RNA matrix models with external interactions and their asymptotic behaviour

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We study a matrix model of RNA in which an external perturbation acts on n nucleotides of the polymer chain. The effect of the perturbation appears in the exponential generating function of the partition function as a factor \((1 - \frac{n\alpha}{L})\) [where \(\alpha\) is the ratio of strengths of the original to the perturbed term and \(L\) is length of the chain]. The asymptotic behaviour of the genus distribution functions for the extended matrix model are analyzed numerically when (i) \(n = L\) and (ii) \(n = 1\). In these matrix models of RNA, as \(n\alpha/L\) is increased from 0 to 1, it is found that the universality of the number of diagrams \(a_{L,g}\) at a fixed length \(L\) and genus \(g\) changes from \(3^L\) to \((3 - \frac{n\alpha}{L})^L\) \((2^L\) when \(n\alpha/L = 1\) and the asymptotic expression of the total number of diagrams \(N\) at a fixed length \(L\) but independent of genus \(g\), changes in the factor \(exp^{\sqrt{L}}\) to \(exp^{1 - \frac{n\alpha}{L}\sqrt{L}}\) \((exp^0 = 1 \text{ when } n\alpha/L = 1)\).

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I. INTRODUCTION

Improved understanding of the process of folding of RNA finds its ultimate use in the prediction of the fully folded, partially folded and completely unfolded structures under physiological conditions \([1]\). Under these conditions, unfolding is a very slow process as compared to folding in the presence of a force. Application of a force increases the unfolding rate and we can therefore get the unfolded structures from the folded ones \([1]\ and references therein). Experimental techniques of force induced measurements have proved successful in probing properties related to different aspects of RNA folding and unfolding, domain unfolding in proteins, in polysacharides and nucleic acids \([2]\ and references therein). Experiments have been performed on the double heliced DNAs to study their elastic and structural properties using electric field, hydrodynamic flow among other methods of force application \([3]\ and references therein). The advent of AFM technique served as an important tool in the study of the basic underlying framework of molecular structural biology. Over the years, optical tweezers and AFM (atomic force microscopy) techniques have been employed to study the physical, elastic and structural properties of the biomolecules by recording their force extension curves (FECs) and studying the force dependent dynamics and folding landscapes of the molecules \([4, 5, 6, 7, 8, 9]\ and references therein). The conformations of biopolymers (DNA, RNA and proteins) which are otherwise not accesible from the conventional methods of measurements: NMR spectroscopy and X-ray crystallography, are possible with the use of AFMs. These conformational changes help in revealing the underlying mechanical framework of the biological systems \([2]\ and references therein). Mechanical unfolding and refolding of single RNA has been studied using force-ramp, hopping and force-jump methods \([10] \text{ and references therein}). In mechanical unfolding experiments, it has been observed that at a critical value of the applied force, the hairpin structure toggles between the folded and the unfolded states \([11, 12, 13]\). In these experiments, ionic concentrations play an important role. Experiments of Bustamante et al \([12, 13]\ have shown that the denaturation of RNA by a constant force involves multiple trajectories (for RNA hairpins and Tetrahymena thermophila ribozyme) while undergoing a transition from the folded structure state to the unfolded state. These trajectories depend on the point at which the force is applied \([1, 14]\). This diverseness in the folding-unfolding pathways is due to the rugged energy landscape of RNA (consisting of many minima). Controlled/monitored force loading and unloading rates can be used to manipulate the single molecules of RNA into either their native or misfolded pathways. Different force unloading rates in experiments on TAR RNA molecules showed different types of trajectories associated with particular refolding characteristics \([15]\ and references therein).

We discuss here very briefly, a generalization of the extended random matrix model of RNA folding proposed in \[16\] where the external perturbation acts on a single nucleotide \((n = 1)\) and on \(n\) nucleotides \((n \leq L)\) in the polymer chain (we will refer to the two RNA models as 1-NP RNA model, with NP being Nucleotide Perturbation and n-NP RNA model respectively). In \[16\], the external perturbation acted on all the nucleotides in the polymer chain \((\text{i.e., } n = L, n\) is the number of bases on which the force is acting). We briskly outline the extended matrix model of \[16\]
II. EXTENDED MATRIX MODELS OF RNA

We review here, the effect when a perturbation acts on all the nucleotides in the polymer chain \((n = L)\) studied in [10]. The nucleotide-nucleotide interaction partition function of the polymer chain with a perturbation on all the bases is

\[
Z_{L,\alpha}(N) = \frac{1}{A_L(N)} \int \prod_{i=1}^{L} d\phi_i \exp^{-\frac{N}{2} \sum_{i,j=1}^{L} (V^{-1})_{i,j} Tr \phi_i \phi_j} \exp^{-N \sum_{i=1}^{L} (W^{-1})_{i,i} Tr \phi_i} \frac{1}{N} Tr \prod_{i=1}^{L} (1 + \phi_i)
\]

where

\[
A_L(N) = \int \prod_{i=1}^{L} d\phi_i \exp^{-\frac{N}{2} \sum_{i,j=1}^{L} (W^{-1})_{i,j} Tr \phi_i \phi_j} \exp(-N \sum_{i=1}^{L} (W^{-1})_{i,i} Tr \phi_i)
\]

is the normalization constant, \(e^{\exp(-N \sum_{i=1}^{L} (W^{-1})_{i,i} Tr \phi_i)}\) is the perturbation term. \(V_{i,j}\) is an \((L \times L)\) symmetric matrix containing information on the interactions between the L nucleotides at positions \(i\) and \(j\) in the polymer chain, \(\phi_i\) are \(L\) independent \((N \times N)\) hermitian matrices and the observable \(\prod_i (1 + \phi_i)\) is an ordered product over \(\phi_i\)’s. We consider \(V_{i,j} = v\) and \(W_i = w\) where \(v\) gives the strength of interaction between the nucleotides at positions \(i\) and \(j\) (in these models, interaction between any two nucleotides of the chain is considered the same and equal to \(v\)) and \(w\) gives the strength of the perturbation. Carrying out a series of Hubbard Stratonovich Transformations, the integral over \(L\) matrices \(\phi_i\) in eq. (1) reduces to an integral over a single \((N \times N)\) hermitian matrix \(\sigma\)

\[
Z_{L,\alpha}(N) = \frac{1}{R_L(N)} \int d\sigma \exp^{-\frac{N}{2} Tr(\sigma^2)} \frac{1}{N} Tr(1 + \sigma)^L
\]

where \(R_L(N) = \int d\sigma \exp^{-\frac{N}{2} Tr(\sigma^2)}\) Following the algebra in [10] (from eq.5 to eq.15), the exponential generating function \(G(t, N, \alpha)\) of the partition function \(Z_{L,\alpha}(N)\) is

\[
G(t, N, \alpha) \equiv \sum_{L=0}^{\infty} Z_{L,\alpha}(N) \frac{t^L}{L!} = \exp{\frac{\pi t^2}{N(1-\alpha)}} \left[ \frac{1}{N} \sum_{k=0}^{N-1} \binom{N}{k+1} (\frac{t^2}{N})^k \right]
\]

where \(\alpha = \frac{v}{w}\) gives the ratio of strengths of the original to the perturbed term.

For \(\alpha = 0\), the extended matrix model of RNA folding reduces to the random matrix model in [18]. However, for \(\alpha = 1\) it is observed that the partition function for odd lengths of the polymer chain vanishes completely. In the extended matrix model, each unpaired base of the polymer chain in the contact diagrams is associated with a factor \((1 - \alpha)\) which becomes zero when \(\alpha = 1\) thus removing structures with any unpaired bases. We can therefore divide the structures into two regimes: (i) \(\alpha \leq 1\) comprising of both the unpaired and paired base structures and (ii) \(\alpha = 1\) comprising of only completely paired base structures (where only structures with fully paired bases remain whereas structures with any unpaired bases are suppressed) [10]. The genus distributions for the extended matrix model are therefore significantly different for different \(\alpha\)’s, especially for \(\alpha = 1\) [where \(Z_{L,\alpha}(N) = 0\) for odd lengths of the polymer chain] as compared with the model of [18]. The addition of a perturbation has thus changed the genus distributions and the overall enumeration of the structures given by this model.

A. EXTENDED MATRIX MODEL OF RNA WITH PERTURBATION ON A SINGLE BASE (1-NP) AND \(n\) BASES (n-NP)

We now consider a generalization of the extended matrix model proposed in [10] by adding a perturbation to a single nucleotide in the polymer chain only, \(n = 1\) (1-NP). The motivation comes from the force induced experiments in obtaining important characteristics of folding and unfolding of RNAs discussed in the introduction [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15]. We keep all the assumptions the same as for the model in [10]. The interaction
FIG. 1: (a) Plot of the asymptotic formula of $N$ in [18] (red dotted curve) with the numerically calculated $N_\alpha$ values for different lengths $L$ corresponding to $\alpha = 0.75$ (boxed curve). (a') The new asymptotic formula of $N'_\alpha$ (red dotted curve) for the extended matrix model of RNA [16] is plotted with the numerical $N_\alpha$ values for different lengths $L$ for $\alpha = 0.75$ (boxed curve).

The diagrammatic representation of the n-NP differs from the diagrammatics of the model with perturbation on all the nucleotides in the factor $(1 - n\alpha_L)$ associated with each unpaired base which replaces the factor $(1 - \alpha)$ in the contact diagrams of figure 1 in [16].

III. ASYMPTOTICS OF THE EXTENDED MATRIX MODELS FROM NUMERICS

The asymptotic behaviour of the genus distribution functions for the matrix model of RNA studied in [18] showed universal characteristics. We investigate here numerically, the changes that the genus distribution functions: (i) the total number of diagrams at a fixed length $L$ but independent of genus $g$, $\mathcal{N}$ [defined as $\mathcal{N} = Z_L(N = 1)$] and (ii) the number of diagrams at a fixed length $L$ and genus $g$, $a_{L,g}$ [defined through $Z_L(N) = \sum_{g=0}^{\infty} a_{L,g} N^g$] of the model in [18] undergo when a perturbation is added to these models. The asymptotics of the genus distribution functions are computed for the extended matrix model (i) with perturbation on all the bases, $n = L$ [16] and (ii) with perturbation on $n$ bases, (n-NP). We will represent the genus distribution functions for the different matrix models as follows: (i) $\mathcal{N}$ and $a_{L,g}$ will represent the asymptotic formulae for the model in [18], (ii) $\mathcal{N}'_\alpha$ and $a_{L,g,\alpha}$ will represent the new asymptotic formulae for the extended matrix model of RNA [16] and (iii) $\mathcal{N}_\alpha$ and $a_{L,g,\alpha}$ will represent the numerical values of the genus distribution functions for different $\alpha$’s. We start with the exact asymptotic expressions (i) $\mathcal{N} = L^{\frac{3}{4}} \exp[-\frac{1}{4} + \sqrt{\mathcal{T}} - \frac{1}{2}] / \sqrt{2}$ and (ii) $a_{L,g} = k_3 3^l L^{(3g - \frac{1}{2})}$ from [18] and compare the behaviour of $N_\alpha$ and $a_{L,g,\alpha}$ for the extended matrix model for lengths up to $L = 40$ for different values of $\alpha (= 0, 0.25, 0.5, 0.75, 1)$. We begin by studying $N_\alpha$ and $a_{L,g,\alpha}$ for the extended models with perturbation on all the bases ($n = L$).
It is observed that as $\alpha$ computed indicating an $\alpha^2(a)$, table I] for different values of $\alpha$ goes from 0 to 1 in the linearly fitted plots of (i) and (ii) (Slope 1 and Slope 2 respectively of table I), strongly verses $L\log L$ (Slope 1, table I), (ii) ($\log\ N$ and we see that the dependence of $\log\ N$ suggesting a dependence of $\alpha$ with the $N$ suggests a dependence of $\alpha = 1$ plots [fig. 2(d) and fig. 2(e)]. In the fitted plots of (iii) we observe a remarkable behaviour for $\sqrt{L}$ for (i) and (ii) respectively. This proves that the factor of $(1 - \alpha)$ with the $\sqrt{L}$ term in the exponent of $N$ is the correct choice. We can therefore write the new asymptotic expression of the total number of diagrams at a fixed length $L$ and $\alpha$ but independent of genus $g$, $N_\alpha'$ for the extended matrix model as

$N_\alpha'(L) \sim \frac{1}{2} L \log L + \frac{1}{2} \sqrt{\frac{1}{2} - \alpha} \log \sqrt{\frac{1}{2} - \alpha}$. We are interested in the large length $L$ behaviour and we see that the dependence of $\log\ N$ on $L$ is strongest in $L\log L$. We linearly fit the plots (i) ($\log N_\alpha - \sqrt{L} + \frac{1}{2}$) versus $L\log L$ (Slope 1), (ii) [$\log N_\alpha - \sqrt{\frac{1}{2} - \alpha} \log L$] versus $L\log L$ [Slope 1(a)], (iii) $(\log N_\alpha - \sqrt{\frac{1}{2} - \frac{1}{2} L\log L})$ verses $L$ (Slope 2) and (iv) [$\log N_\alpha + (1 - \alpha)\sqrt{\frac{1}{2} - \frac{1}{2} L\log L}$] verses $L$ [Slope 2(a)].

TABLE I: Table lists slopes of the linearly fitted plots for different values of $\alpha$ before and after the multiplication of $(1 - \alpha)$ with the $\sqrt{L}$ term of (i) $(\log N_\alpha + \frac{1}{2} - \sqrt{L})$ versus $L\log L$ (Slope 1), (ii) $(\log N_\alpha + \frac{1}{2} - (1 - \alpha)\sqrt{L})$ versus $L\log L$ [Slope 1(a)], (iii) $(\log N_\alpha - \sqrt{\frac{1}{2} - \frac{1}{2} L\log L})$ verses $L$ (Slope 2) and (iv) [$\log N_\alpha + (1 - \alpha)\sqrt{\frac{1}{2} - \frac{1}{2} L\log L}$] verses $L$ [Slope 2(a)].

| $\alpha$ | Slope 1 | Slope 1(a) | Slope 2 | Slope 2(a) |
|---------|--------|------------|--------|------------|
| 0       | 0.499  | 0.499      | -0.5026| -0.5026    |
| 0.25    | 0.4885 | 0.499      | -0.5353| -0.5022    |
| 0.5     | 0.4767 | 0.4987     | -0.5683| -0.5027    |
| 0.75    | 0.4624 | 0.4981     | -0.6025| -0.5060    |
| 1       | 0.4556 | 0.5003     | -0.6331| -0.4992    |

1. Asymptotics for $N_\alpha$

Figure 1(a) shows the combined plot of the asymptotic expression of $N$ (red dotted curve) with the numerically computed $N_\alpha$ values for $\alpha = 0.75$ (boxed curve). We have shown here for illustration, the plot for only $\alpha = 0.75$. It is observed that as $\alpha$ is increased from 0 to 1, the boxed curves (for different $\alpha$’s) shift downward continuously indicating an $\alpha$ dependence in $N_\alpha$ for the extended matrix model of RNA. We investigate this dependence in the following numerical analysis.

Taking $\log\ N$ we get: $\log\ N \sim \frac{1}{2} L \log L - \frac{1}{2} + \sqrt{\frac{1}{2} - \frac{1}{4} - \log\sqrt{\frac{1}{4}}}$. We are interested in the large length $L$ behaviour and we see that the dependence of $\log\ N$ on $L$ is strongest in $L\log L$. We linearly fit the plots (i) ($\log N_\alpha - \sqrt{L} + \frac{1}{2}$) versus $L\log L$ (Slope 1, table I), (ii) ($\log N_\alpha - \sqrt{\frac{1}{2} - \frac{1}{2} L\log L}$) verses $L$ (Slope 2, table I) and (iii) ($\log N_\alpha + \frac{1}{2} - \frac{1}{2} L\log L$) versus $\sqrt{\frac{1}{2} - \alpha}$ for different $\alpha$ and find their slopes. We find that there is a continuous decrease in the slopes as $\alpha$ goes from 0 to 1 in the linearly fitted plots of (i) and (ii) (Slope 1 and Slope 2 respectively of table I), strongly suggesting a dependence of $N_\alpha$ on $\alpha$. In the fitted plots of (iii) we observe a remarkable behaviour for $\alpha = 0.75$ and $\alpha = 1$ plots [fig. 2(d) and fig. 2(e)]. In the $\alpha = 0.75$ plot [fig. 2(d)], the points for odd and even lengths separate out into two very distinct curves and for the $\alpha = 1$ plot [fig. 2(e)], the odd lengths vanish completely leaving only the even length points in the figure. This indicates that ($\log N_\alpha + \frac{1}{2} - \frac{1}{2} L\log L$) versus $\sqrt{L}$ is very sensitive to changes in $\alpha$.

We try a factor of $(1 - \alpha)$ with the $\sqrt{L}$ term in the exponent of the $N$ expression and then fit the plots: (i) [$\log N_\alpha + \frac{1}{2} - (1 - \alpha)\sqrt{L}$] versus $L\log L$ [Slope 1(a), table I] and (ii) [$\log N_\alpha + (1 - \alpha)\sqrt{L} - \frac{1}{2} L\log L$] verses $L$ [Slope 2(a), table I] for different values of $\alpha$. We observe that now all the slopes are nearly the same and equal to $+\frac{1}{2}$ and $-\frac{1}{2}$ for (i) and (ii) respectively. This proves that the factor of $(1 - \alpha)$ with the $\sqrt{L}$ term in the exponent of $N$ is the correct choice. We can therefore write the new asymptotic expression of the total number of diagrams at a fixed length $L$ and $\alpha$ but independent of genus $g$, $N_\alpha'$ for the extended matrix model as
FIG. 3: The asymptotic formula for $a_{L,g}$ in [18] (black dotted curve) is plotted with the numerical $a_{L,g,\alpha}$ values (green boxed curve) for different lengths $L$ for $\alpha = 0.75$.

Note: The figure plots $a_{L,g,\alpha}$’s for all genii corresponding to a particular length $L$ of the polymer chain. The lowest curve (black dotted or green boxed) corresponds to genus $g = 0$ for all the lengths (0 to 40) and the successive curves in the upward direction correspond to next higher genii with the maximum genus given by $g_{\text{max}} = L/4$.

$$N'_\alpha = L^{\frac{L}{2}} \exp\left[-\frac{L}{4} + (1-\alpha)\sqrt{\frac{L}{4}}\right]/\sqrt{2}.$$  

(4)

We see from eq. (4) that the total number of structures for the extended matrix model changes considerably for example, when $\alpha = 1$ the $\sqrt{L}$ term vanishes from the exponent. We repeat the exercise as before and plot the new asymptotic formula $N'_\alpha$ for the extended matrix model of RNA given by eq. (4) [fig. 1(a'), red dotted curve] with the numerically obtained $N'_\alpha$ values for different $\alpha$’s (represented by boxed curve, shown here for only $\alpha = 0.75$). The plot for the new asymptotic formula coincides with the numerical data $N'_\alpha$ confirming the new formula.

2. Asymptotics for $a_{L,g,\alpha}$

The plot (fig. 3) of the asymptotic formula for $a_{L,g}$ (black dotted curve) with the numerically calculated $a_{L,g,\alpha}$ values (green boxed curve) for different $\alpha$’s (shown for $\alpha = 0.75$) clearly indicates that the asymptotic formula of the model in [18] needs to be changed to give the asymptotic behaviour of the extended matrix model of RNA folding [16].
TABLE II: Table lists the measures of slopes for different values of α obtained from the linear fits to the plots between L and Log \(a_{L,g=1,α}\) (Slope 1), the \(x(α)\) values for each α and slopes from the linear fit of plots between Log L and [Log \(a_{L,g=1,α} - LLog(3 - α)\)] for each α (Slope 2).

| α     | Slope 1 x(α) | Slope 2 |
|-------|--------------|---------|
| 0     | 1.198        | 3.313   | 1.646 |
| 0.25  | 1.109        | 3.63    | 1.639 |
| 0.5   | 1.012        | 2.75    | 1.633 |
| 0.75  | 0.9065       | 2.476   | 1.623 |
| 1     | 0.7891       | 2.2     | 1.655 |
| Analytical | 1.24           | 3.4556  | 1.495 |

The curves for different α’s (shown here for only α = 0.75, fig. 3) move further and further away from the asymptotic expression curve [18] as α goes from 0 to 1. This behaviour is studied and the correct asymptotic expression \(a'_{L,g,α}\) for the extended matrix model is found.

We start with the asymptotic expression of \(a_{L,g} = k_g 3^L L(3g - \frac{1}{2})\), where \(k_g = \frac{1}{3(3g - \frac{1}{2})2^{2g+1}p\sqrt{π}}\). Taking Log on both the sides and fixing \(g = 1\) (for simplicity) we get \(Log(a_{L,g=1}) \sim Log \frac{1}{3(3g - \frac{1}{2})2^{2g+1}p\sqrt{π}} + LLog3 + \frac{1}{2}LogL\). In Log \(a_{L,g=1}\), L dependence is present in the form of L and LogL. We are interested in the large L behaviour so we first look for the dominant L dependence. The linear fits to the plots of \(Log(a_{L,g=1,α})\) verses L in table II (Slope 1) shows that the slopes of the numerical \(a_{L,g,α}\) curves for different α’s are not the same and not equal to the slope of the \(a_{L,g}\) asymptotic curve (slope should be Log 3 for a plot between \(Log(a_{L,g=1,α})\) and L according to [18]). This indicates an α dependence in the factor 3 of the \(3^L\) universal part of \(a_{L,g}\) which we represent by \(x(α)\) in table II [where \(x(α) = Log(Slope1)\)]. We write the asymptotic formula by replacing 3 with \(x(α)\). The expression for \(a'_{L,g,α}\) after taking Log on both the sides becomes \(Log a'_{L,g,α} \sim Log k_g + LLog[x(α)] + [3g - \frac{3}{2}]LogL\). To determine the form of \(x(α)\), we plot \(x(α)\) verses α which is a straight line with slope \(-1.133\) and intercept \(3.466\). In the same way as the asymptotic expression for \(a_{L,g} \) in [18] had the universal term \(3^L\), we find \(x(α)\) to be \(x(α) = (-α + 3)L\) for all α. We therefore have \(Log a'_{L,g,α} \sim Log k_g + LLog(3 - α) + [3g - \frac{3}{2}]LogL\). The universal \(3^L\) part in the \(a_{L,g} \) [18] has been modified to \((3 - α)L\) for the extended matrix model [16]. The asymptotic formula gets modified to \(a'_{L,g,α} \sim k_g(3 - α)L^{(3g - \frac{3}{2})}\).

Analyzing the Log(L) dependence now, we assume that there exists an α dependence in the exponent of L which we represent by \(f(α)\). We can therefore modify the modified equation after taking Log on both the sides and substituting \(g = 1\), \(Log(a'_{L,g=1,α}) \sim Log \frac{1}{3(3g - \frac{1}{2})2^{2g+1}p\sqrt{π}} + LLog(3 - α) + \frac{1}{2}LogL\). Linear fitted plots of \[Log(a_{L,g=1,α}) - LLog(3 - α)\] verses Log L for different α values is shown in fig. 4. The figure shows a continuous separation of data points belonging to the even and odd lengths as α is increased from 0 to 1. There are two distinct lines at small lengths L which merge into a single line at higher lengths L. For α = 1 the points for odd lengths vanish completely from the plot. The slopes [table II Slope 2] show that the difference between analytical and numerical values for different α is \sim 0.01, which is small. The Log(L) term therefore shows no significant α dependence. So we fix \(f(α) = 1\). This gives the asymptotic formula of the number of diagrams at a fixed length L, genus g and α, \(a'_{L,g,α}\) for the extended matrix model of RNA as

\[a'_{L,g,α} \sim k_g(3 - α)L^{(3g - \frac{3}{2})}\] (5)

The asymptotic formula [eq. (3)] thus obtained is plotted with the numerically found \(a_{L,g,α}\) values for different α’s [fig. 4] shown here for only α = 0.75) and it is seen that the formula matches with the numerical results for large L. To verify the final form of the formula, we substitute different α’s and \(g = 1\) in eq. (5) and plot \(Log a'_{L,g=1,α} - LLog(3 - α)\) verses Log L. The slopes are found to be 1.495 in all the cases. This result will hold for any genus g, though we have shown here the result for only \(g = 1\). It is interesting to note here that the universality of \(a'_{L,g,α}\) for the extended matrix model changes from \(3^L\) in [18] to \(2^L\) when \(α = 1\) (the completely paired base region).

The asymptotic behaviour of \(a_{L,g,α,n}\) and \(N_{α,n}\) for the model with perturbation on n bases is the same as for the model with perturbation on all the bases except that α is replaced by \(\frac{α}{n}\) [as is evident from the expression of the exponential generating function \(G(t, N, α)\) given by eq. (3) with \(\frac{α}{n}\) in place of α]. Thus we can write the asymptotic expressions of the genus distribution functions for a perturbation acting on n bases as
FIG. 4: \[\text{Loga}_{L,g} = 1, \alpha - L\text{Log}(3 - \alpha)\] verses Log L plots for different values of \(\alpha\), (a) \(\alpha = 0\), (b) \(\alpha = 0.25\), (c) \(\alpha = 0.5\), (d) \(\alpha = 0.75\) and (e) \(\alpha = 1\). The slopes for these values of \(\alpha\) are listed in Table 2 (Slope 2).

\[a'_{L,g,\alpha,n} \sim k_g (3 - \frac{n\alpha}{L})^L L^{(3g - \frac{3}{2})}\]  

(6)

and,

\[N'_{\alpha,n} = L^L \exp\left[-\frac{1}{4} + (1 - \alpha)\sqrt{\frac{L}{4}} - \frac{\sqrt{\alpha}}{\sqrt{2}}\right] / \sqrt{2}\]  

(7)

The asymptotics for the extended matrix models therefore show marked changes in the presence of the perturbation in the universal term of \(a_{L,g}\) and in the total number of structures \(N\) of the model in [18].

IV. CONCLUSIONS

In this work, we develop on the footsteps of the extended matrix model of RNA folding proposed in [16], the effect of an external perturbation on only one nucleotide in the polymer chain of length \(L\). We argue that \(\alpha\) in the exponential generating function of the partition function of model in [16] will be replaced by \(\frac{n\alpha}{L}\) if perturbation acts on only one nucleotide in the chain. Further, we generalize this result to a finite number \(n \leq L\) of perturbations on the nucleotides of the chain, where \(\alpha\) in the exponential generating function of the partition function gets replaced by \(\frac{n\alpha}{L}\), eq. (3).

Next, we find numerically the asymptotic behaviour of the genus distribution functions for the extended matrix model of RNA folding in [16] and the n-NP model. We find from the numerical analysis that the universality of \(a_{L,g,3L}\) found in [18], changes to \((3 - \alpha)L\) when the perturbation acts on all the bases in the polymer chain [which becomes \((3 - \frac{n\alpha}{L})L\) when the perturbation is on \(n\) bases]. The power law term \(L^{3g - \frac{3}{2}}\) of \(a_{L,g}\) [18] remains the same for the asymptotic formula of \(a'_{L,g,\alpha}\) in the extended matrix models with perturbation on all the bases [16] and on \(n\) bases. The total number of diagrams \(N\) also changes from its form in [18] to \(N'_{\alpha} = L^L \exp\left[-\frac{1}{4} + (1 - \alpha)\sqrt{\frac{L}{4}} - \frac{\sqrt{\alpha}}{\sqrt{2}}\right] / \sqrt{2}\) with the term \(\exp\sqrt{T}\) in [18] changing to \(\exp\sqrt{(1 - \alpha)\sqrt{\frac{T}{4}}}\) for the matrix model with perturbation on all the bases [which becomes \(\exp\sqrt{(1 - \frac{n\alpha}{L})\sqrt{T}}\) when the perturbation is on \(n\) bases]. The most striking change found in the universality of \(a'_{L,g,\alpha}\) is when \(\alpha\) takes the value 1 (and \(n = L\)) as the universality goes from \(3L\) to \(2L\) and in the \((1 - \alpha)\sqrt{T}\) term in the exponent of \(N'_{\alpha}\) which goes to zero when \(\alpha = 1\) and \(n = L\). It is shown in fig. 2 and fig. 4 that as \(\alpha\) is increased from 0 to 1 in steps of 0.25, the points corresponding to even and odd lengths of the chain start splitting up into two different curves at small lengths, but converge into a single linear curve as the length is increased. Note that at small lengths, this difference is most pronounced for \(\alpha = 0.75\), for both \(N'_{\alpha}\) and \(a_{L,g,\alpha}\). The \(\alpha = 1\) plots of \(N'_{\alpha}\) and \(a_{L,g,\alpha}\) [fig. 4(e) and fig. 4(e)] respectively show the absence of odd length data points. It is interesting to note that the genus distributions show different behaviour at small and large lengths (analysis has been done for \(L = 40\)). The large \(L\) (asymptotic) behaviour of the distribution functions [eq. (4), (5), (6) and (7)] found for the RNA matrix model with external perturbation show prominent changes.
FIG. 5: The plot for the new asymptotic formula for $a'_{L,g,\alpha}$ (black dotted curve) for the extended matrix model of RNA is shown with the numerically obtained $a_{L,g,\alpha}$ for $\alpha = 0.75$ (green boxed curve).

We have studied the effect of an external perturbation on the RNA matrix model. In order to compare the results of the matrix model of RNA folding with external perturbations (discussed here and in [16]) with experiments (where the perturbations may be due to the constant forces discussed in the introduction or due to natural processes like transcription and translation taking place inside a living cell), a more detailed study will be undertaken.

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