## **Progress Report**

Modeling the mechanism of topoisomerase

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## Outline

- 1. Goals
- 2. Literature Review
- 3. Initial Ideas

## Goals

#### Goals

## Overall goal

• Understand the interaction of *TOP2* and the topology of DNA.

## This week goal

- · Review Matlab programming.
- Understand the dynamics and fluid-coupled system of DNA.
- (Hopefully) Start to model.

Literature Review

## Topology of DNA

## Linking number

$$Lk(C_1, C_2) = \frac{1}{4\pi} \oint_{C_1} \oint_{C_2} \frac{\mathbf{x}_1'(s_1) \times \mathbf{x}_2'(s_2) \cdot \left[\mathbf{x}_1(s_1) - \mathbf{x}_2(s_2)\right]}{\left|\mathbf{x}_1(s_1) - \mathbf{x}_2(s_2)\right|^3} ds_2 ds_1$$

Writhe

$$Wr(C) = \frac{1}{4\pi} \oint_{C} \oint_{C} \frac{\mathbf{x}'(s_{1}) \times \mathbf{x}'(s_{2}) \cdot \left[\mathbf{x}(s_{1}) - \mathbf{x}(s_{2})\right]}{\left|\mathbf{x}(s_{1}) - \mathbf{x}(s_{2})\right|^{3}} ds_{2} ds_{1}$$

**Twist** 

$$Tw(C_2, C_1) = Lk(C_1, C_2) - Wr(C_1)$$

## Simplified Model (Swigon, 2009)

## **Elastic Energy**

$$\Psi = \frac{1}{2} \int_{0}^{L} \overbrace{A \left| t' \right|^{2}}^{\text{bending}} + C \underbrace{\left( \left[ t_{1} \times d \right] \cdot d'(s) - \bar{\Omega} \right)^{2}}_{\text{squared difference of twist density}} ds \implies A \left( t \times t'' \right) + C \Delta \Omega t' = F \times t$$

Under standard condition:  $A \approx 50kT \cdot nm$ ,  $C \in [25, 100]kT \cdot nm$ 

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## **Electrostatic Energy**

For M charged sites,

$$\Phi = \frac{4\delta^2}{4\pi\epsilon} \sum_{m=1}^{M-1} \sum_{n=m+1}^{M} \frac{\exp\left(-\kappa |\mathbf{x}_m - \mathbf{x}_n|\right)}{|\mathbf{x}_m - \mathbf{x}_n|}$$

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## Simplified Model (con't) (Swigon, 2009)

#### Generalized Kirchhoff's Rod Dynamics

$$\begin{split} \partial_t P &= F' + f \\ \partial_t R &= M' + x' \times F + m \end{split}$$

(linear momentum)
(angular momentum)

## Biochemistry of TOP2

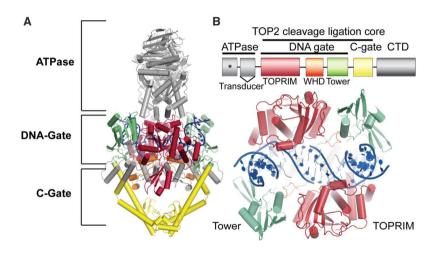


Figure 1: TOP2 Schematic on S. cerevisiae (Riccio et al., 2020)

## Biochemistry of TOP2 (con't)

# "Cleavage site selection" Protein-induced bending cleavage : Target Non-target No bending

Figure 2: Possible mechanism of identifying cleavage site (Jang et al., 2019)



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## Naive Ideas (con't)

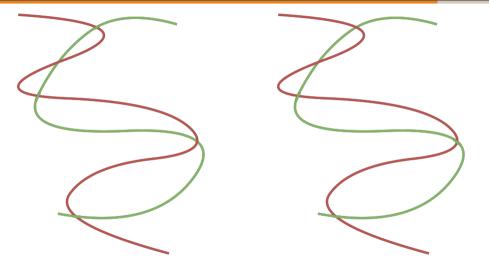


Figure 3: Visualize the process. Left side is original and right side is randomly transformed

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