Single Stranded DNA Translocation Through A Nanopore: A Master Equation Approach

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We study voltage driven translocation of a single stranded (ss) DNA through a membrane channel. Our model, based on a master equation (ME) approach, investigates the probability density function (pdf) of the translocation times, and shows that it can be either double or mono-peaked, depending on the system parameters. We show that the most probable translocation time is proportional to the polymer length, and inversely proportional to the first or second power of the voltage, depending on the initial conditions. The model recovers experimental observations on hetro-polymers when using their properties inside the pore, such as stiffness and polymer-pore interaction.

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1. INTRODUCTION

Translocation of biopolymers through a pore embedded in a membrane is a fundamental step in a variety of biological processes. Among the examples are the translocation of some species of m-RNA through the nucleus membrane which is the first stage of gene expression in eucarvotic cells [1], and the attack of cells by viruses that occurs by injecting the genetic information through a hole in the cell membrane [2]. The translocation importance in bio-systems, and the possibility for developing fast sequencing methods, have been the motivation for recent experiments, in which a voltage-driven ssDNA is translocated through α -hemolysin channel of a known structure [3]. In these experiments one measures the time it takes a single ssDNA molecule to pass through a membrane channel [4-7]. Since ssDNA is negatively charged (each monomer has an effective charge of zq, where z (0 < z < 1) is controlled by the solution pH and strength), when applying a voltage the polymer is subject to a driving force while passing through the membrane from the negative (cis) side to the positive (trans) side. Because the presence of the ssDNA in the transmembrane pore part (TPP) blocks the cross-TPPcurrent, one can deduce the translocation times pdf from the current blockade duration times [4-7]. It has been found that the shape of the translocation times pdf is controlled not only by the voltage applied to the system, the temperature and the polymer length but also by the nature of the homo-polymer used: poly-dA (A-adenine); poly-dC (C-cytosine); poly- T_{nu} (T_{nu} -thymine), and the sequence of hetro-polymers [4-7].

The translocation process can be roughly divided into two stages. The first stage is the arrival of the polymer in the vicinity of the pore and the second stage is the translocation itself. Several models have been suggested for describing the translocation stage. In [8] an equation for the free energy of the translocation, obtained from the partition functions of the polymer parts outside the TPP, was derived and used to calculate the mean first passage time (MFPT). Other investigators used similar ideas with improved free energy terms by taking into consideration effects such as the membrane width [9-10], or assumed that only the part of the ssDNA inside the TPP affects the dynamics of the translocation rather than the polymer parts outside the TPP [11-12].

In this work we present a new theoretical approach that allows to consider both the polymer parts outside the TPP and within the TPP. Using the ME we are able to map the three dimensional translocation onto a discrete space one-dimensional process. Based on the ME we compute the pdf of the first passage times (FPT) of the translocation, F(t), and the MFPT, as a function of the system parameters. We relate our theoretical results to recent experimental observations and by analyzing them using our model, we come up with physical understanding of these observations.

2. THE MODEL

An n = N + d - 1-state ME is used to describe the translocation of an N-monomer long ssDNA subject to an external voltage V, and temperature T, through a TPP of a length that corresponds to d(=12) monomers. A state is defined by the number of monomers on each side of the membrane and within the TPP. A change in the state of the system (only nearest states transitions are allowed) is assumed to be controlled mainly by the behavior of the polymer within the TPP in the presence of the applied voltage. In addition, it is assumed to be influenced by entropic and interaction factors of the polymer outside and within the TPP. Absorbing ends are used as boundary conditions, which are the natural choice for this system because the polymer can exit the TPP on both sides. The state i = n represents the arrival of the first monomer into the TPP from the cis side, and the state i = 0 represents the departure of the far end monomer from the trans side of the TPP. Let $P_i(t)$ be the pdf of state j that contains m_i nucleotides occupying

the TPP according to:

$$m_{j} = \begin{cases} j, & j \leq d \\ d, & N > j > d \text{ given } N \geq d, \\ n+1-j, & j \geq N \end{cases}$$
 (1.1)

and a similar set of equations for a short polymer, $N \leq d$, which is obtained by exchanging N and d in Eqs.(1.1) through (1.3). The governing equations of motion are:

$$\partial P_{j}(t)/\partial t = a_{j+1,j}P_{j+1}(t) + a_{j-1,j}P_{j-1}(t) -(a_{j,j+1} + a_{j,j-1})P_{j}(t); \quad j = 2, \dots, n-1, \partial P_{y}(t)/\partial t = a_{y+1,y}P_{y+1}(t)\delta_{y,1} + a_{y-1,y}P_{y-1}(t)\delta_{y,n} -(a_{y,y-1} + a_{y,y+1})P_{y}(t); \quad y = 1, n.$$
 (2)

Equations (2) can be written in matrix representation $\partial \vec{P}/\partial t = \mathbf{A} \vec{P}$. The propagation matrix \mathbf{A} , is a tridiagonal matrix that contains information about the transitions between states in term of rate constants. We assume that the rate constants can be decoupled into two terms:

$$a_{j,j+/-1} = k_j(T)p_{j,j+/-1}(V,T).$$
 (3)

The first term provides the rate to perform a step, while the second term gives the probability to jump from state j in a given direction, and obeys: $p_{j,j+1} + p_{j,j-1} = 1$. To obtain k_j , we first consider the bulk relaxation time of a polymer [13] $\tau_b \propto \beta \xi_b b^2 N^\mu$, where $\beta^{-1} = k_B T, \; b$ is a monomer length, ξ_b is the Stokes bulk friction constant per segment, $\xi_b = 6\pi b\eta$ (where η is the solvent viscosity), N is the number of monomers in the polymer and the dimensions dependant μ represents the effect of the microscopic repulsion on the average polymer size. In three dimensions $\mu = 3,9/5,3/2$ for rod-like, self-avoiding and Gaussian (Zimm model) chains, respectively. To compute the relaxation time inside the TPP, the confined volume of the TPP must be taken into account. For a rod-like polymer the restricted volume dictates a onedimensional translocation, whereas for a flexible polymer the limitations are less restricted. We implement this by taking μ as a measure of the polymer stiffness inside the TPP that obeys: $0 \le \mu \le 1.5$. The expression for the relaxation rate of state j is therefore,

$$k_j = 1/(\beta \xi_p b^2 m_j^{\mu}) \equiv R/m_j^{\mu}.$$
 (4)

From Eq.(4) it is clear that as μ becomes smaller the rate to preform a step becomes larger, namely k_j for a rod-like polymer increases. This feature appears, at first sight, to be in contradiction to the relaxation time behavior of a bulk polymer, where a rod-like polymer has a larger relaxation time than that of a flexible polymer. This contradiction is resolved by taking into account the different dimensional demand for a rod-like polymer relative to a flexible polymer inside the TPP. Because μ is a measure of the polymer stiffness inside the TPP, it is

controlled by the interaction between the monomers occupying the *TPP*, e.g base stacking and hydrogen bonds, and therefore is affected by the monomer type and the sequence of the ssDNA.

The friction constant per segment inside the TPP, ξ_p , represents the interaction between the ssDNA and the TPP. The physical picture is that during translocation there are few or no water molecules between the polymer and the TPP. Consequently the water molecules inside the TPP can hardly be viewed as the conventional solvent and the Stokes friction constant is replaced by ξ_p representing the ssDNA-TPP interaction.

To calculate $p_{j,j-1}$, the second term on the right hand side of Eq.(3), we assume a quasi-equilibrium process and use the detailed balance condition for the ratio of the rate constants between neighboring states: $a_{j,j-1}/a_{j-1,j} = e^{-\beta \Delta E_j}$, where $\Delta E_j = E_{j-1} - E_j$. We then use the approximation $a_{j,j-1}/a_{j-1,j} \approx p_{j,j-1}/(1-p_{j,j-1})$, and deduce the jump probabilities by computing ΔE_j . To compute E_j the contributions from three different sources are considered: electrostatic, E_j^p , entropic, E_j^s , and an averaged interaction energy between the ssDNA and the pore, E_j^i .

For the calculations of the electrostatic energy difference between adjacent states, ΔE_j^p , we assume a linear drop of the voltage along the TPP and write for m_j monomers occupying the TPP penetrating from the cis side of the membrane for a length of i_jb :

$$E_j^p = zq(V/d) \sum_{n=i_j}^{m_j+i_j-1} n = zq(V/2d)m_j(m_j + 2i_j - 1).$$
(5)

The effective charge per monomer in the TPP is taken to be the same as of the bulk. For states that contain monomers at the trans side of the membrane, zqV should be added for ΔE_j^p . This contribution represents the additional effective charge that passed through the potential V. Accordingly, the expression for ΔE_j^p is (see Appendix A):

$$\Delta E_i^p = zqV(m_i + \alpha_i)/d. \tag{6}$$

Here α_j takes the values: $\alpha_j = \{-1; 0; 1\}$ for cases described by equations $\{(1.1); (1.2); (1.3)\}$ respectively $(\alpha_j = 1 \text{ and } \alpha_j = -1 \text{ correspond to the entrance and exit states of the translocation, whereas <math>\alpha_j = 0$ corresponds to the intermediate states of the translocation). For a short polymer, α_j has the same values as for a large polymer.

The contribution to ΔE_j from ΔE_j^s is composed of two terms. One term is the entropic cost needed to store m_j monomers inside the TPP, and the second term originates from the reduced number of configurations of a Gaussian polymer near an impermeable wall. Combining these terms leads to (see Appendix B):

$$\Delta E_j^s = \gamma_j/\beta,\tag{7}$$

where $\gamma_j = \{-1 + g_j; g_j; 1 + g_j\}$, for cases described by equations $\{(1.1); (1.2); (1.3)\}$, respectively. g_j is given in Appendix B in terms of $N_{j,cis}$ and $N_{j,trans}$, which are the number of monomers on the cis and trans sides correspondingly. For a short polymer γ_j behaves similarly but for intermediate states g_j =0.

For computing ΔE^i_j we focus on the average interaction between the ssDNA and pore (not only its transmembrane part). Due to the asymmetry of the pore between the cis and the tran sides of the membrane [3], the ssDNA interacts with the pore on the cis side of the membrane and within the TPP but not on the trans side of the membrane. Assuming an attractive interaction, $E^i_j = -k_B T(N-N_{j,trans})$ (more properly, $E^i_j = -\varepsilon(N-N_{j,trans})$, and we set $\epsilon = k_B T$ in the relevant temperature regime) we obtain:

$$\Delta E_i^i = \zeta_i/\beta,\tag{8}$$

where $\zeta_j = \{1; 1; 0\}$, for the cases described by equations $\{(1.1); (1.2); (1.3)\}$, respectively, and for a short polymer $\zeta_j = \{1; 0; 0\}$.

Using the above relations, and defining $\delta_j = \gamma_j + \zeta_j$ we obtain

$$p_{j,j-1} = (1 + e^{\beta \Delta E_j^p + \delta_j})^{-1}.$$
 (9)

For the system to be voltage driven $\beta |\Delta E_j^p| > \delta_j$ must be fulfilled, which translate into the condition: $V/V_C > 1$, where a characteristic voltage is introduced: $V_C^{-1} \equiv (1 + 1/d)\beta z|q|$. This inequality ensures that there is a bias towards the trans side of the membrane. Otherwise the polymer is more likely to exit from the same side it entered than to transverse the membrane. Under experimental conditions [6] $V_C = 46mV$, when using $z \approx 1/2$.

In Figure 1 we show the different contributions to ΔE_j : $\beta \Delta E_j^p$ (for $\beta z|q|V=1$) and δ_j . $\beta \Delta E_j^p$ decreases for the entrance states of the translocation, increases at the exit states of the translocation, and is a negative constant for intermediate states. Clearly $\beta \Delta E_j^p \leq 0$ reflects the field directionality. On the other hand, δ_j opposes the translocation for the entrance and intermediate states. For the entrance states $\delta_j > 0$ due to both entropic terms, but approaches zero (from below) for the exit states of the translocation, due to the cancellation of ΔE_j^i against the entropic gain of storing less monomers within the TPP. At intermediate states $\delta_j \approx 1$, where its shape near the crossover between the different situations is controlled by g_j .

3. RESULTS AND DISCUSSION

3.i. The FPT pdf

In this subsection we compute the FPT pdf, F(t), and examine its behavior as a function of the system parameters. F(t) is defined by:

$$F(t) = \partial(1 - S(t))/\partial t, \tag{10}$$

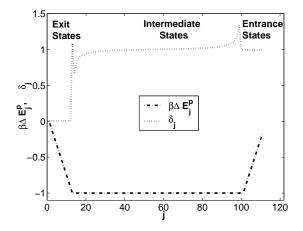


FIG. 1: The components of the ΔE_j , $\beta \Delta E_j^p$ ($\beta z | q | V = 1$) and δ_j , are shown for N = 100.

where the survival probability, namely, the probability to have at least one monomer in the TPP, S(t), is the sum over all states pdf

$$S(t) = \overrightarrow{U} \mathbf{C} e^{\mathbf{D}t} \mathbf{C}^{-1} \overrightarrow{P}_{0}. \tag{11}$$

Here \overrightarrow{U} is the summation row vector of n dimensions, \overrightarrow{P}_0 is the initial condition column vector, $(\overrightarrow{P}_0)_j = \delta_{x,j}$, where x is the initial state, and the definite negative real part eigenvalue matrix, \mathbf{D} , is obtained through the transformation: $\mathbf{D} = \mathbf{C}^{-1}\mathbf{AC}$.

Substituting Eq.(11) into Eq.(10), F(t) is obtained. Figure 2 shows the double-peaked F(t) behavior as a function of V/V_C and N (inset), for starting at x=N+d/4. The left peak represents the non-translocated events. Its amplitude decreases as V/V_C increases but remains unchanged (along with the position) with the increase in N, because only the 'head' of the polymer is involved in these events. As x decreases, namely when the translocation initial state shifts towards the trans side, the non-translocation peak and the translocation peak merge and for x=n/2, namely, for an initial condition for which $N_{j,cis}=N_{j,trans}$, F(t) has one peak (data not shown) independent of V/V_C .

For a convenient comparison to experimental results, we calculate and examine the behavior of the most probable average translocation velocity, $v = xb/t_m$, where t_m is the time that maximizes the translocation peak.

Figure 3 shows the v(N) behavior, for $V/V_C=2.60.$ v(N) is a monotonially decreasing function of N for $N \leq d$, but is independent of N for $N \geq d$. This agrees with the experimental results [6]. The origin for v(N) behavior, stems from Eqs.(1) and (4), according to which the minimal k_j is a decreasing monotonic function of N for $N \leq d$, but is independent of N for $N \geq d$.

The velocity, v(V), depends on x, $v(V) = v_x(V)$, and changes from a linear to quadratic function of the voltage when changing x, as shown in the inset of $figure\ 3$, for N=30.

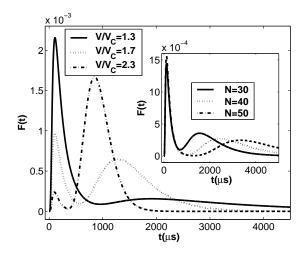


FIG. 2: F(t), for several values of V/V_C , with: $N{=}30$, $x{=}N{+}d/4$, $z\approx 1/2$, $T{=}2^oC$, $V_C{=}46mV$, $\mu{=}1.14$ and $R{=}10^6{\rm Hz}$. The left peak represents the non-translocated events, whereas the right peak represents the translocation. Inset: F(t) as a function of N, with $V/V_C = 1.5$, and the other parameters as above. The non-translocation peak remains unchanged when increasing the polymer length, while the translocation peak shifts to the right with N.

Starting at x=N+1, a linear scaling is obtained: $v_{N+1}(V)=b_1(V-b_2/b_1)$. The coefficient b_2/b_1 can be identified as an effective characteristic voltage: $\widetilde{V_C}^{-1}\equiv (1+1/d)\beta\widetilde{z}|q|=b_1/b_2$. From the last equality \widetilde{z} can be extracted.

Starting at x = N/2, i.e. when initial state is close to the exit states, a square dependence is obtained: $v_{N/2}(V) = c_1(V - c_2)^2 + c_3$, with $c_1 = o(10^{-5})$, $c_2 = 40mV$ and $c_3 = o(10^{-2})$. These coefficients are similar to the measured values [6].

We note that both linear and square scaling behaviors have been observed experimentally [4,6]. A possible explanation for the different functional behavior of v(V) might originate from different data analysis that can be interpreted as having a different initial condition.

To get numerical values for ξ_p and μ , we use the experimental data in refs. [6-7], and obtain: $\mu(C) = 1$, $\mu(A) = 1.14$, $\mu(T_{nu}) = 1.28$, and $\xi_p(A) \approx 10^{-4} meVs/nm^2$, $\xi_p(C) = \xi_p(T_{nu}) = \xi_p(A)/3$. From these values we find the limit in which the relaxation time of the polymer parts outside the TPP can be neglected. We estimate the maximal bulk number of monomers, N_{max} , for which the bulk relaxation time is much shorter (5%) than of the TPP relaxation time. For a poly-dA bulk Zimm chain we get $N_{max} \approx 271$, by taking for the viscosity the value for water at $2^{o}C$, $\eta \approx 1.7 \cdot 10^{-3}Ns/m^2$. Using this value, ξ_b can be calculated from the Stokes relation to be: $\xi_b \approx 10^{-7} meVs/nm^2$, which is three order of magnitude smaller than ξ_p .

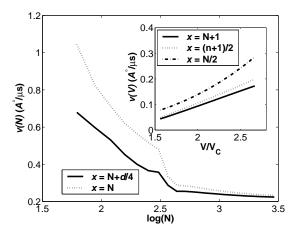


FIG. 3: The velocity as a function of the polymer length, for the same parameters as in figure 2, various initial conditions (linear-log scales) and $V/V_C=2.6.\ v(N)$ tends towards a length independent, but display a sharp decrease for short polymers. Note for the step feature of v(N) when N becomes larger than the TPP length, d. Inset: v(V), for N=30, showing linear and quadratic scaling depending on the initial condition, x.

3.ii. The MFPT

Additional information about the translocation can be obtained by computing the MFPT, $\overline{\tau}$. To compute an analytical expression for $\overline{\tau}$, we consider a large polymer, N>d, and replace $p_{j,j-1}$ and k_j by state independent terms: $p_+=[1+e^{(-V/V_C+1)}]^{-1}$, valid for $x\approx N$, and $k=1/(\beta\xi_pb^2d^\mu)$. This leads to $a_+=p_+k$ and $a_-=(1-p_+)k$, which defines a one dimensional state invariant random walk. The MFPT is obtained by inverting \mathbf{A} [14]: $\overline{\tau}=\int_0^\infty tF(t)dt=-\overrightarrow{U}\mathbf{A}^{-1}\overrightarrow{P}_0$. The calculations of the elements of the state independent \mathbf{A}^{-1} yields (see Appendix C):

$$(-\mathbf{A}^{-1})_{s,x} = \frac{\Delta(p^s)\Delta(p^{n+1-x})}{\Delta(p)\Delta(p^{n+1})} \frac{p_+^{x-s}}{k}; \qquad s < x, \quad (12)$$

where $\Delta(p^m) = p_+^m - p_-^m$ and $(-\mathbf{A}^{-1})_{s,x}$ for $s \geq x$ is obtained when exchanging s with x and p_+ with p_- in Eq.(12). Summing the x column elements of $(-\mathbf{A}^{-1})$ we obtain $\overline{\tau}$ (see Appendix C):

$$\overline{\tau} = \frac{\Delta(p^{n+1-x})p_+^x x - \Delta(p^x)p_-^{n+1-x}(n+1-x)}{k\Delta(p)\Delta(p^{n+1})}, \quad (13)$$

which in the limit of a weak bias, $V/V_C \gtrsim 1$, can be rewritten as (see Appendix C)

$$\overline{\tau} \approx \frac{2x\xi_p b^2 d^{\mu}}{z|q|(1+1/d)} \frac{1}{V - V_C}.$$
(14)

Although $\overline{\tau}$ and t_m are different characteristics of F(t) and differ significantly when slow translocation events dominate, Eq.(14) captures the linear scaling with

N and 1/V. The quadratic scaling of t_m with 1/V is obtained when using Eq.(9) rather than its state invariant version, for starting at, or near, an initial state for which $\delta_{j=x} \leq 0$.

3.iii. The sequence effect

Under the assumptions that are presented below, we now construct ξ_p and μ for every ssDNA sequence and thus examine the sequence effect on t_m . For a given ssDNA sequence occupying the TPP in the j state, we write an expression for the average friction of that state, $\xi_{p,j}$, assuming additive contributions of the monomers inside the TPP:

$$\xi_{p,j} = (1/m_j) \sum_{s=1}^{m_j} \xi_p(nu_s). \tag{15}$$

Here nu_s stands for the nucleotide s occupying the TPP. To construct a compatible state dependent stiffness parameter, μ_j , we first argue that only nearest monomers can interact inside the TPP and thus contributes to the rigidity of the polymer, which in turn increases k_j . We then examine the chemical structure of the nucleotides and look for 'hydrogen-like' bonds between adjacent bases. The term 'hydrogen-like' bonds is used because the actual distance between the atoms that create the interaction may be larger than of a typical hydrogen bond. The pairs AA and CC can interact but not the pairs $T_{nu}T_{nu}$ and CA. For the pair CT_{nu} the interaction is orientation dependent; namely, for the l pairs sequence, poly- $d(CT_{nu})_l$, the interaction is within each of the pairs but not between the pairs. Accordingly we have: $\mu(nu \ nu) = \mu(nu), \ \mu(CA) = \mu(AC) = \mu(T_{nu}),$ $\mu(CT_{nu}) = \mu(C), \ \mu(T_{nu}C) = \mu(T_{nu}), \text{ which allow the}$

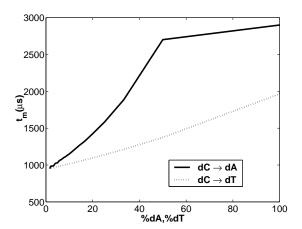


FIG. 4: t_m as a function of the percentage of equally spaced monomers substitutions $C \to A$ and $C \to T_{nu}$, for N=60, $x=N, z\approx 1/2, V/V_C=1.63$ and $T=292^oK$. The curves emphasize the effects of the rigidity and the friction on the translocation dynamics. See text for discussion.

calculation of μ_i following the definition:

$$\mu_j = \frac{1}{m_j - 1} \sum_{s=1}^{m_j - 1} \mu(nu_s \ nu_{s+1}), \tag{16}$$

with $(\mu_j)_{m_j=1} = 0$. Figure 4 shows t_m as a function of equally spaced substitutions $C \to T_{nu}$ and $C \to A$. The linear scaling of $t_m(C \to T_{nu})$ is due to the linear scaling of $\mu_j(C \to T_{nu})$. The saturating behavior of $t_m(C \to A)$ is a combination of two opposing factors: the linear scaling of $\xi_{p,j}(C \to A)$ and the nonmonotonic behavior of $\mu_j(C \to A)$. Our model also predicts that for sufficiently large l

$$t_m[(CA)_l] > t_m(C_lA_l). \tag{17}$$

This feature is explained by noticing that $2t_m[(CA)_l] > t_m(C_{2l}) + t_m(A_{2l})$, see figure 4, which follows from the expression for μ_j , Eq.(16), and then using $2t_m(C_nA_n) \approx t_m(C_{2l}) + t_m(A_{2l})$, which follows from the linear scaling of t_m with N, for $N \geq d$ in addition to Eq.(15). The above findings regarding the behavior of t_m for hetro-ssDNA, fit the experimental results [7].

4. CONCLUSIONS

In the presented model, the translocation of ssDNA through α -hemolysin channel is controlled, in addition to the voltage, by the interaction between the polymer and the pore $(\Delta E_j^i \text{ and } \xi_p)$, and between nearest monomers inside the TPP (μ) , as well as by an entropic factors originate from polymer segments outside and within the TPP. Based on the model, we showed that F(t) can be mono or double peaked depending on x and V/V_C . We calculated the MFPT to be: $\overline{\tau} \sim N/(V - V_C)$, for N > d and $V/V_C \gtrsim 1$, and $t_m \sim N/v_x(V)$ for $N \geq d$, where $v_x(V)$ changes from a linear to a quadratic function of V with x. In addition we estimated that $\xi_p \approx 10^3 \xi_b$, and by constructing ξ_p and μ for hetro-ssDNA explained experimental results regarding the various behaviors of t_m for hetro-ssDNA.

An extended version of this model that describes translocation through a fluctuating channel structure, can be used to describe unbiased translocation, which displays long escape times [16]. Translocation of other polymers through proteins channels can be described using the same framework by changing μ , ξ_p and ΔE_j .

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APPENDIX A

We wish to calculate the electrostatic energy difference between sates, ΔE_j^p . There are three cases during translocation, which are described by Eqs.(1.1)-(1.3).

For any polymer length, Eq.(1.1)(exit states) describes a case for which $N_{j,cis}$ =0 and Eq.(1.3) (entrance states) describes a case for which $N_{j,trans}$ =0. For the case described by Eq.(1.2) (intermediate states), there are monomers on both sides of the membrane for a large polymer, or no monomers on both sides of the membrane for a short polymer. Starting from Eq.(5) we have for the entrance states:

$$\Delta E_j^p = \frac{zqV(m_j + 1)}{d}.$$
 (A1)

For the exit states ΔE_j^p is composed of two contributions. One contribution stems from the passage of a monomer with an effective charge of zq through the potential V:

$$\Delta E_{j,1}^p = zqV. \tag{A2}$$

The second contribution calculated from Eq.(5) is:

$$\Delta E_{j,2}^p = \frac{-i_j zqV}{d}.$$
 (A3)

Combining the two contributions we find

$$\Delta E_j^p = \frac{(d-i_j)zqV}{d} = \frac{(m_j - 1)zqV}{d}, \quad (A4)$$

when using $m_i = d + 1 - i_i$.

For the intermediate states and a large polymer, we have only the contribution given by Eq.(A2) (the number of monomers within the *TPP* is constant), which can be written as:

$$\Delta E_j^p = \frac{m_j zqV}{d},\tag{A5}$$

when using $m_j = d$ which holds for the intermediate states. For a short polymer, we have to consider only the contribution given by Eq.(5), which leads again to Eq.(A5). Eq.(6) is obtained from adding the above contributions.

APPENDIX B

For calculating ΔE_j^s , we start by writing an expression for the entropic energy that consists of two terms:

$$E_j^s = E_{j,1}^s + E_{j,2}^s. (B1)$$

 $E_{j,1}^s$ represents the entropy cost of storing m_j monomers within the TPP and is a linear function of m_j [10]. $E_{j,2}^s$ originates from the reduced number of configurations of a Gaussian polymer near an impermeable wall, and can be approximated by [8]:

$$E_{j,2}^{s} = \begin{cases} \frac{1}{2} k_{B} T ln(N_{j,trans}), & j \leq d; \\ \frac{1}{2} k_{B} T ln(N_{j,trans}N_{j,cis}), & N > j > d; \\ \frac{1}{2} k_{B} T ln(N_{j,cis}), & j \geq N. \end{cases}$$
(B2)

Separating the translocation into three regimes, described by Eqs.(1.1)-(1.3), we find that for the entrance states $\Delta E_{i,1}^s$ is given by:

$$\Delta E_{i,1}^s \propto k_B T,$$
 (B3)

while for the exit states

$$\Delta E_{i,1}^s \propto -k_B T,$$
 (B4)

with a proportional constant of o(1).

For the intermediate states $\Delta E_{j,1}^s = 0$ because the same number of monomers occupy the TPP between adjacent states. $\Delta E_{j,1}^s$ for a short polymer has the same values as for a large polymer, when adjusting the conditions for the three cases (exchanging N and d in Eqs.(1)).

Computing $\Delta E_{j,2}^s$ from Eq.(B2) results in $\frac{1}{2}k_BTg_j$, where

$$g_{j} = \begin{cases} ln(1+1/(N-j)), & j \leq d; \\ ln(1+1/(N-j))(1-1/(j-d)), & N > j > d; \\ ln(1-1/(j-d)), & j \geq N. \end{cases}$$
(B5)

For a short polymer, g_j is similar to Eq.(B5) for the entrance and exit states, but $g_j = 0$ for the intermediate states because $N_{j,cis} = N_{j,trans} = 0$ for these states. Note that $|g_j| < 1$ for all j. Special care is needed when computing g_j for states that belong to the crossover between the three situations. For these states a combination of Eqs.(B2) was used. From the above contributions we obtain Eq.(7).

APPENDIX C

To compute $\overline{\tau}$ which is given by

$$\overline{\tau} = \sum_{s=1}^{x-1} (-\mathbf{A}^{-1})_{s,x} + \sum_{s=x}^{n} (-\mathbf{A}^{-1})_{s,x},$$
 (C1)

we have to calculate the elements of the general inverse Toeplitz matrix $(\mathbf{A}^{-1})_{s,x}$ [17]:

$$(-\mathbf{A}^{-1})_{s,x} = \frac{\Delta(\lambda^s)\Delta(\lambda^{n+1-x})}{\Delta(\lambda)\Delta(\lambda^{n+1})} \frac{p_+^{x-s}}{k}; \qquad s < x, \quad (C2)$$

where $\lambda_{+/-} = [1+/-\sqrt{(1-4p_+p_-)}]/2$. Substituting the expression for p_+ and p_- into the expressions for $\lambda_{+/-}$, we obtain $\lambda_{+/-} = p_{+/-}$, which when used in Eq.(C2) results in Eq.(12). The summation of each of the terms in Eq.(C1) is straight forward. The first term yields

$$I = \alpha \sum_{s=1}^{x-1} (1 - y^s) = \alpha \left(x - \frac{1 - y^x}{1 - y}\right)$$
 (C3)

where $y = p_{-}/p_{+}$ and

$$\alpha = \frac{p_+^x \Delta(p^{n+1-x})}{\Delta(p)\Delta(p^{n+1})k}.$$
 (C4)

The second term in Eq.(C1) is:

$$II = \widetilde{\alpha} \sum_{s=x}^{n} \Delta(p^{n+1-s}) p_{-}^{s-x} = \widetilde{\alpha} p_{-}^{n+1-x} \cdot \left[y^{x-n-1} \frac{1-y^{n+1-x}}{1-y} - (n+1-x) \right],$$
 (C5)

where

$$\widetilde{\alpha} = \frac{\Delta(p^x)}{\Delta(p)\Delta(p^{n+1})k}.$$
 (C6)

Combining I and II and rearranging terms results in Eq.(13).

Rewriting Eq.(13) as

$$\overline{\tau} = \frac{x}{k\Delta(p)} - \frac{(n+1)(1-y^{-x})}{k\Delta(p)(1-y^{-n})},$$
 (C7)

we find that for $V/V_C \gtrsim 1$, the second term in Eq.(C7) vanishes as y^{n-x} . Keeping the first term in the expression for $\overline{\tau}$, Eq.(C7), and expanding to first order in V/V_C the explicit form of $\Delta(p)$

$$\frac{1}{\Delta(p)} = \frac{1 + e^{-V/V_C + 1}}{1 - e^{-V/V_C + 1}} \approx \frac{2}{V/V_C - 1}$$
 (C8)

Eq.(14) is obtained.

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