms should have improved accuracy as compared to older algorithms. In addition, I aim to empirically verify the time complexities of my chosen algorithms. The Zuker algorithm was the first thermodynamic algorithm to achieve usable prediction accuracy, and it forms the basis for all the methods I shall hence discuss.

1.2 Relevant Algorithms

1.2.1 The Zuker Algorithm

In 1981 Zuker & Stiegler [16] described an algorithm that predicted RNA structure by minimizing molecular free energy. The lower free energy a molecule has, the more stable it is. This was done by introducing a number of thermodynamic rules for canonical substructures like hairpin loops, internal bulges, multiloops (also called bifurcation loops), unbonded bases, and stacked base pairs. For examples of these structures, refer to Figure 1. The Zuker algorithm uses a mutually recursive dynamic programming recurrence to achieve a relatively comprehensive scoring scheme. This is possible because RNA structures are nested, and hence substructures with minimum free energy need not be recomputed. It follows naturally that

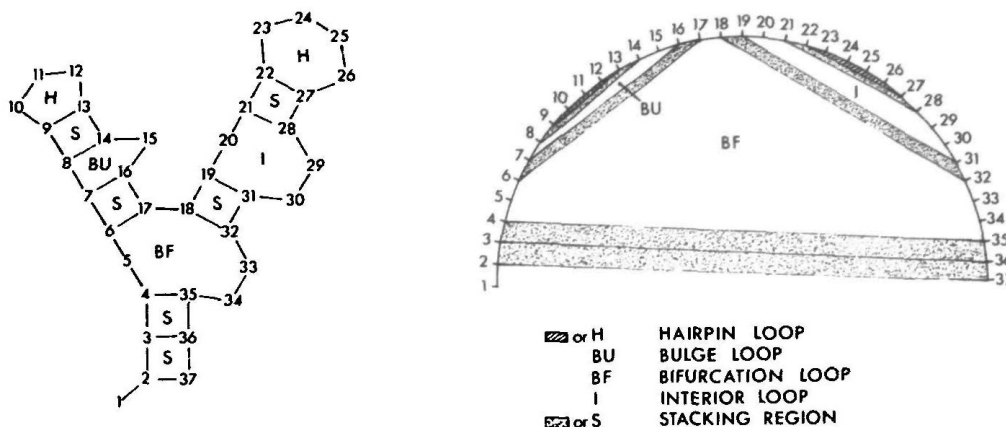


Figure 1: Diagram of substructures used in the Zuker algorithm. On the left is a diagram of a RNA secondary structure. On the right is the same structure laid out on a semi-circle. Bonds are represented as lines crossing the semi-circle. Taken from original publication [16].

dynamic programming can then be used to find a global minimum. The thermodynamic scoring system is borrowed from the work of Studnicka et al. [15] who presented a complex but theoretically similar algorithm, albeit having much worse asymptotic and implementation complexity. It was then later improved by Matthews et al. [8, 7]. The time complexity of the Zuker algorithm is $O(n^3)$, where n is the number of nucleotides in the RNA. In short, it is able to efficiently predict secondary structures for RNAs with hundreds of bases, on modern hardware. Because of its efficiency, robustness, and extensibility, this method is, even today, still the most popular available. The most widely used packages for RNA secondary structure prediction all contain implementations of the Zuker algorithm [5, 14].

1.2.2 Maximum Expected Accuracy

The Maximum Expected Accuracy (MEA) technique for RNA prediction was first applied by Do, Woods & Batzoglou as part of the CONTRAfold algorithm [3] in 2006, and is newer than the Zuker method. This was the second class of algorithm I tested. The Zuker algorithm essentially finds the most likely structure under a thermodynamic model. A MEA prediction method is more compromising; it finds a structure containing the most probable set of bonds. This is done by computing the partition function for a RNA, as described by McCaskil [10]. The partition function computation is achieved by a modified version of the Zuker algorithm, and can be done in $O(n^3)$ time. It should be noted that this computation uses the underlying thermodynamic model of the Zuker algorithm. This partition function can be processed to produce a two dimensional matrix of base pairing probabilities. Each pair of indexes in the matrix represents the probability that the bases corresponding to those indexes will bond. Intuitively this represents the entire folding landscape of a RNA, rather than a single minimum free energy structure as

computed by the Zuker algorithm. A MEA algorithm builds a structure by selecting bonds from this bond probability matrix. However, if the sum probability is naively maximized, it tends to produce structures with too many bonds. As such, a MEA algorithm must find a compromise between the number of bonds selected, and the total probability of the computed structure. Usually this is achieved by introducing some cut-off value, or, in the case of CONTRAfold, a scaling factor.

1.2.3 Cotranscriptional Folding

There is compelling evidence that RNA structures form during transcription. Put simply, this means that RNA structures begin to form before the molecule has been fully assembled. This thesis is called ‘cotranscriptional folding’. Kramer & Mills [4] reported seeing preliminary secondary structures form, break apart, and reform into other structures during transcription. Over a decade later Morgan & Higgs [11] examined many RNA molecules and found that typical structures had suboptimal free energy. They postulated that this was due to cotranscriptional folding. Recently, Proctor & Meyer [13] purportedly improved secondary structure prediction accuracy by simulating cotranscriptional folding in an algorithm they called ‘CoFold’. The effects of cotranscriptional interactions were captured using a scaling function in which closer nucleotides are weighted higher than distant nucleotides. Proctor & Meyer [13] reported that this improved prediction accuracy; particularly for RNA molecules comprising greater than 1000 nucleotides. CoFold extends the Zuker algorithm by injecting the aforementioned scaling function into the recurrence relation. As such, it also has a $O(n^3)$ time complexity. CoFold was the third algorithm chosen for testing.

2 Materials and Methods

2.1 Environment and Software

All software was run on the Debian 7.5 “wheezy” operating system using the default configuration. Debian was run on top of an Intel i7-4770k processor with 32 gigabytes of RAM. The GNU C Compiler (gcc) version 4.8.2 was used to compile all the required code. Though the processor used was multicore, OpenMP was disabled at compile time to prevent the use of multiple cores during testing. The source code for all the algorithms tested was compiled using makefiles provided as part of their source. The latest version of the Vienna RNA Suite (version 2.1.7, released April 13th 2014) was used as the reference implementation of the MEA algorithm and the Zuker algorithm. This was because it contains widely used versions of both. The entire Vienna RNA Suite was compiled from source, then was linked as a static library at compile time for testing. The latest version of CoFold was downloaded from the CoFold webserver (ref). Because CoFold is based on an older version of RNAfold, it was compiled separately, and linked as a separate static library. In addition, the GNU Regression, Econometrics, and Time-series Library (also called ‘gretl’) was used for all statistical tests, and to produce the graphics found in Section

2.2 Data Set

The RNA secondary structures used to test algorithms presented in this paper were taken from the RNA STRAND database [2]. The RNA STRAND database is a free-to-use, curated collection of RNA secondary structures taken from various publicly available databases and publications. A subset of RNA structural data was extracted from the database. This subset contained only RNA structures that were marked having been verified using X-Ray crystallography, or nuclear magnetic resonance imaging. It also comprises only whole RNAs; none of the RNAs used were fragments or subsequences of larger RNA molecules. Finally, no duplicates were allowed in the selected set. Hereafter, I shall refer to this collection of RNA secondary structures as the ‘testing set’. The testing set contained 392 different RNA molecules ranging in length from 20 to 3032 nucleotides.

2.3 Accuracy

Well established procedures have been developed over the history of RNA structure prediction for comparing accuracy. Usually accuracy is determined by comparing predicted structures to known structures. True Positives (TP) is defined as the number of base pairs which appear in both the predicted structure and the actual structure. False Positives (FP) is the number of predicted base pairs not in the true structure [5]. Similarly, False Negatives (FN) is defined as the number of base pairings in the reference structure but not present in the predicted structure [5]. Sensitivity, also called the True Positive Rate (TPR), can be defined using the previously introduced values. I have given a mathematical definition of the TPR in Equation 1.

$$\frac{TP}{TP + FN} \quad (1)$$

Precision, also known as Positive Predictive Value (PPV), can also be calculated using these values (see Equation 2).

$$\frac{TP}{TP + FP} \quad (2)$$

For the results presented in this report, the F-score was used as a measure of accuracy. F-score is defined as the harmonic mean of sensitivity and precision. It provides a good balance between these two metrics.

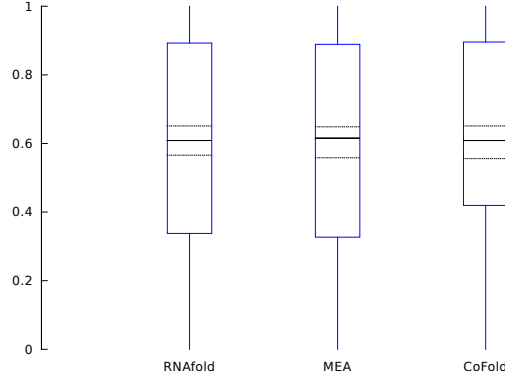


Figure 2: Box plots depicting the spread of F-scores for RNAfold, MEA, and CoFold.

Algorithm	Mean	Median	Std. Dev.
RNAfold	0.574834	0.608696	0.341977
MEA	0.564584	0.615385	0.346070
CoFold	0.580802	0.608696	0.337973

Table 1: Summary statistics for the F-scores of RNAfold, MEA, and CoFold.

3 Results

3.1 Accuracy

To compare the accuracy of my three chosen algorithms, I ran each of them using the testing set as input. The structures computed by each algorithm were then compared to the actual, experimentally determined structures for the corresponding RNAs, and an F-score was computed. A summary of the recorded F-scores is shown graphically in Figure 2. In addition, summary statistics can be found in Table 1. A more fine grained comparison was achieved by using the Wilcoxon signed-rank test. This statistical test was chosen over the more standard t-test because the data was not normally distributed, and the Wilcoxon signed-rank test is less sensitive to non-parametric variables. A Wilcoxon signed-rank test compares the difference between samples from the same population. In our case, the sample refers to the algorithm used, and the population is the testing set, which was the same for all algorithms. Hence the assumptions of the test are satisfied. The test was run to compare each pair of algorithms. A summary of these results can be found in Table 2. Because none of the results were statistically significant ($p > 0.05$), we cannot reject the null hypothesis of the Wilcoxon signed-rank test. Specifically, the null hypothesis is that any difference in the compared samples is due to chance. To test the claim that CoFold is more accurate for larger RNA, the Wilcoxon signed-ranks test was repeated for only RNAs larger than 1000 nucleotides. Again the results were not statistically significant ($p > 0.05$), and the null hypothesis can be safely rejected (see Table 3).

Algorithms	z -value	p -value
MEA & CoFold	-0.225675	0.410727
RNAfold & CoFold	-0.85571	0.196079

Table 2: The results of Wilcoxon signed-rank tests for CoFold versus other algorithms using only RNA > 1000 nucleotides in length. The z -value indicates the magnitude of difference between population F-scores. The p -value indicates statistical significance.

Algorithms	z -value	P-value
MEA & CoFold	-0.97557	0.164639
RNAfold & CoFold	-0.284113	0.388162
RNAfold & MEA	0.290959	0.385541

Table 3: The results of Wilcoxon signed-rank tests between RNAfold, MEA, and CoFold for only RNA with length ≥ 1000 . The z -value indicates the magnitude of difference between population F-scores. The P-value indicates statistical significance.

3.2 Time

4 Discussion and Conclusions

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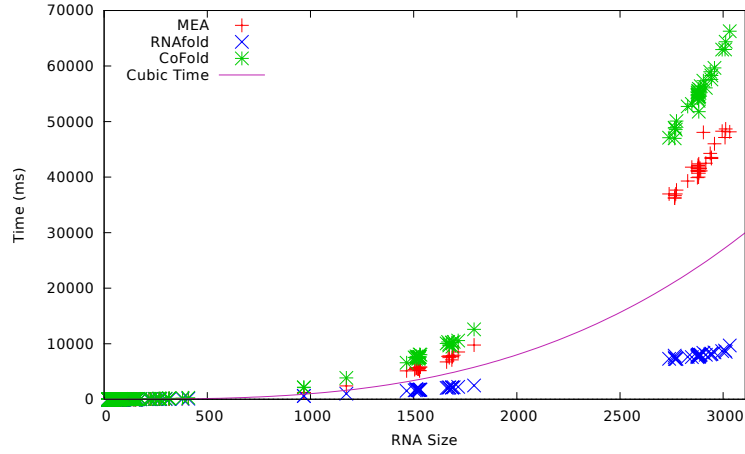


Figure 3: Here the recorded run time for RNAfold, MEA, and CoFold is depicted as a scatter plot. The time used by all algorithms increases with increasing RNA length. The length of an RNA is defined as the number of nucleotides it comprises. A purple line representing a generic cubic curve is included for comparison. This line has been scaled by a constant so that it remains visible on the diagram.

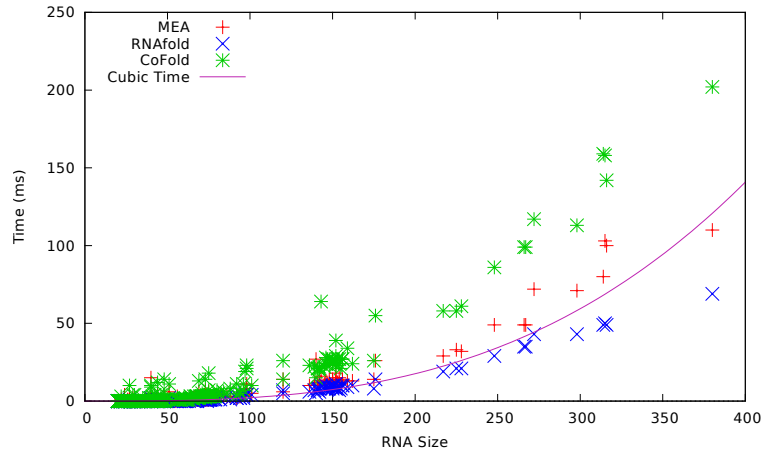


Figure 4: Here the recorded run time for only smaller RNAs (< 400 nucleotides) is depicted as a scatter plot. A purple line representing a generic cubic curve is included for comparison. This line has been scaled by a constant so that it remains visible on the diagram.

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