Two-dimensional DNA Crystal as Energy Minimizer

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APh 161, Physics of Biological Structure and Functions
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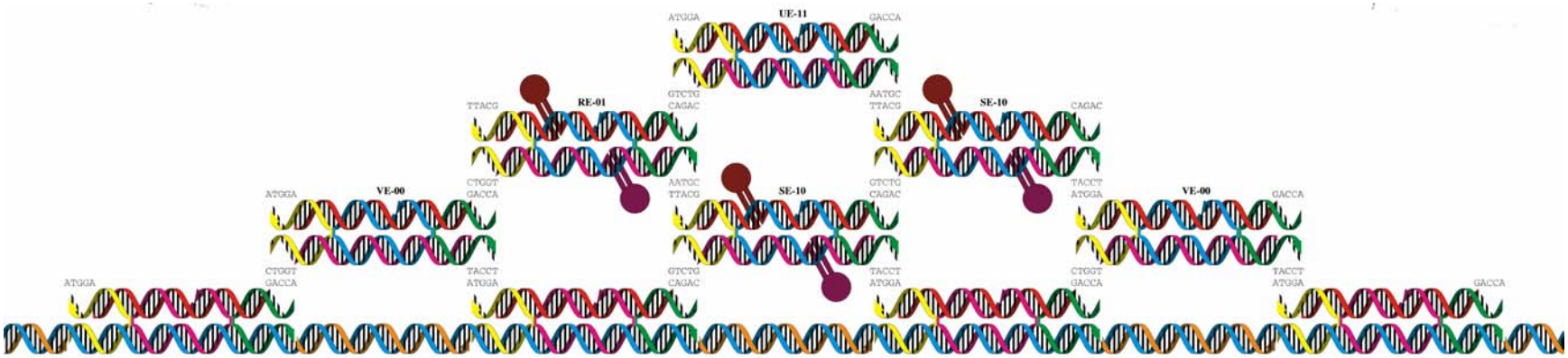
Introduction



2D DNA crystal is formed by self-assembly of synthetic DNA molecules

“Intermolecular interactions between the structural units
are programmed by the design of 'sticky ends' that associate
according to Watson–Crick complementarity,
enabling us to create specific periodic patterns on the nanometre scale.“
(Winfree et al. *Nature* **394**, 539-544 (1998))

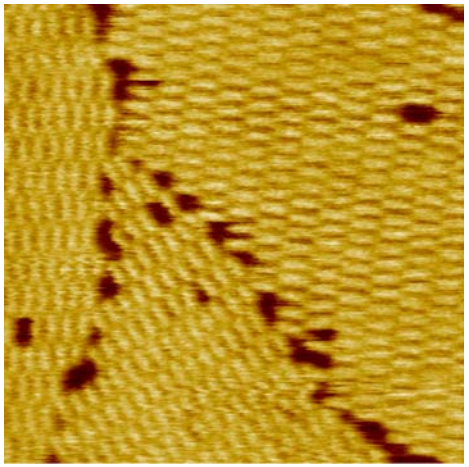
Introduction

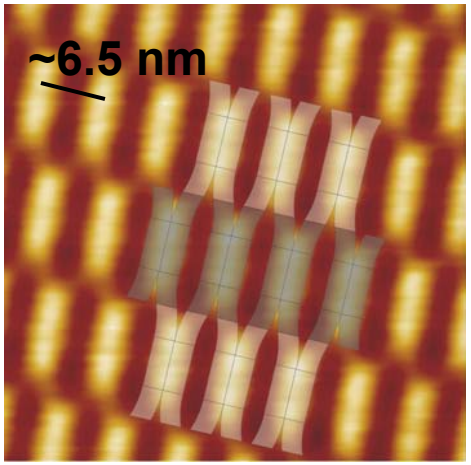
- Recently, high resolution Atomic Force Microscopy image of the lattice is routinely achieved in our lab. The DNA crystal was deposited on mica before/during the imaging process

- The high resolution image reveals that the 2D DNA crystal structure is not closely packed, instead, it is “separated”. There are ~6.5 nm spacing between DNA molecule.

- Using beam theory and Coulomb interaction, I am able to show that the structure arises from the interplay between
  - electrostatics and
  - bending deformation energy

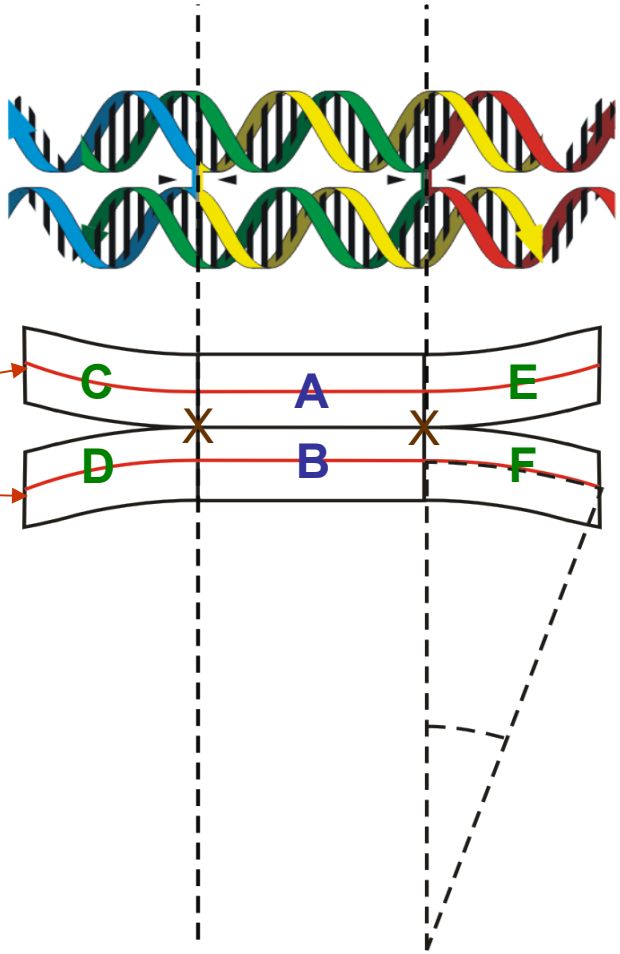
  in the energy of the lattice.





The Model

- DNA double helix is a cylinder that has
  - persistence length of ~50 nm, follow linear elastic theory of beam
  - line charge density of $2e^-$/0.34 nm, does not depend on major/minor grooves
- The DX molecule is modeled as six connected beams with two line charges in the center of each beam (red lines)
- Two of the beams (A,B) are fixed due to the two cross over points (X's) and four of other beams (C,D,E, and F) are bendable, this bending is due to the electrostatics repulsion between 2 helices
- The bending curvatures are 4 identical circular arc due to lattice symmetry

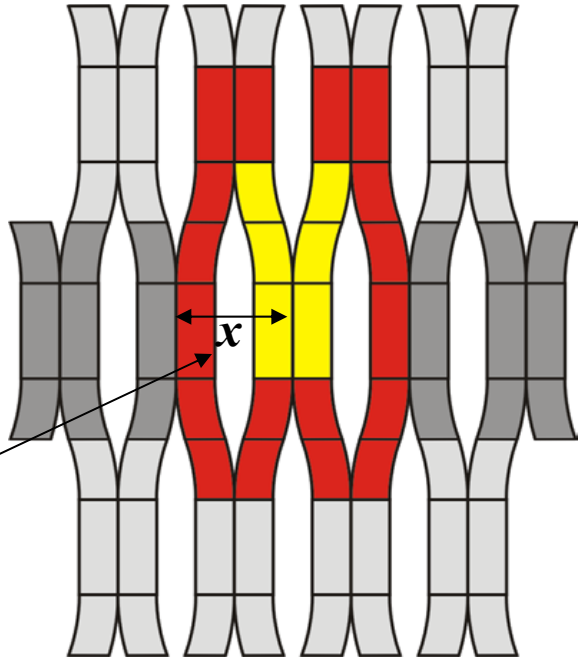


The Energetics of 2D DNA Crystal Structure

STRATEGY

1. Parameterized the lattice
2. Calculation
   - 2.1 Bending Energy
   - 2.2 Interaction energy between single unit cell (yellow segments) with its nearest neighbors (red segments).

   Both 2.1 and 2.2 are functions of the radius of curvature only
   - 2.3 Sum 2.1 and 2.3, and
   - 2.4 Find the spacing (x) where the "energy" is minimum



1. Parameterized the lattice

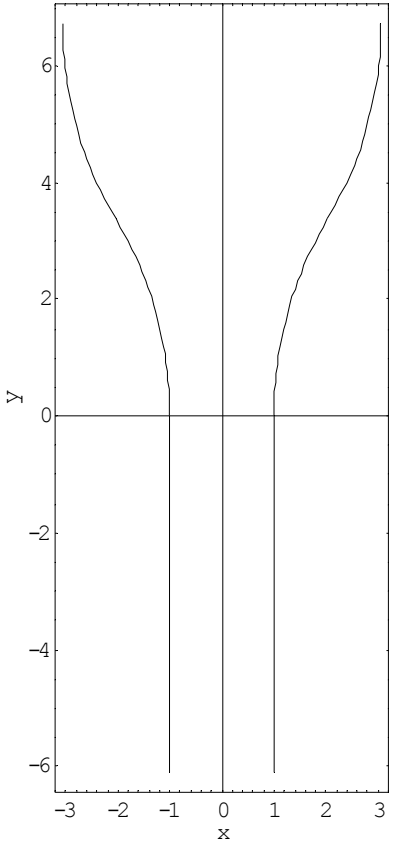
- The lattice was constructed using parametric equations. Each curved curvature is a circular arc, with radius of curvature R.

- From this geometry, the spacing between the unit cell (x) is

$$x(R) = 4\left\{ r_{DNA} + R\left[1 - \cos\left(\frac{\Gamma}{R} \right) \right] \right\}$$

, where
R is the radius of curvature,
r_{DNA} is the radius of a DNA helix (~ 1 nm),
and Γ is the arc length (21 bp x 0.34 nm)

- CAVEAT: The formula of spacing gives *apriori* result spacing to be shorter than 14 nm 



2. Calculation

- We only consider the energy term that depends strongly to the bending radius, which are
  - bending energy terms, and
  - electrostatics

Assumptions

- Other energy terms, such as
  - Elastic energy from twist
  - base-pairs (nearest-neighbor interaction)

  are assumed to be independent from bending. Since we will take the derivative with respect to the radius of curvature,

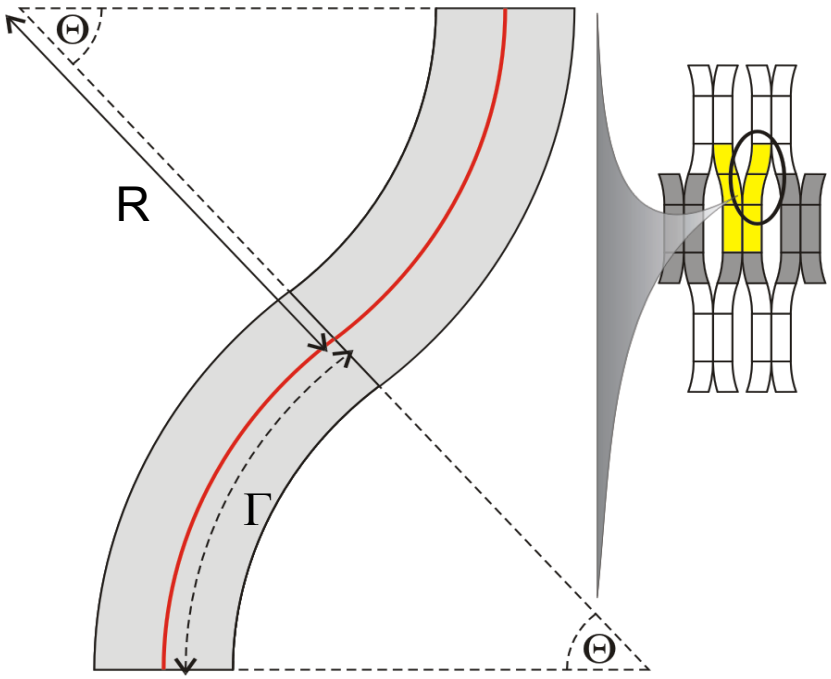
  these energy terms are not computed.
- The curve is smooth, i.e. there is no base de-stacking at the nicks
- The DNA-mica interaction does not induce structural change from the structure in the solution.
- Linear elastic theory of beam is followed

2.1. Bending Contribution

The bending energy of an arc is

$$E_{bending} = n \frac{\Gamma}{2\pi R} \frac{\xi_p \pi}{R}$$

, where
n is the number of the curved segment
(4 curved segments in 1 unit cell),
Γ is the arc length,
ξ_p is the persistence length
of a DNA double helix (~50 nm),
and R is the radius of curvature



2.2. Electrostatics Contribution

The electrostatic interactions are calculated as

$$E_{elec} = \int ds_i \int ds_j \lambda^2 V_{DH}\left(|\vec{s}_i - \vec{s}_j|\right)$$

, where s_i parameterizes the position on the line charge
V_{DH} is the Debye-Hückel potential
between 2 line charges in the solution

$$V_{DH} = k_B T \frac{l_B}{|\vec{s}_i - \vec{s}_j|} e^{-\kappa|\vec{s}_i - \vec{s}_j|}$$

, where l_B is the Bjerrum length

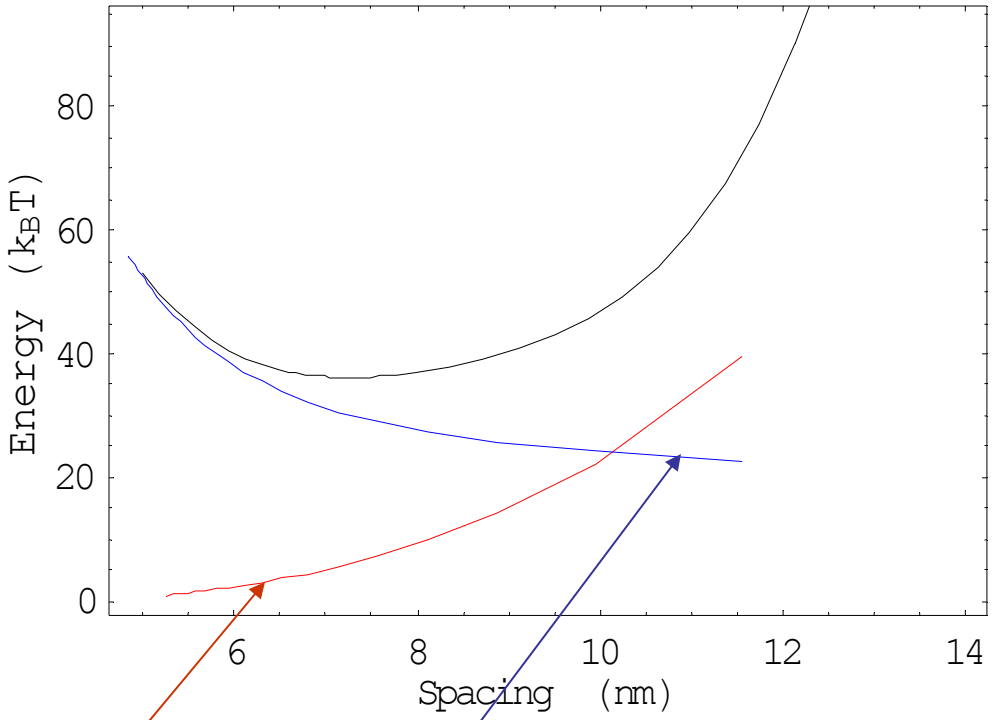
$$l_B = e^2 \Big/ \varepsilon k_B T$$

and $1/\kappa$ is the Debye screening length, defined via

$$\kappa^2 = 4\pi l_B \sum_i Z_i^2 c_i$$

, where Z_i and c_i are the valence and concentration
of the salt species i

2.3. Numerical Result

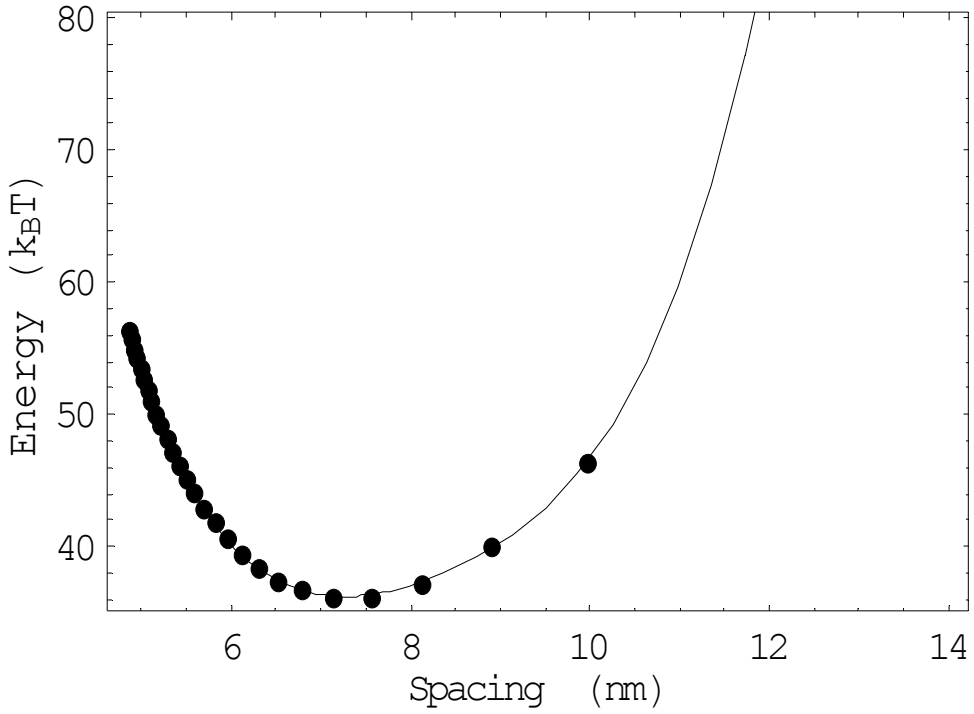


Red : Bending Energy [] Blue : Electrostatics Interaction Energy

Black : Bending + Electrostatics

- The contribution from the nearest neighbor interaction is ~ 200 $k_B T$. Thus, the total energy is negative

2.4. Energy of the configuration as a function of DX spacing



- The sum of the bending and electrostatic interactions is minimum at separation = 7.3 nm, which is in a good agreement with ~ 6.5 nm spacing measured from AFM images
- From this plot, we can estimate the k to be 0.021 N/m

Conclusion

- As demonstrated consistently in APh 161 lectures,
  simple calculation based on naive model is capable to give insight of a physical phenomena

- My “unsophisticated” model of the 2D DNA crystal gives minimum energy at 7.3 nm lattice spacing, which is in agreement with ~6.5 nm spacing from the experimental measurement.

- I plan to extend the study by two different experiments
  - extending the curved segments by 21 nucleotides
  - changing the buffer salt concentration and its salt species
    , i.e. modifying the Debye screening length

  and compare the spacing with the prediction by this calculation.

Acknowledgements

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