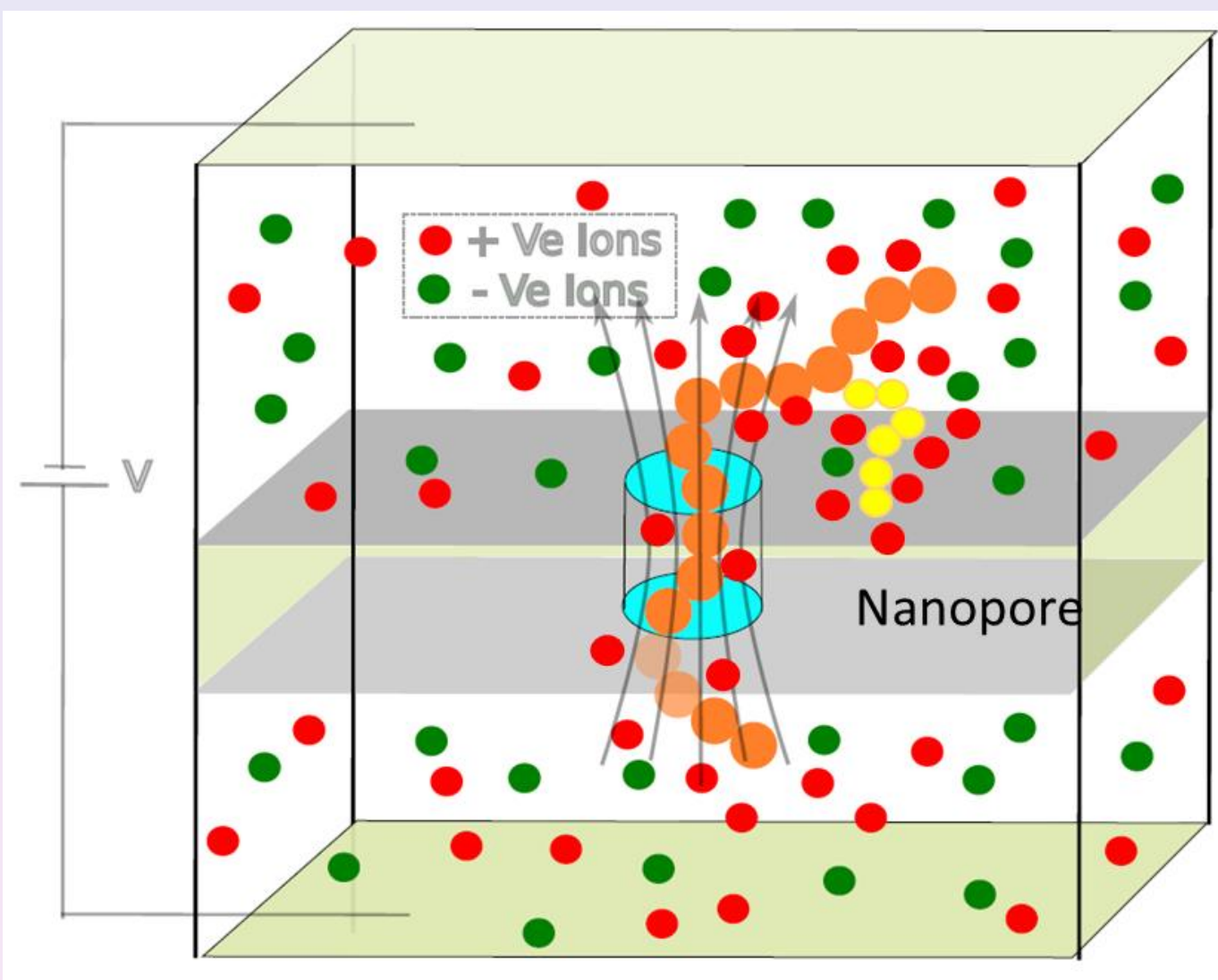


## Abstract

- Accurate genome mapping has direct applications in identifying and characterizing unknown species, restoring biodiversity, unambiguously labeling food specimens, authenticating herbal products, protecting endangered species, and in taxonomical research.
- Detection the genomic motifs relies on the accuracy **current blockade traces** measured at the nanopores which is often very noisy.
- We implement full fledge **electrokinetic transport of dsDNA** with sidechains in presence of explicit co and counter ions.
- We also propose a novel protocol to reconstruct current blockade from the Brownian dynamics (BD) simulation. When compared with the ionic current, we get an excellent correlation that can be exploited to get current data for a longer DNA.

## Model & the Method

Single Nanopore setup with explicit Co & Counter ions



Motion of the dsDNA

We coarse-grain 128 nm long  $\lambda$ phage DNA into 64 beads. This implies  $\sigma \sim 1bp$  (2 nm resolution).

Positive Ions = 500  
Negative Ions = 500

Nanopore diameter =  $4\sigma$

## Simulation Details

Bead Spring Model of DNA

$$U_{LJ}(r) = 4\epsilon \left[ \left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^6 \right] + \epsilon \quad \text{for } r \leq 2^{1/6}\sigma$$

$$= 0 \quad \text{for } r > 2^{1/6}\sigma.$$

LJ Potential

$$U_{FENE}(r) = -\frac{1}{2}kR_0^2 \ln(1 - r^2/R_0^2)$$

Spring Potential

$$U_{bend}(\theta_i) = \kappa(1 - \cos \theta_i)$$

Bending Potential

Electrostatic Interaction

Coulombic interactions between any two charged particles  $q_i$  and  $q_j$ , and separated by a distance  $r_{ij}$

$$U_{electrostatic}(r_{ij}) = k_B T l_B \frac{q_i q_j}{r_{ij}}, \quad l_B = \frac{e^2}{4\pi\epsilon_0 \epsilon k_B T}$$

The monomers are charged with  $q_{bead} = -1.0$  &  $q_{tag} = 0.5$ .

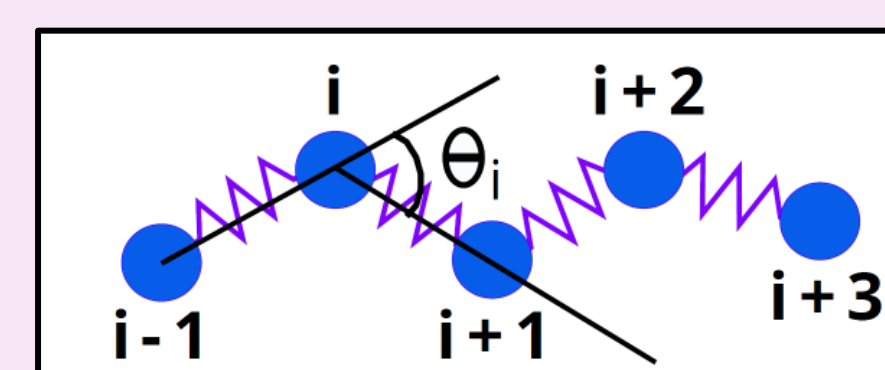
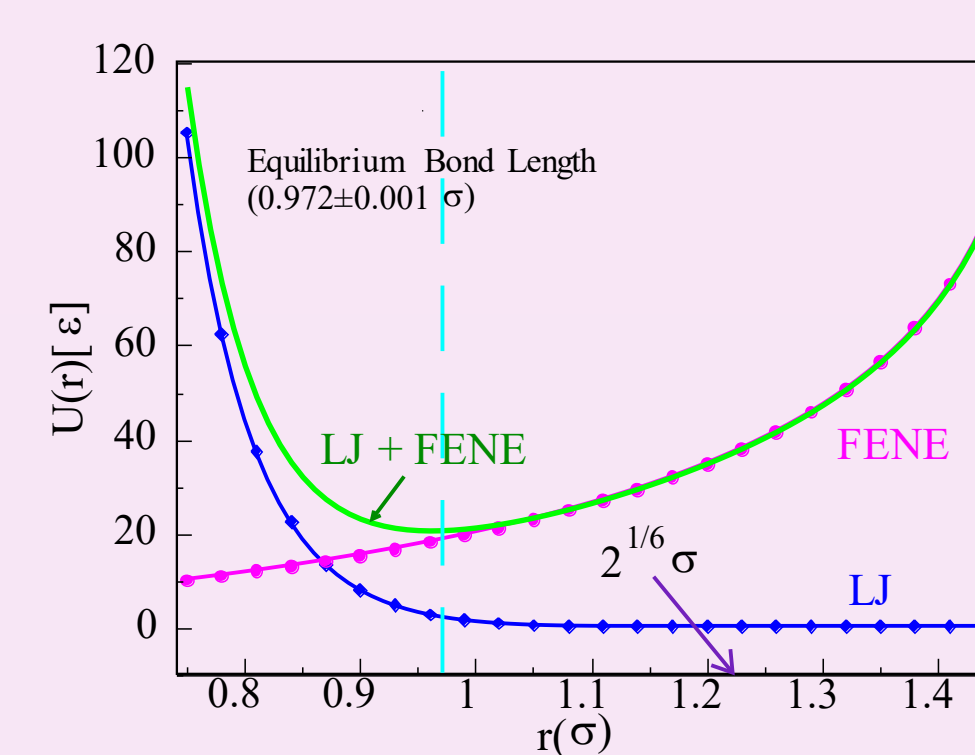
Due to the extended electric field, each monomer experience an additional force  $\vec{F}_{elec}(m) = q(m)\vec{E}$ .

Equation of Motion:

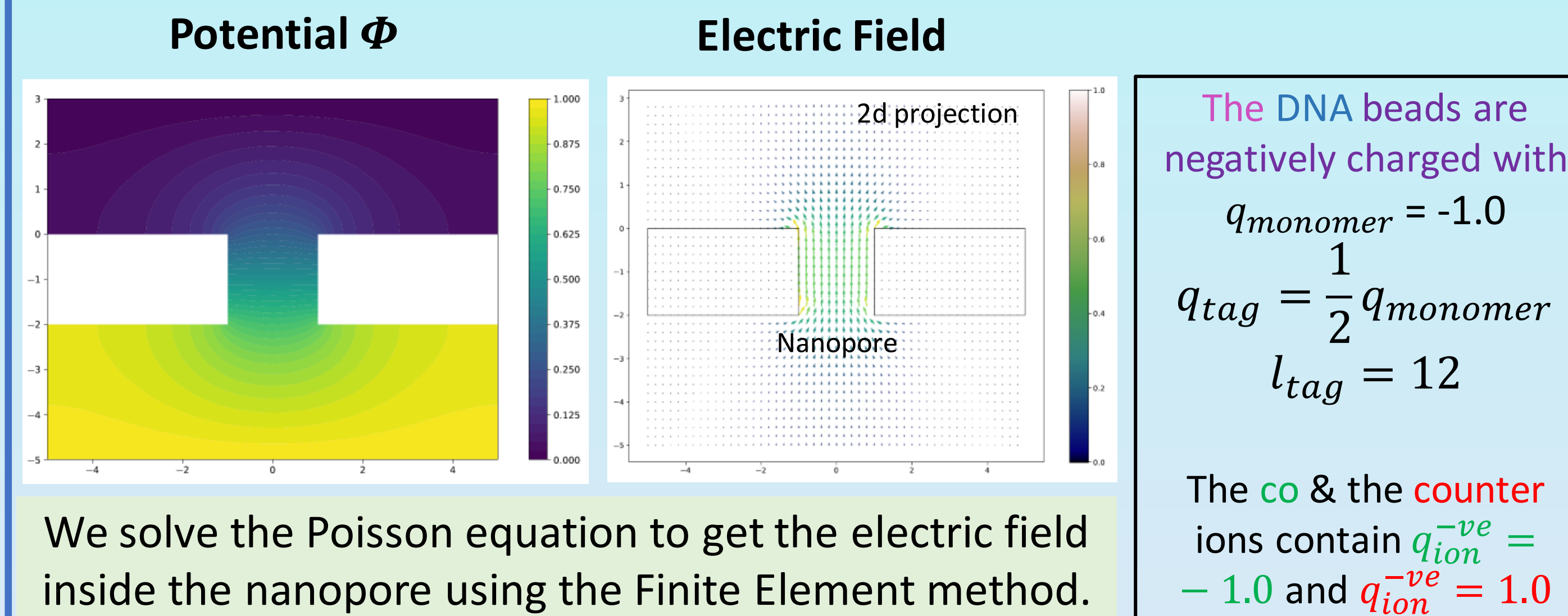
$$m_i \frac{d^2 \vec{r}_i}{dt^2} = -\vec{\nabla}(U_{LJ} + U_{FENE} + U_{Bend}) - \gamma \frac{d\vec{r}_i}{dt} + \vec{R}_i(t)$$

With  $\langle \vec{R}_i(t) \cdot \vec{R}_j(t') \rangle = 2dk_B T \gamma \delta_{ij} \delta(t - t')$

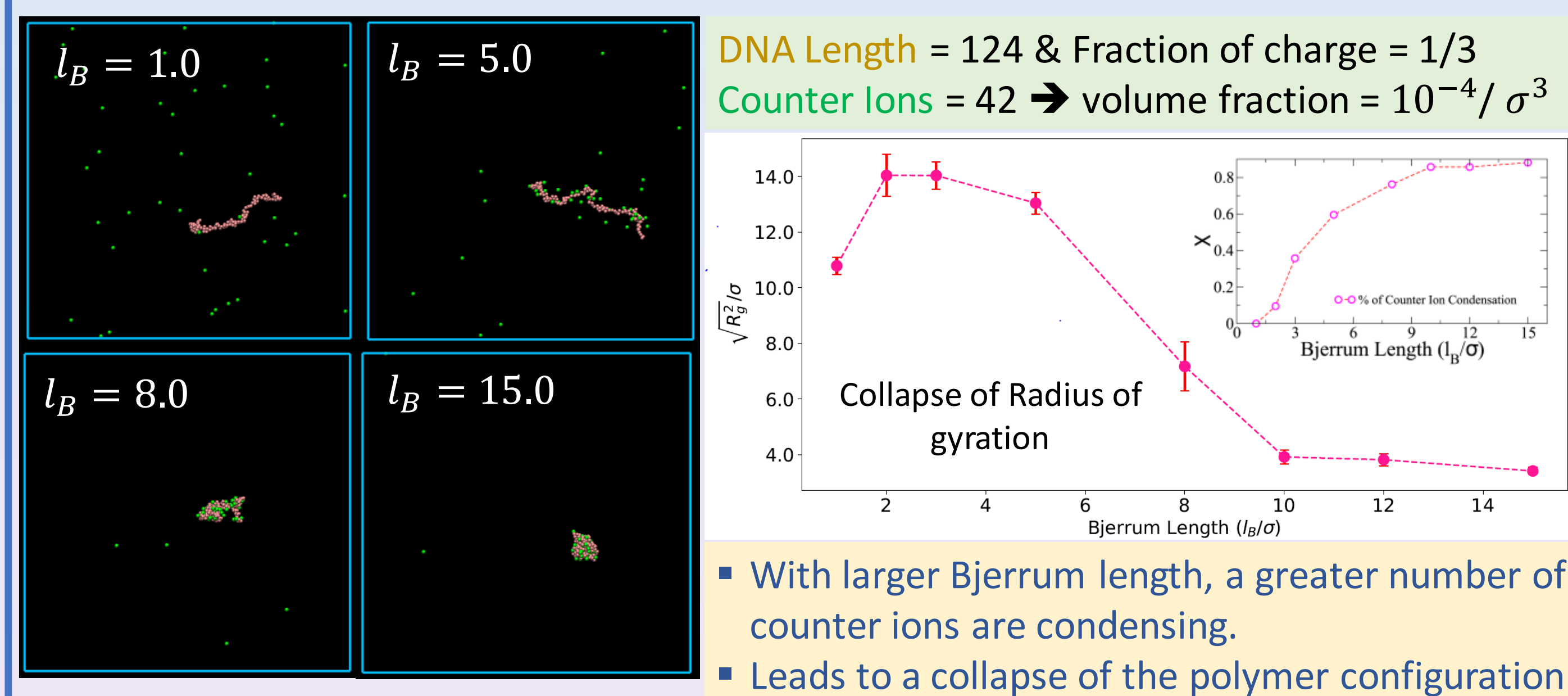
$d$  = dimension of the system,  $\gamma$  = Frictional Coefficient



## Extended Electric Field

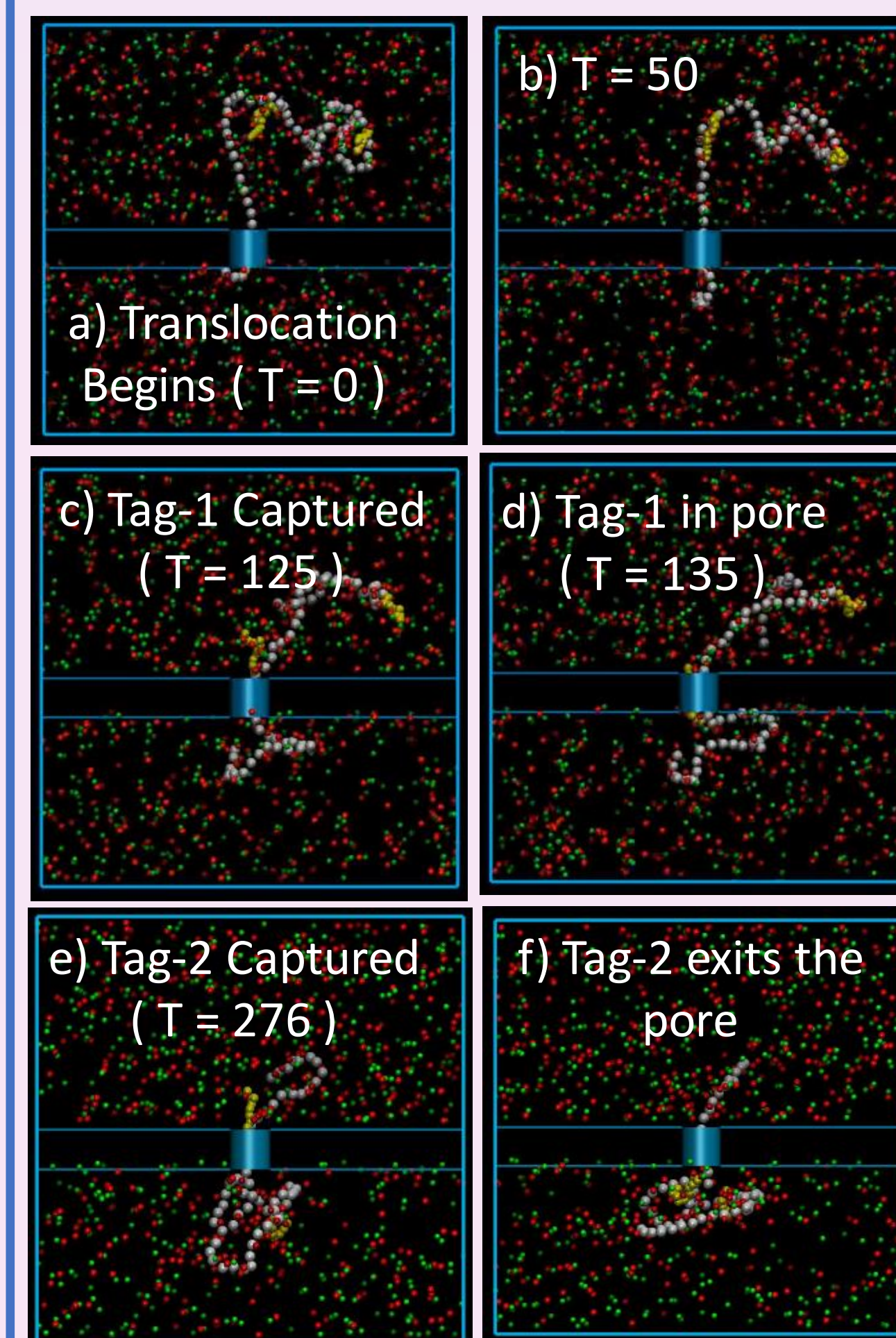


## Collapse of polymer with Bjerrum Length

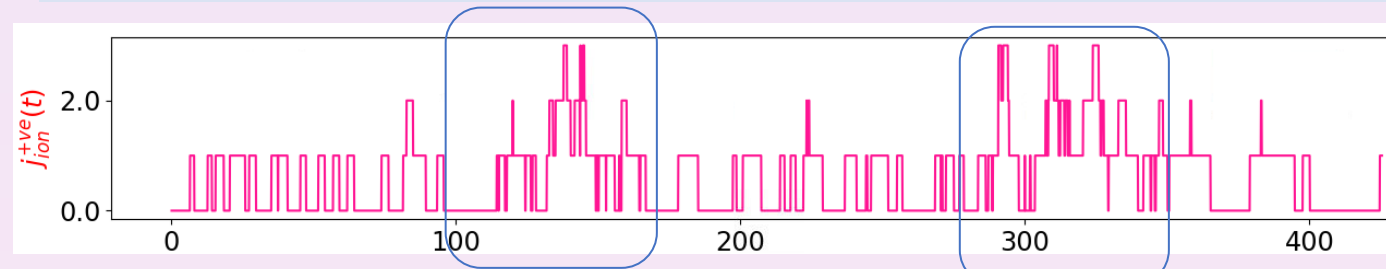


## Ion Flow through nanopore

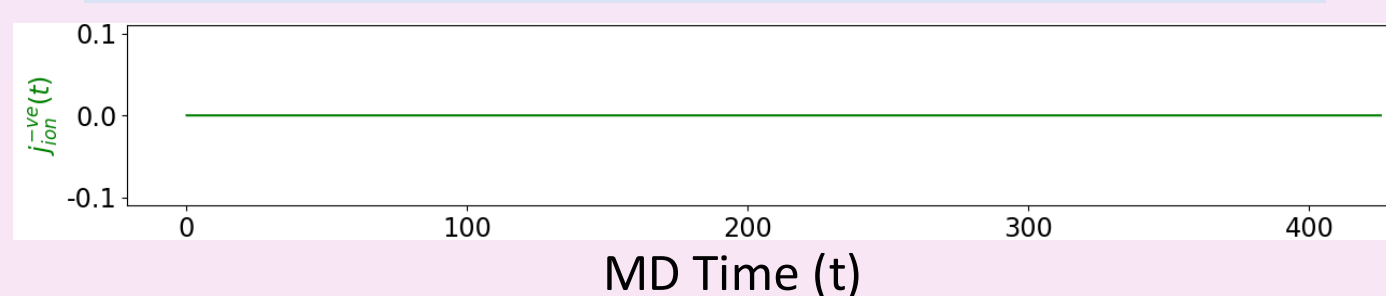
Simulation snapshots of translocation events



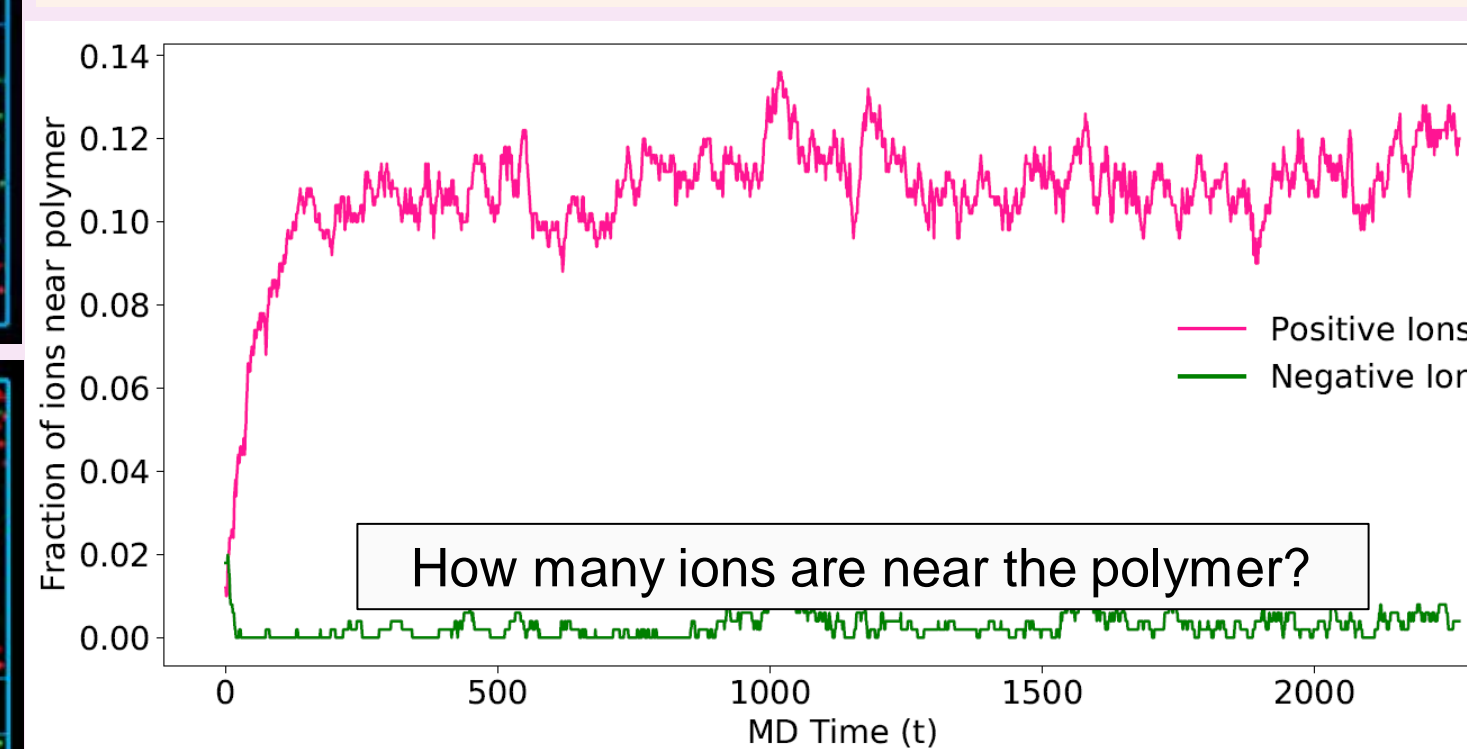
Counter Ion Flow through the nanopore:



Co Ion Flow through the nanopore:

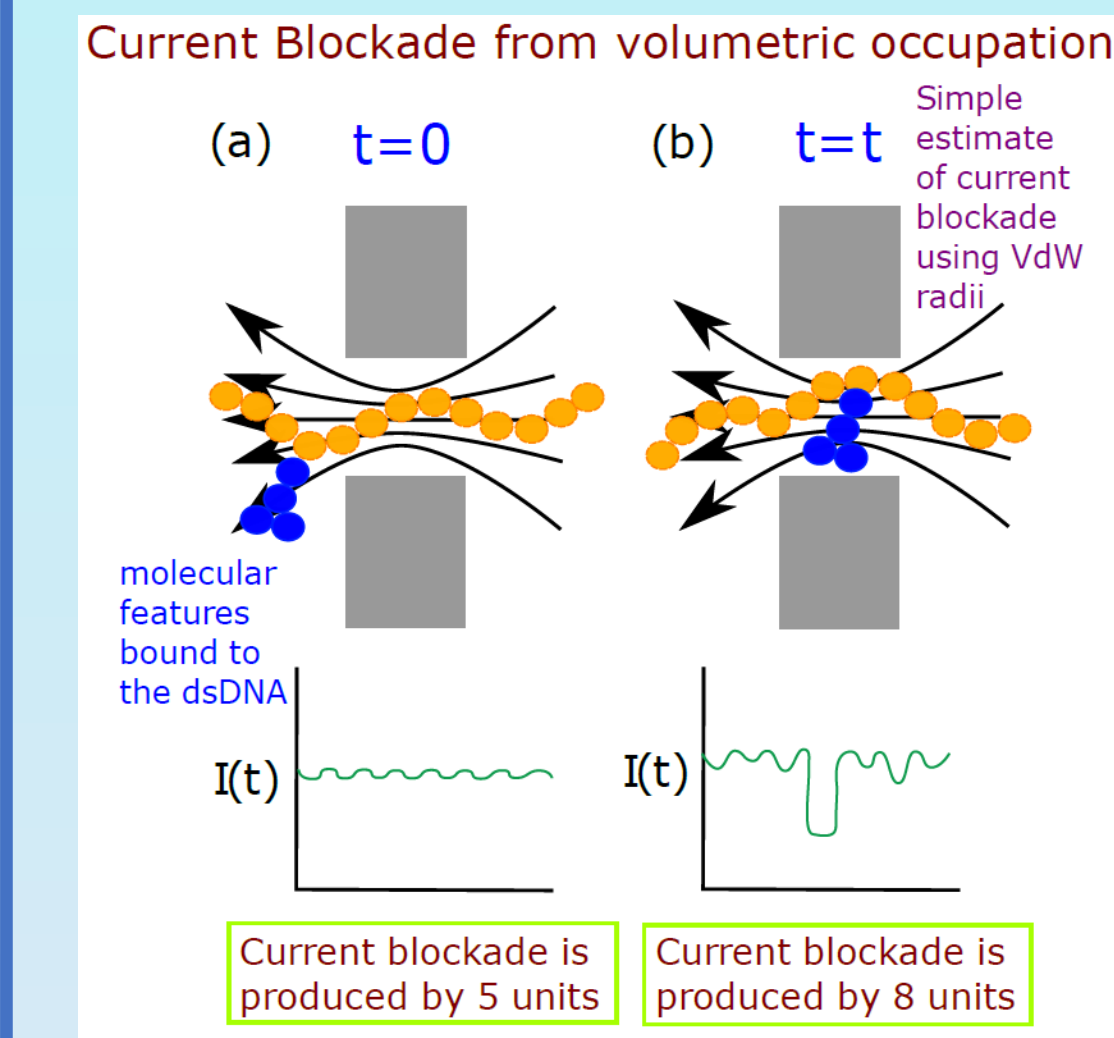


- ❖ Counter ions (+ve) are flowing in the opposite direction of the polymer motion.
- ❖ However, co-ion (-ve) flow is completely hindered.



- The +ve counter ions are significantly larger in number in the near vicinity of the dsDNA.
- The -ve co-ions are repelled by the electrostatic interactions.

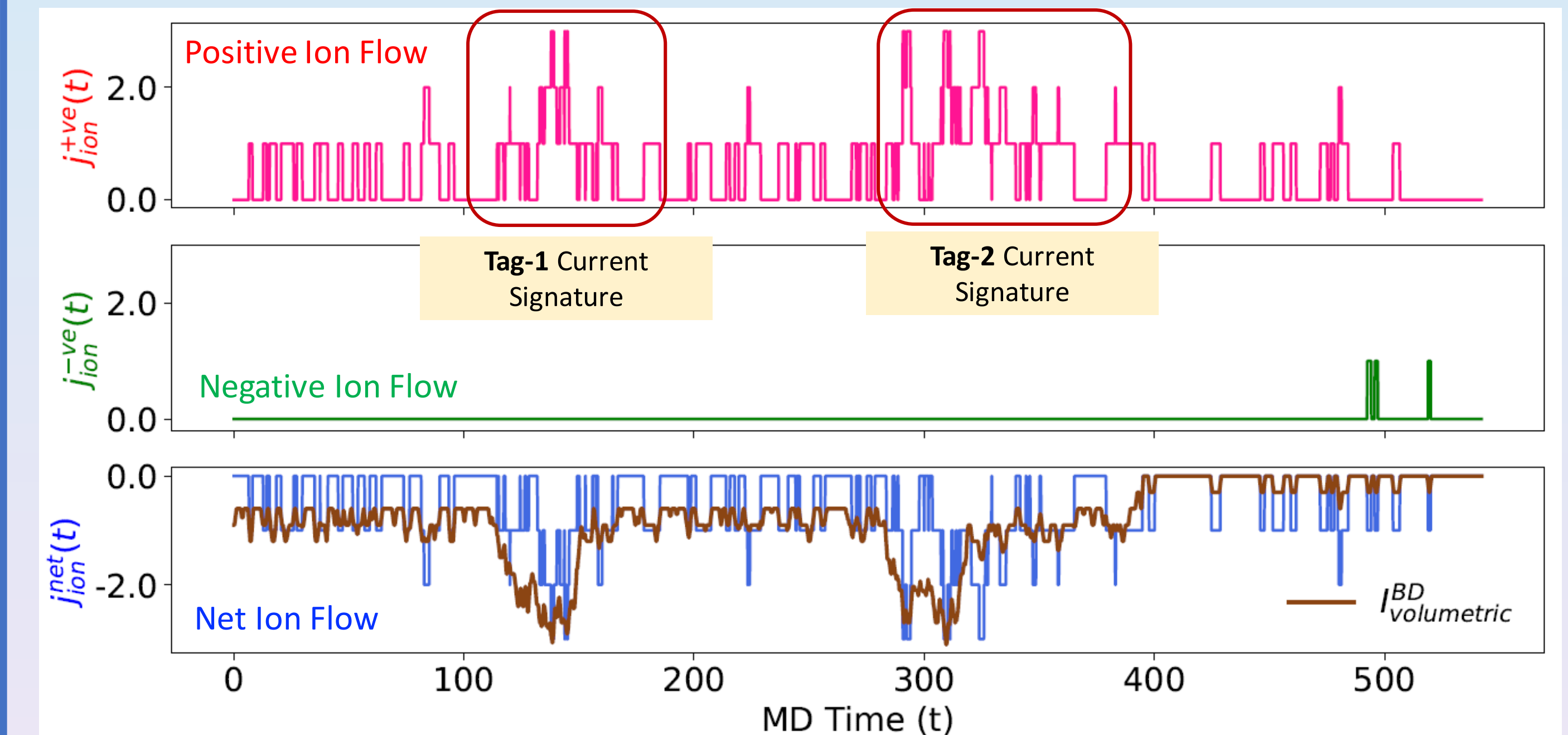
## Volumetric Occupation Model



Is there other way to get current blockade from simulation?

Volumetric occupation inside the pore are translated to current blockade magnitude as monomers and side chains pass through the pore as time progresses.

We observe an upsurge in the counter ion flow while sidechain ssDNA tags are in the nanopore.



## Conclusions

- ❖ Implementation of the **explicit (co & counter) ions** along with the charged dsDNA with tags provide **accurate current traces**.
- ❖ By measuring the **volumetric occupation** of the species inside the nanopore from BD simulation, current blockade traces can be generated.
- ❖ Our BD simulation confirms that there is a **high correlation** between the **actual ion flow** and the **volumetric occupation current traces**.

## References

1. Seth S., Rand A., Reisner W., Dunbar W. B., Sladek R. and Bhattacharya A. "Discriminating protein tags on a dsDNA construct using a Dual Nanopore Device." *Sci Rep*, 2022, 12 (1), 11305.
2. Seth S. and Bhattacharya A. "How capture affects polymer translocation in a solitary nanopore." *J. Chem. Phys*, 2022, 156 (24), 244902.
3. Seth S. and Bhattacharya A. "DNA barcodes using a double nanopore system." *Sci Rep*, 2021, 11 (1), 9799.
4. Seth S. and Bhattacharya A. "DNA barcode by flossing through a cylindrical nanopore." *RSC Advances*, 2021, 11 (34), 20781-20787.

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