Attraction between the polycyclic aromatic surface elements of carbon nanotubes (CNT) and the aromatic nucleotides of deoxyribonucleic acid (DNA) leads to reversible adsorption (physisorption) between the two, a phenomenon related to hybridization. We propose a Hamiltonian formulation for the zipper model that accounts for the DNA-CNT interactions and allows for the processing of experimental data, which has awaited an available theory for a decade.

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Deoxyribonucleic acid (a.k.a. DNA) is a biomolecule, comprised of two polymer chains, stabilized by hydrogen bonds (H-bonds) in the perpendicular direction to its axis. If the H-bonds are broken and the two strands are separated, each single strand DNA (ssDNA) will remain stabilized by the $\pi$-stacking of neighbour nucleotides in the direction parallel to the axis. Being one of the most rigid polymers, with probably the largest ratio of longitudinal to lateral dimensions, ssDNA can be considered as a one-dimensional (1D) object even at the scale of one Kuhn segment [1–3]. Another constituent of this complex under study, carbon nanotubes (CNT), are a system with cylindrical symmetry, that have unique electronic properties due to the relevant size-quantization effects, as well as outstanding mechanical properties thanks to their amazing structure [4, 5]. Not surprisingly, CNTs have found numerous applications in varied areas such as nanoelectronics, medicine, environmental safety, and microbiology. Due to the large longitudinal to lateral dimension ratio, in the same way as for DNA, CNTs can be considered as one-dimensional objects. Attraction between these two rigid 1D objects results in the formation of a ssDNA-CNT complex, which, at a later stage of hybridization, serves as a landing site for free ssDNAs from solution.

There are several reasons motivating the study the DNA-CNT complex. One is the insolubility or extremely poor solubility of CNTs, which imposes a considerable challenge when it comes to applications. Different techniques were developed to improve CNT dispersion including the use of surfactants, oligomers, biomolecules, polymer-wrapping, and chemical functionalization. One of the most efficient dispersing agents for water solutions is single-stranded DNA (ssDNA), which forms a (very) stable complex with CNTs [6]. Another line of reasoning originates from the wide range of existing applications for the DNA-CNT complexes in various nanotechnologies.

Despite the fact that there are several reviews on biological or biosensing applications for carbon nanomaterials, there is a negligibly small number of both theoretical and experimental studies devoted to the equilibrium picture of reversible adsorption (physisorption) of DNA on CNTs.

The standard approach in the field consists of the application of First Principles Calculations (mostly, using DFT software) to estimate the energies of interaction between the nucleotides and carbon-based substrates with and without water (see e.g., [9] and references therein). Another wide group of approaches is through the use of all-atom Molecular Dynamics simulations to reach conclusions about the thermodynamics of ssDNA-SWCNT interactions (see, e.g., [10] and references therein).

Recently, several phenomenological models have been employed towards the problem, mainly through the modifications of adsorption theories known from the past. Thus, to process the experimental data, a recent experimental study [11] has treated the adsorption of ssDNA oligomers and dimers as a simple chemical reaction.

Kato et al. [12] have applied the Hill formula to estimate the adsorption free energy of single-stranded cytosine oligo-DNAs on single wall nanotubes (SWNT). In a recently published article [13], an extended version of Langmuir’s approach is developed to describe the histidine and alanine adsorption on CNT. While simple and seemingly effective, adsorption isotherm models adopted to the biopolymer-CNT story suffer from the apparent and long-known limitations of the Hill-Langmuir approach in describing the cooperative adsorption of polymers.

A general problem in the field is the absence of a Statistical Mechanical approach with a model Hamiltonian, that would provide a link between the microscopic properties of the system and its macroscopic behavior, as described by Thermodynamics.

A recent experimental study serves as a bright example illustrating this apparent gap in knowledge. In 2009 Al-
Albertorio et al reported an experiment on the association of ssDNA oligomers with CNTs [14]. The authors managed to process the results of kinetics experiments and to extract the association enthalpies with the help of the Eyring equation [14]. At the same time, they failed in extracting the data from the equilibrium measured curves of the temperature dependence of DNA/CNT fraction, because of the absence of a corresponding theory. The best they could do was to fit what they called sigmoidal function to their measured points, without providing any roots. The authors considered the Hamiltonian of the Zimm-Bragg model [20]. The so-called characteristic equation of ZB:

$$\lambda^2 - \lambda(W - 1 + Q) + (W - 1)(Q - 1) = 0,$$  \hspace{1cm} (2)

where $W = e^{U/T}$ and $T$ is temperature. Using mapping

$$\frac{\lambda}{Q} \rightarrow \lambda; \quad \frac{W - 1}{Q} \rightarrow s; \quad \frac{1}{Q} \rightarrow \sigma,$$  \hspace{1cm} (3)

allows us to transform Equation (2) into the original characteristic equation of ZB:

$$\lambda^2 - \lambda(s + 1) + s(1 - \sigma) = 0,$$  \hspace{1cm} (4)

with obvious roots

$$\lambda_{1,2}(s, \sigma) = \frac{1}{2} \left[ 1 + s \pm \sqrt{(1-s)^2 + 4\sigma s} \right] =$$

$$\frac{1}{2} \left[ 1 + s \pm (1-s)\sqrt{1 + \frac{4\sigma s}{(1-s)^2}} \right].$$  \hspace{1cm} (5)

Since the Thermodynamics is fully determined by the characteristic equation of the model, Eq. (4) can be considered the Hamiltonian of the ZB model [20]. The solutions of Eq. (4) are eigenvalues that provide the link between model parameters $s, \sigma$ and the partition function:

$$Z(\sigma, s) = c_1 \lambda_1^N + c_2 \lambda_2^N = \lambda_N^N \left[ e^{c_1} + e^{-N/\sigma} \right],$$  \hspace{1cm} (6)

FIG. 1: Scheme illustrating the similarity between the mixture of adsorbed and desorbed nucleotides of ssDNA on a CNT (above) and the helical and coil nucleotide pairs in ds-DNA (below). Both systems can be reduced to the same sequence of ordered (o) and disordered (d) repeat units, giving rise to the sequence of statistical weights of Zimm-Bragg type.
where \( N \) is the number of repeat units, \( c_1 = \frac{1-\lambda_1}{\lambda_1-\lambda_2} \), \( c_2 = \frac{\lambda_1-1}{\lambda_1-\lambda_2} \) and

\[
\xi(\sigma, s) = 1/\log(\lambda_1/\lambda_2)
\]

is the spatial correlation (or persistence) length, a curve with its maximum at the transition point. For finite correlation lengths (\( \xi < \infty \)) the effect of the second eigenvalue on the partition function decreases exponentially with the increase of \( N \):

\[
Z(\sigma, s) \xrightarrow{N \gg \xi} c_1 \lambda_1^N \approx \lambda_1^N.
\]

This is the regular, large \( N \), limit of the Zimm-Bragg theory, meaningful for longer polymer chains, but not applicable to our problem of interest: oligomer DNA adsorption on carbon nanotubes. In their experiment, Albertorio et al. used DNA oligomers of 12 nucleotide bases long, which is on the order of the Kuhn length of a single strand DNA (ssDNA, i.e. \( N \sim 2\xi \)). Therefore we need to return to Eq. (5) and apply the single-sequence approximation of the Zimm-Bragg model. At the heart of the single-sequence approximation is the impossibility of having more than one uninterrupted sequence of helical (ordered) repeat units due to small system sizes (\( N < 2\xi \)). For this regime, the role of the small parameter is played by

\[
\frac{4\sigma s}{(1- \sigma)^2} \ll 1.
\]

After resolving Eq. (9) into the Taylor series by this small parameter and keeping the first terms, we obtain the eigenvalues

\[
\lambda_1(\sigma, s) = 1 + \frac{\sigma s}{1 - \sigma}; \quad \lambda_2(\sigma, s) = s - \frac{\sigma s}{1 - \sigma}.
\]

When inserted into Eq. (10), we obtain:

\[
Z(\sigma, s) = \frac{(1 - s + \frac{2\sigma s}{1 - \sigma})(1 + \frac{2\sigma s}{1 - \sigma})^N + \frac{2\sigma s}{1 - \sigma}s(N - \frac{2\sigma s}{1 - \sigma})^N}{1 - s + \frac{2\sigma s}{1 - \sigma}}.
\]

After resolving the powers into series, rearranging the results and keeping only terms linear in \( \sigma \), we obtain

\[
Z(\sigma, s) = 1 + \frac{\sigma s}{(1- \sigma)^2}(N - 1 - Ns + sN) + O(\sigma^2).
\]

The order parameter (helicity degree) is calculated from the partition function as

\[
\theta(\sigma, s) = \frac{1}{N} \frac{\partial \log Z(\sigma, s)}{\partial \log s} = \frac{NZ(\sigma, s)}{\partial s} = \frac{\sigma s}{N(s-1)^3} \left[ \frac{1}{1 + \frac{\sigma s}{N-1}}(N - 1 - Ns + sN) \right].
\]

Eq. (13) is a well-known helicity degree formula, appearing in many papers and books [21–23]. Thus, using the analogy between the adsorption of one DNA strand onto another in double-stranded DNA and single-strand DNA adsorption onto a nanotube, we have derived Eq. (13) as a theoretical formula, describing the order parameter, the fraction of adsorbed nucleotides. However, before making a comparison with experiments we need to translate the Zimm and Bragg parameters \( s \) and \( \sigma \) into experimental variables. There have been many definitions of the Zimm and Bragg parameters in the past [21]. Following our past studies [16, 19, 20], we define the stability parameter \( s \), which has the meaning of a statistical weight and is usually represented in terms of a (Gibbs or Helmholtz) free energy change between the bound and unbound states, as:

\[
s = \exp \left( -\frac{\Delta G}{RT} \right) = \exp \left( -\frac{\Delta H - RT\Delta S}{RT} \right).
\]

The cooperativity parameter \( \sigma \), by its definition, describes how much the original probability of bounded region growth, \( s \), is hindered by the fact that there is no preceding bounded repeated unit. It can be estimated (see [16, 14, 20]) as

\[
\sigma = Q^{1-l}.
\]

In the formulas above \( \Delta H = -U \) is the enthalpy of binding per nucleotide; \( \Delta S = \ln Q \) is the entropic price of adsorption per nucleotide; \( l (=6\text{ nucleotides}) \) is the persistence length of ssDNA. After inserting the definitions of \( s \) and \( \sigma \) into Eq. (13), we arrive at

\[
\theta(s, \sigma) = \theta(T, U, Q, l = 6, N = 12) = \theta(T, U, Q),
\]

a formula, that contains only two free parameters: \( U \) and \( Q \).

In order to check how adequately the proposed theory describes the phenomenon, we have chosen an experimental study which reports the measured fraction of adsorbed nucleotides, namely, the study by Albertorio et al. [14]. In their study, a solution of 12-base-long single stranded DNA homopolymers consisting of poly \( d(A)_{12} \), poly \( d(T)_{12} \), poly \( d(C)_{12} \), and poly \( d(G)_{12} \), as well as regular heteropolymers poly \( d(AC)_{6} \) and poly \( d(GT)_{6} \)
was added to single-wall carbon nanotubes (SWNT) at a 1:1 DNA:SWNT mass ratio. The DNA/SWNT mixture was sonicated and then the bundles of non-dispersed nanotubes and the remaining free DNA were removed. The thermal stability of the obtained hybrids was quantified indirectly by measuring the extent to which 12-base-long ssDNA polymers dissociated from the nanotubes after incubation in an aqueous buffer solution at different temperatures in the 4-99°C range for 10 min by the detection of optical absorption at 815 nm.

We have digitized Figures 2 and 3 of Ref. [14], reporting the temperature-dependent fractions remaining in solution and fit them with Eq. [15]. Results of the fit are shown in Figure 2 and in Table 1. As one can see, the fit is close to perfect, which, considering that there are just two free parameters, ensures the validity of the statistical approach developed. The values of fitted energies (enthalpies) of adsorption (Table 1) are all in the range of 10 kJ/mol per nucleotide, in complete agreement with previously reported values (see Ref. [14]). Regarding the particular ordering of adsorption enthalpies by nucleotide type, there is a long history of contradictory reports, as is nicely reviewed by Pramanik and Maiti [10]. Based on the data provided in Ref. [14], we cannot support a particular view on the adsorption strength ordering of nucleotides, since the experimental curves for poly d(C)12 and poly d(G)12 span outside the experimentally accessible range of temperatures, and their desorption is incomplete (Figure 2 of [14]), thus essentially decreasing the quality of the fit (not shown). However, based on the available data on poly d(A)12 and poly d(T)12, our analysis confirms purines having larger enthalpy of adsorption as compared to pyrimidines (i.e. A > T order), in agreement with many reported studies (see Ref. [10] and references therein). Since we are not aware of any other published data on the temperature dependence of the ratio of adsorbed nucleotides on CNT, more experimental data are needed to make conclusion about the order of adsorption strengths for different nucleotides.

However, not only are the fitted numbers relevant per se, but also the model itself, since it provides a language for the treatment of the phenomenon. For instance, in the same paper, Albertorio et al. [14] also mentions problems with the stability of adsorbed DNA because of desorption. They have introduced extra stabilization by increasing the free DNA concentration in solution. This stabilizing effect is reported, but not explained or modelled. Instead, a line of naive argumentation could lead to the opposite expectations that the presence of extra free ssDNAs in solution will result in the promotion of ssDNA-ssDNA interactions, which should introduce a destabilizing effect onto the ssDNA-CNT complex because of obvious competition between the two targets for adsorption. In view of our previous studies of the osmotic stress effects onto DNA conformations [17], the reported increase in stability of bound conformations finds its explanation as arising because of the increased osmotic stress due to the increased excluded volume effects (crowding) from the free DNA added.

Thus, by providing a Statistical Mechanical Hamiltonian to describe the DNA-CNT interaction, which is at the heart of numerous Nano(Bio)technologies, we open the doors for a better understanding of the principles behind the relevant biotechnologies and suggest a route towards the predictable design of nanodevices.

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