



A new approach to the mechanics of DNA

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- stores all genetic information of humans, animals, plants and bacteria
- mechanics important for:
 - replication
 - gene expression
 - folding and packing of DNA
- knowing properties
→ better understanding diseases
(e.g. cancer, genetic disorders)

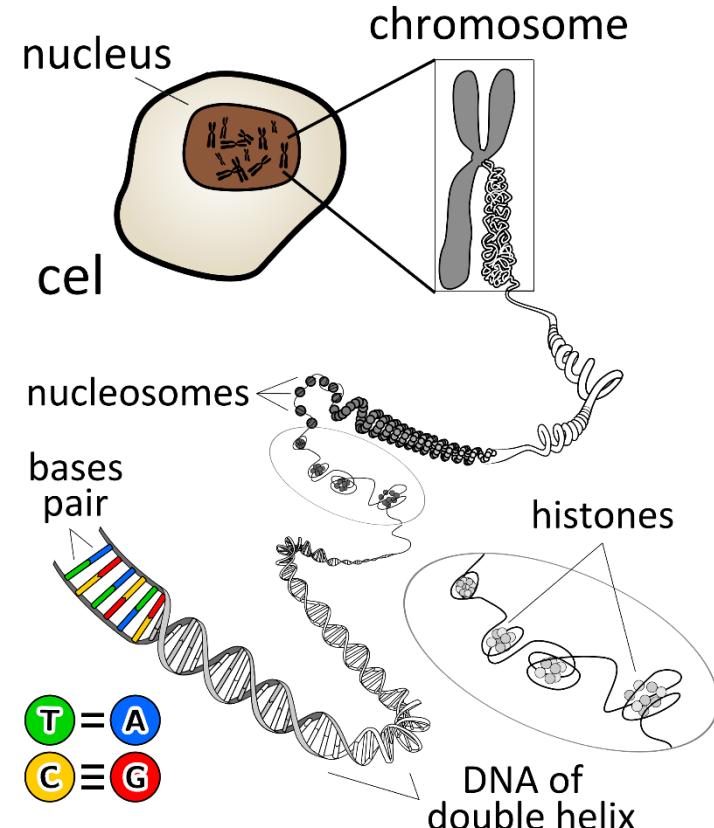
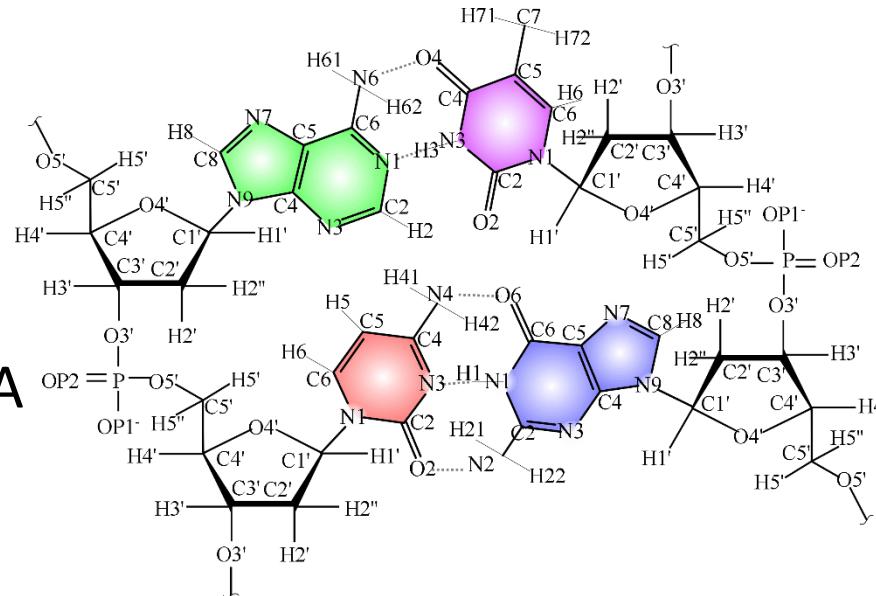
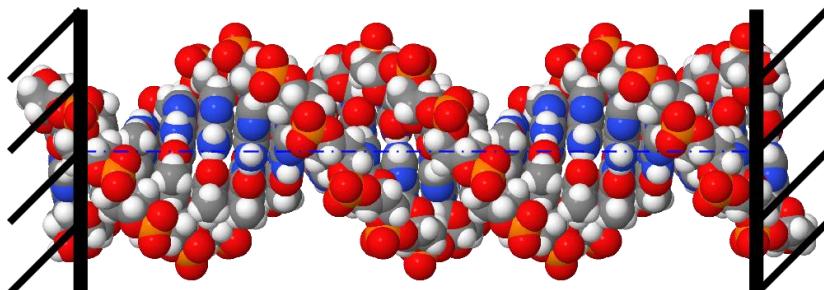
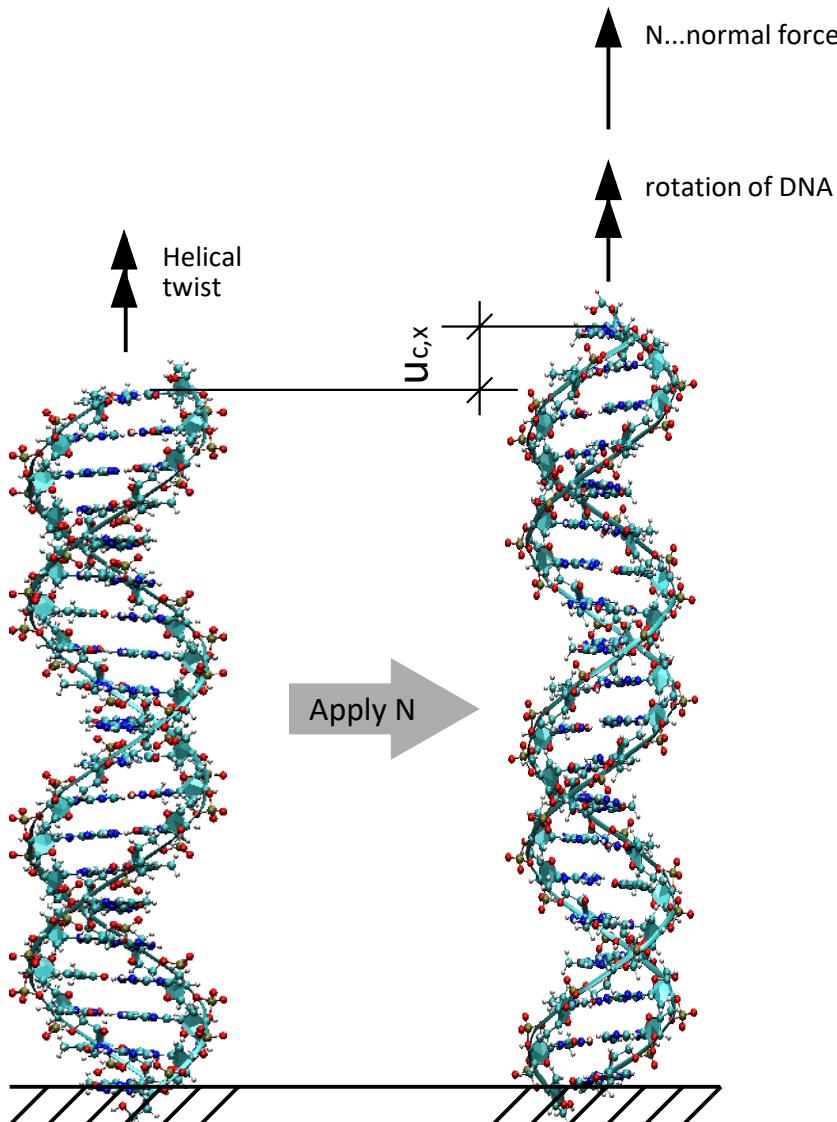


image: CC-BY-SA 3.0 KES47
[https://commons.wikimedia.org/wiki/
File:Chromosome_en.svg](https://commons.wikimedia.org/wiki/File:Chromosome_en.svg)

Force-moment interaction



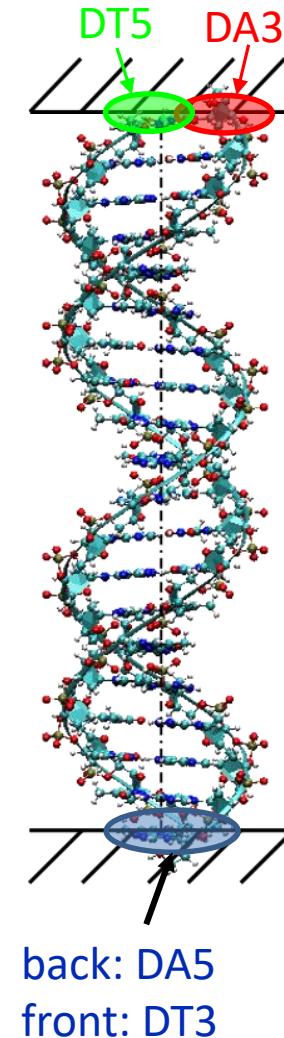
- coupling between stretch and torsion shown experimentally
- state of the art (so far): modeling DNA as **homogeneous, isotropic, cylindrical rod**
→ coupling not reproducible
- molecular dynamics to beam

Molecular dynamics model

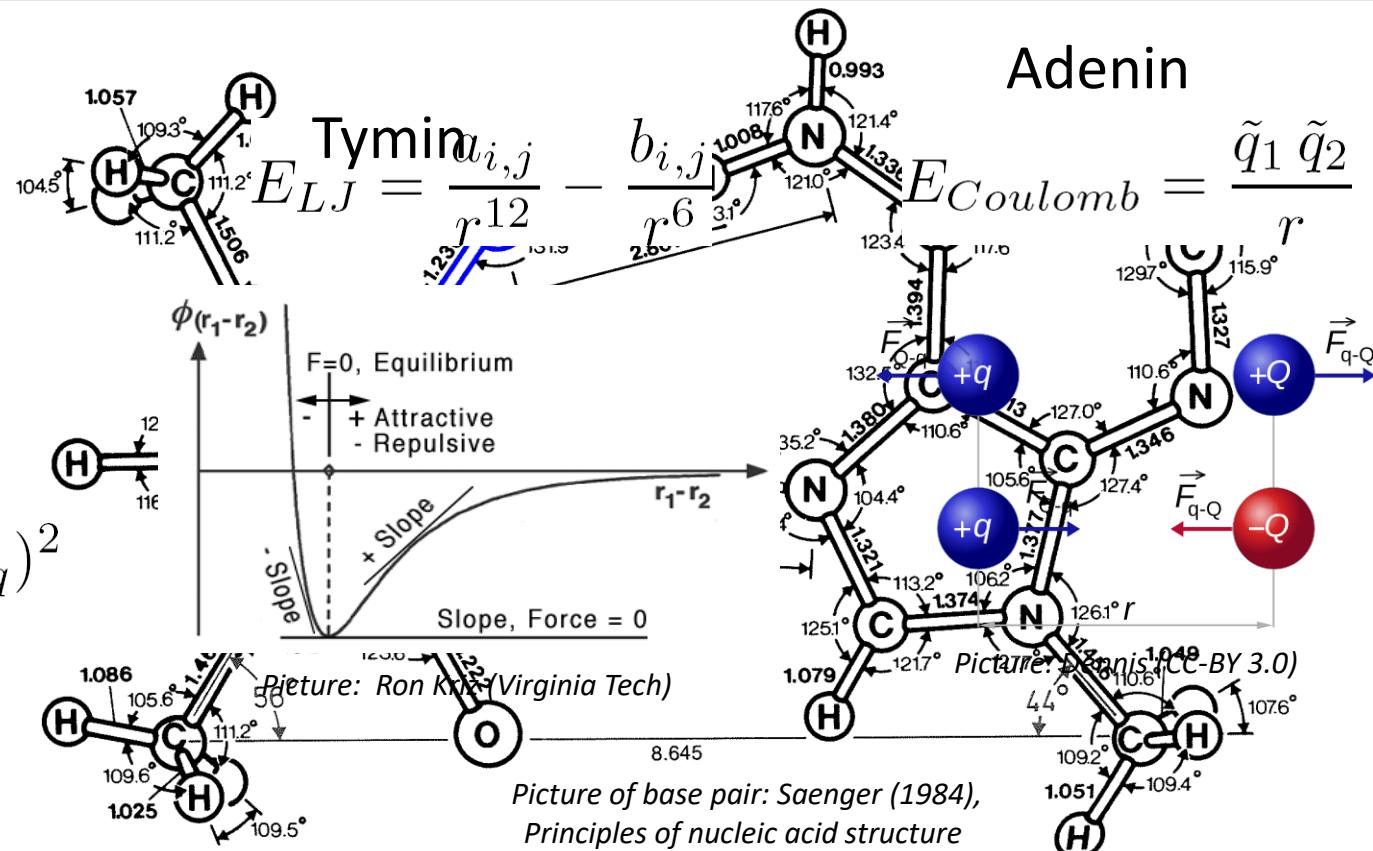
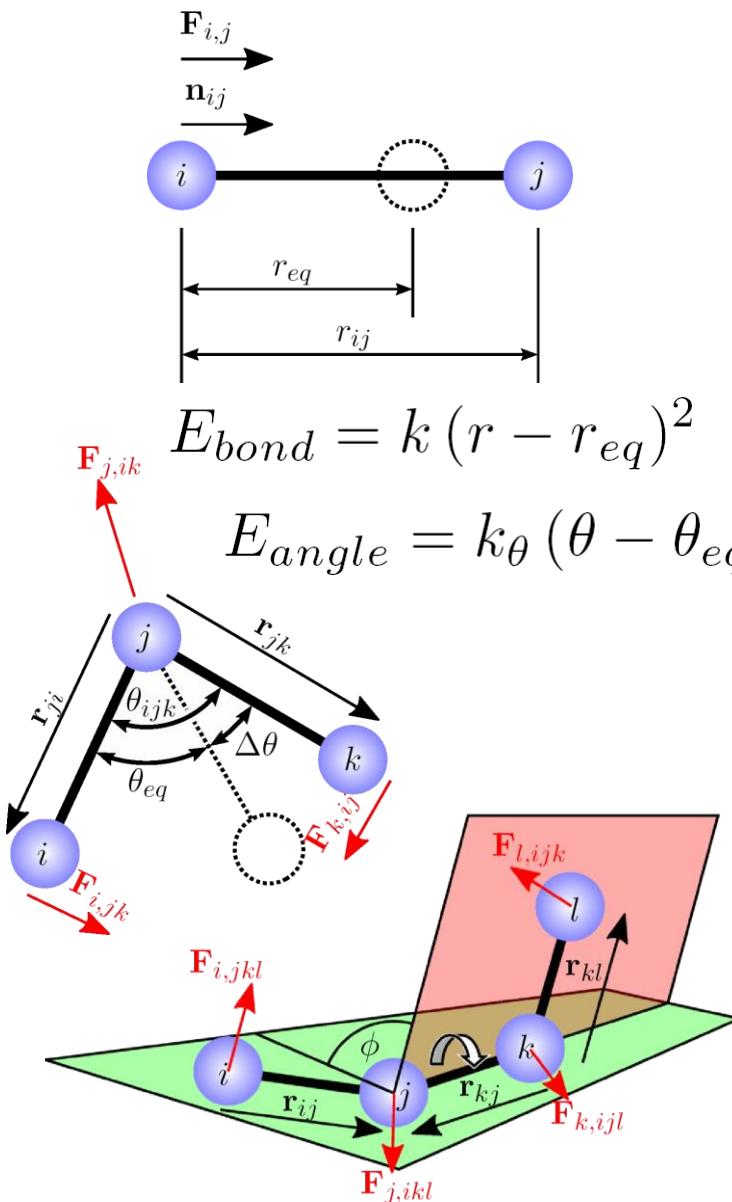
- 20 polyadenine-polythymine-base pairs (two full turns)
 - helical twist of 36° per base-pair
 - helical rise of 3.38 \AA per base-pair
- initial displacement field
 - beam-related homogeneous stretches and twists
 - rigid body cross sections

$$\mathbf{u}(x, y, z) = \epsilon_x x \mathbf{e}_x - \sin \left(\arctan \left(\frac{z}{y} \right) + \vartheta_x x \right) \sqrt{y^2 + z^2} \mathbf{e}_y \\ + \cos \left(\arctan \left(\frac{z}{y} \right) + \vartheta_x x \right) \sqrt{y^2 + z^2} \mathbf{e}_z$$

- fixed upper end:
3end adenine(DA3) and **5end thymine (DT5)**
- fixed lower end:
5end adenine (DA5) and **3end thymine (DT3)**



Interatomic potentials with DNA



applied method:
generalized Born Implicit Solvent

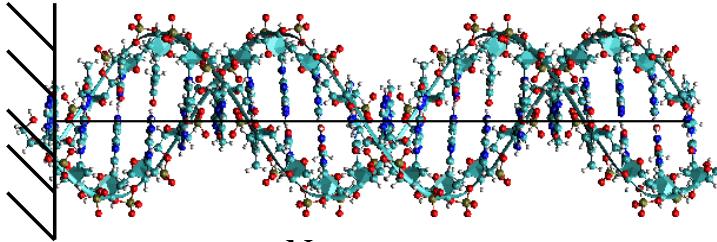
$$E_{torsion} = k_{tor} (1 + \cos(n \phi + \psi))$$

[Kalliauer et al., JMPS , 2020]

Molecules-to-beam-element homogenization

[Kalliauer et al., JMPS , 2020]

molecular system



$$p^{\text{int}} = \frac{1}{\ell_{\text{RLE}}} \sum_{i=1}^{N_{\text{atom}}} \mathbf{F}_i^{\text{int}}(\mathbf{x}_i) \cdot \hat{\mathbf{v}}^{\text{int}}(\mathbf{x}_i)$$

\mathbf{F}_i ... atom-specific internal force vector

\mathbf{x}_i ... atom-specific location vector

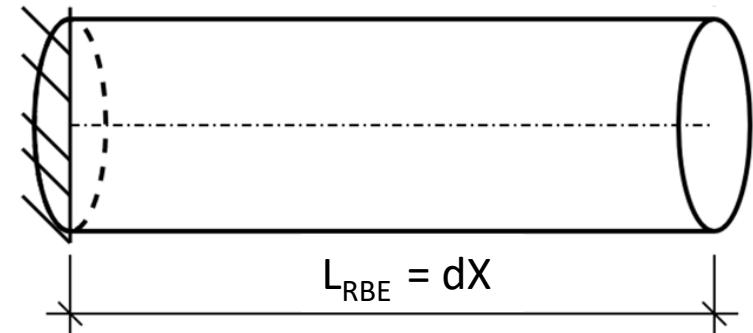
\mathbf{v}_i ... atom-specific virtual velocity vector

ℓ_{RLE} ... length of representative beam element

with beam-informed molecular virtual velocity field:

$$\hat{\mathbf{v}}^{\text{int}}(\mathbf{x}) = x_i \left(\frac{\partial \hat{V}(X)}{\partial X} \mathbf{e}_x + \frac{\partial \hat{\Omega}(X)}{\partial X} (-z_i \mathbf{e}_y + y_i \mathbf{e}_z) \right)$$

continuum beam system (element)



$$p_{\text{int}}(X) = -N(X) \frac{\partial \hat{V}(X)}{\partial X} - M_x(X) \frac{\partial \hat{\Omega}(X)}{\partial X}$$

N ... normal force

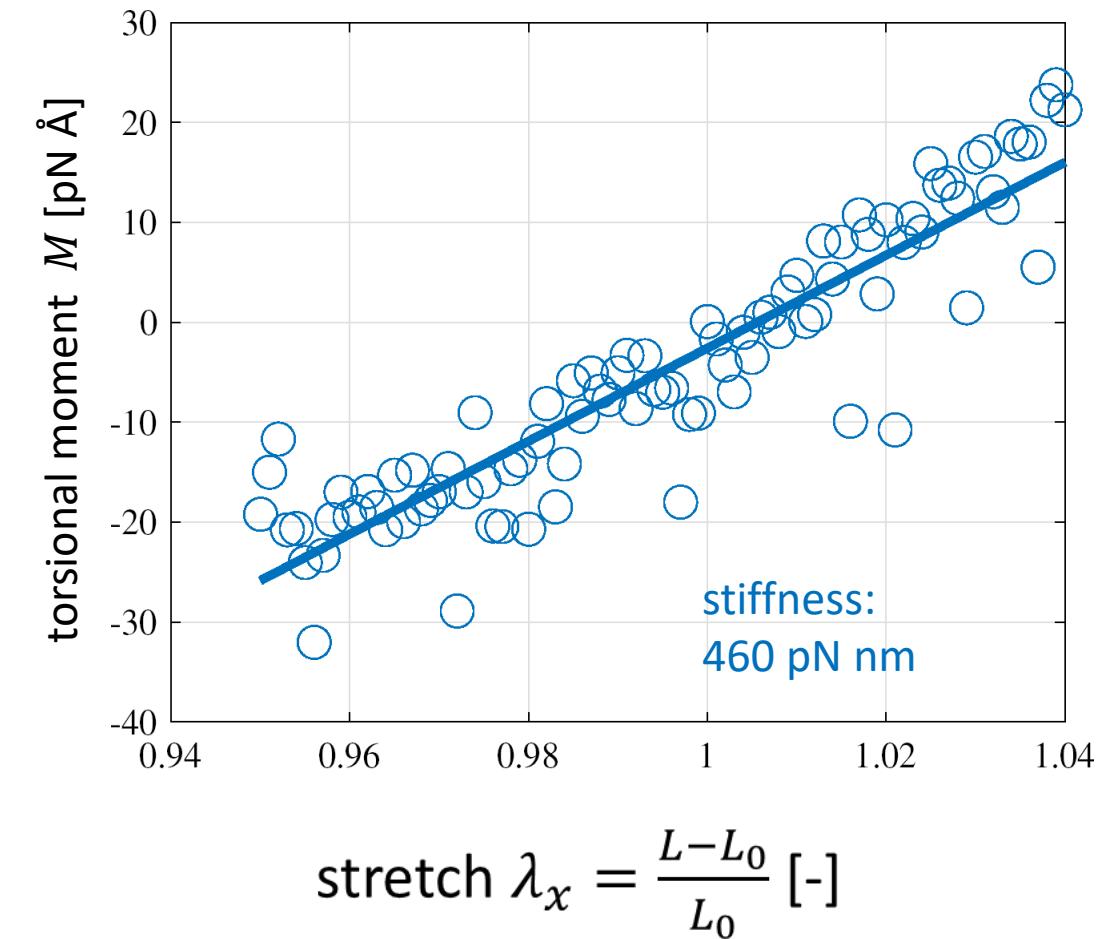
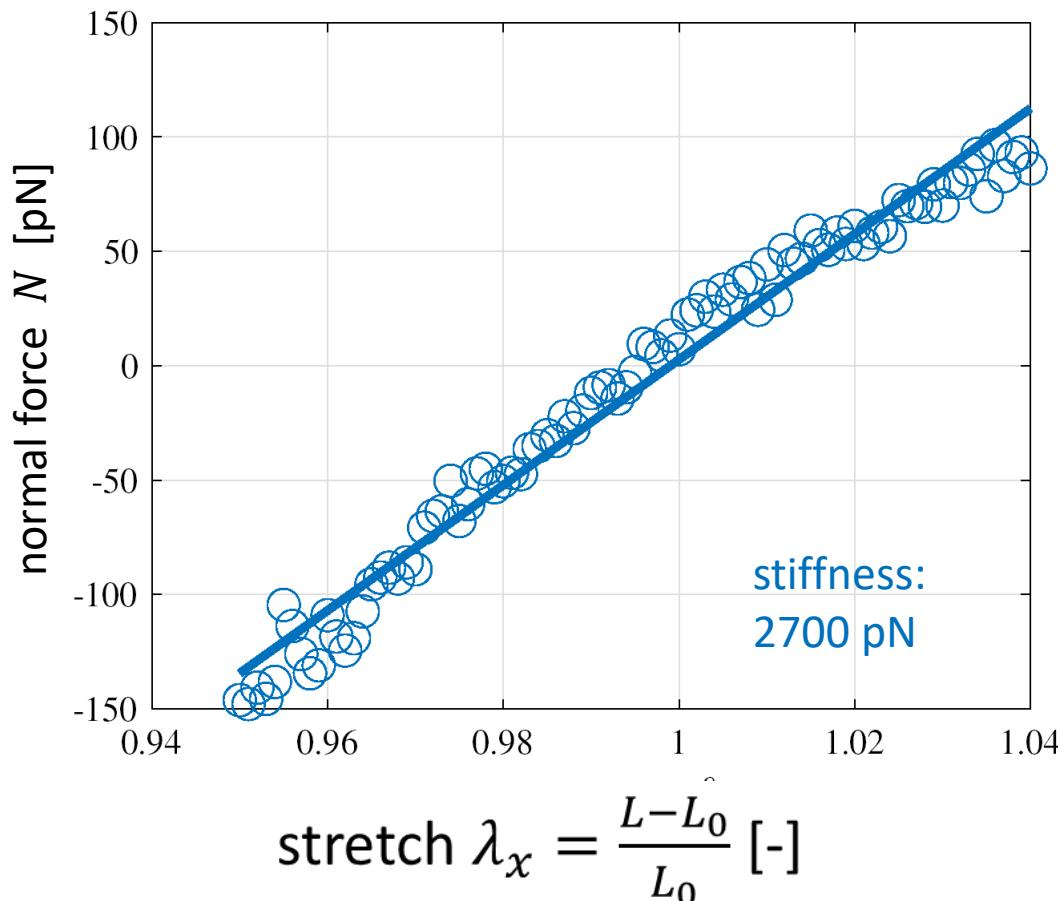
V ... virtual axial velocity

X ... beam element-specific location vector

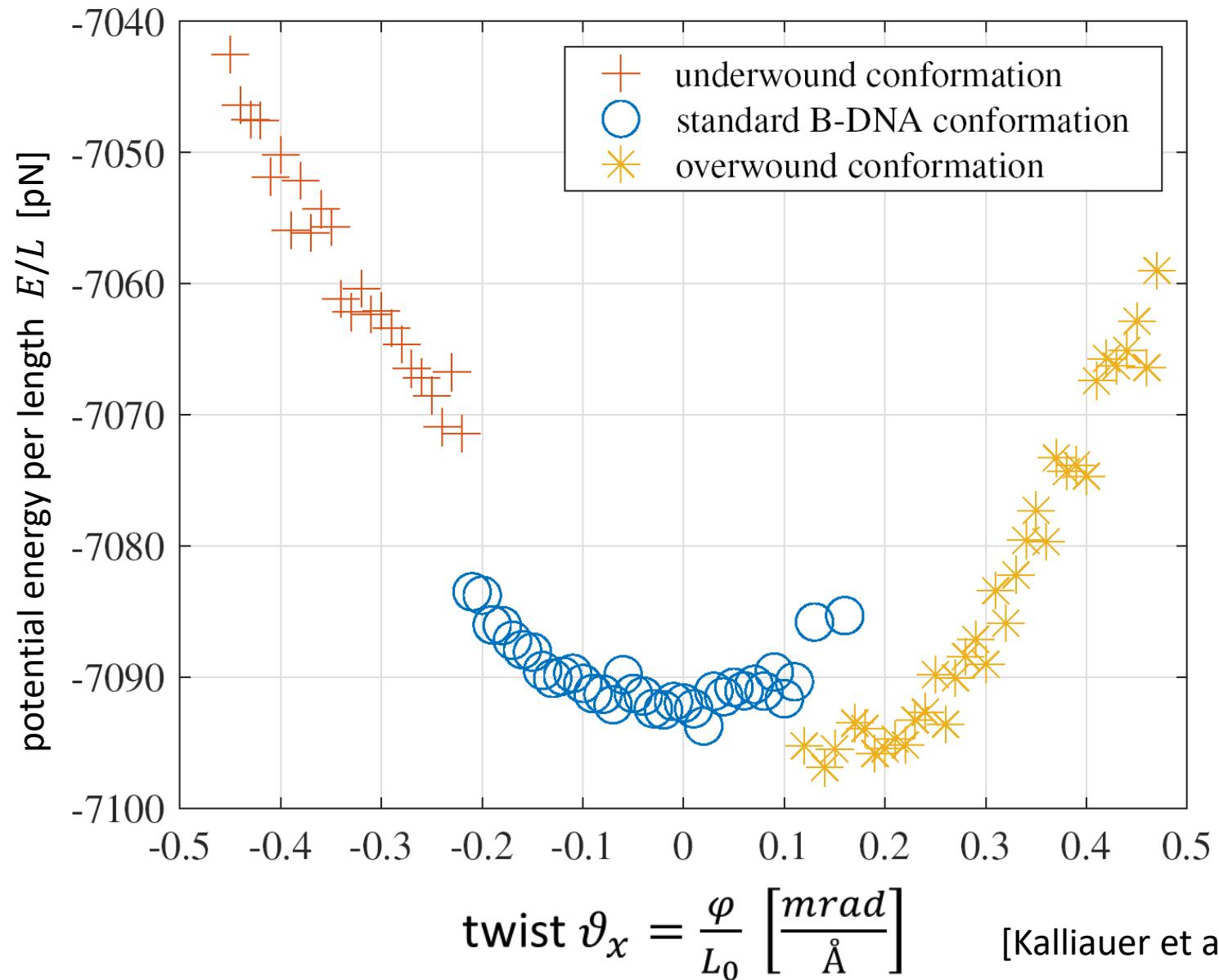
$$N(X) = \frac{-1}{\ell_{\text{RLE}}} \sum_{i=1}^{N_{\text{atom}}} x_i F_{i,x}^{\text{int}}$$

$$M_x(X) = \frac{-1}{\ell_{\text{RLE}}} \sum_{i=1}^{N_{\text{atom}}} x_i (-z F_{i,y}^{\text{int}} + y F_{i,z}^{\text{int}})$$

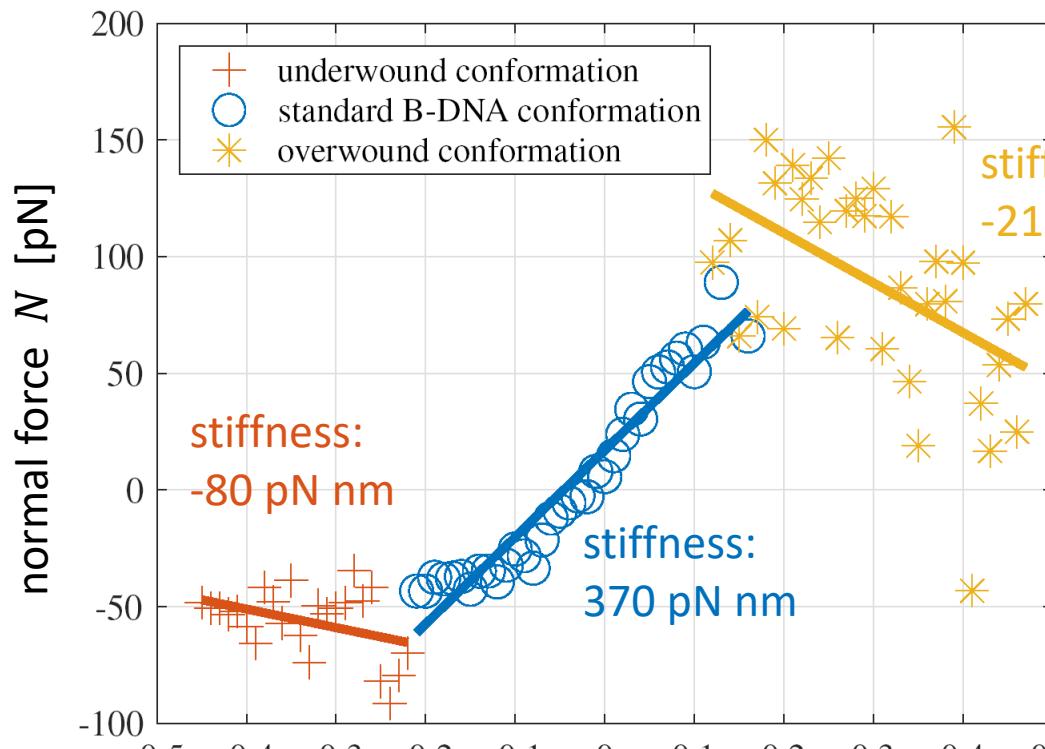
Stretching at zero twist



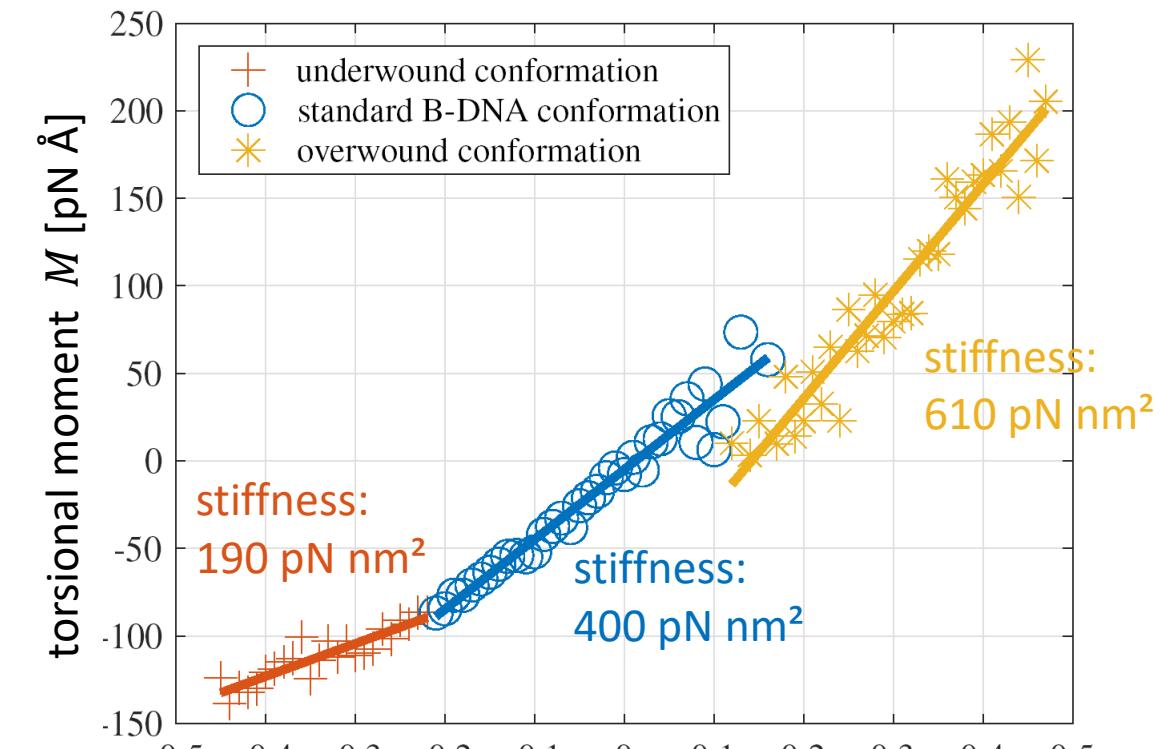
Twisting at constant length



Twisting at constant length

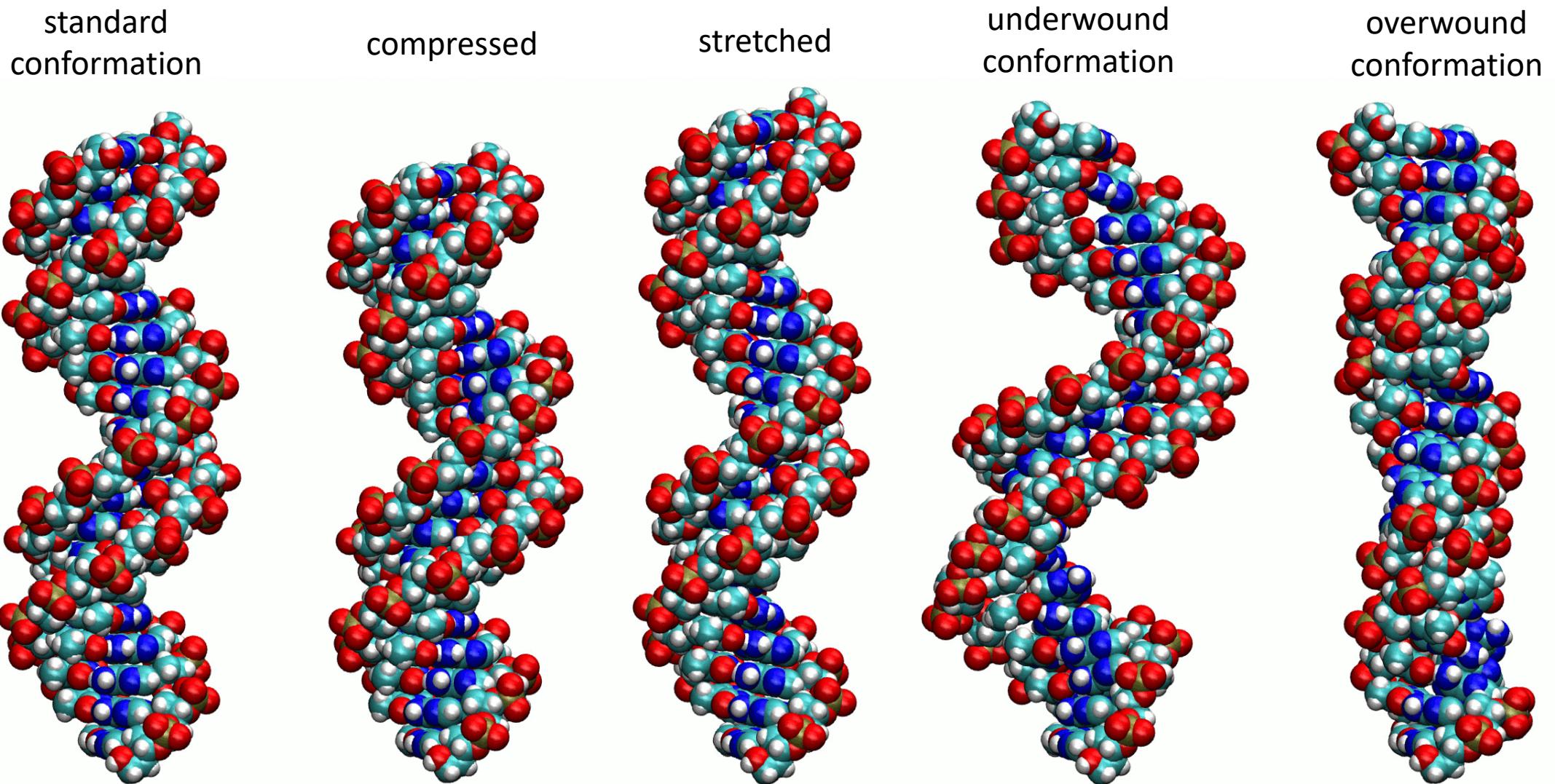


$$\text{twist } \vartheta_x = \frac{\varphi}{L_0} \left[\frac{mrad}{\text{\AA}} \right]$$



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Snapshots of deformations



Conclusions and Outlook

- ❖ first ever beam model derived directly from molecular dynamics
- ❖ this model includes the stretch-to-torsion coupling known from DNA experiments
- ❖ stiffness below persistence length (~50nm)
- ❖ theory of large strains
- ❖ bending stiffness
- ❖ DNA origami
- ❖ other polymers (other sequences of DNA, RNA, collagen, ...)