Modeling Electric-Field Induced Modulation of Ligand-Receptor Binding Kinetics Towards Adaptive MC Receivers

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***Abstract*—We present a first-principles model for electric-field-controlled DNA hybridization on biosensor surfaces based on Scheutjens-Fleer self-consistent field (SF-SCF) theory. The model derives voltage-dependent probe layer structure by solving the Edwards diffusion equation coupled with Poisson-Boltzmann electrostatics iteratively until self-consistency. Hybridization kinetics are computed via the Halperin-Buhot-Zhulina framework augmented with electrophoretic contributions. We introduce a mechanistic asymmetry wherein association is treated as nucleation-limited, while dissociation is governed by the field-dependent stability of the full duplex. The model predicts sharp transitions between hybridizing and non-hybridizing regimes, offering a theoretical foundation for adaptive MC receivers.**

***Index Terms*—DNA hybridization, self-consistent field theory, polyelectrolyte brushes, biosensors, molecular communications**

I. INTRODUCTION

Molecular communication (MC) systems encode information in signaling molecules, but a fundamental challenge lies in the fixed kinetic parameters of ligand-receptor interactions at the receiver [1]. Unlike electronic receivers with tunable gain, passive MC receivers cannot dynamically adjust their binding characteristics. This limitation manifests critically as inter-symbol interference (ISI), where molecules from previous transmissions persist at the receiver, preventing subsequent symbol detection.

Adaptive receivers with dynamically reconfigurable binding kinetics offer a solution to ISI [2], with modulation mechanisms including thermal [3], photoresponsive [4], magnetic [5], and electric field approaches. Electric field modulation is particularly suited to MC: it offers fast switching, requires no reagents, and integrates with microelectronic fabrication. Experiments confirm that applied fields modulate hybridization rates by orders of magnitude, with high-density probes exhibiting sharp transitions between hybridizing and non-hybridizing regimes [6], [7]. However, existing treatments address equilibrium thermodynamics and electrostatic barriers without deriving brush conformation self-consistently with applied voltage.

We present the first theoretical framework that couples voltage-dependent brush structure with hybridization kinetics, integrating the SF-SCF theory [8] with the Halperin-Buhot-Zhulina framework [9] and electrophoretic contributions [7] for adaptive MC receiver design.

II. MODEL FORMULATION

A. SF-SCF Theory for Polyelectrolyte Brushes

We consider ssDNA probes of N nucleotides at areal density σ_P on an electrode. Following [8], polymer volume fraction $\phi(z)$ and reduced potential $\psi(z) \equiv e\Phi/(k_B T)$ are solved self-consistently on a lattice with spacing $a \approx 0.43$ nm. The brush height H is derived as the first moment of $\phi(z)$ (computed from Edwards diffusion equation), which is coupled to the $\psi(z)$ through the Poisson-Boltzmann equation:

$$\frac{d^2\psi}{dz^2} = \kappa^2 \sinh\psi + 4\pi\ell_B \alpha\phi(z)/a^3, \tag{1}$$

where $\kappa = \sqrt{8\pi\ell_B c_s}$ is the inverse Debye length, c_s the bulk salt concentration, $\ell_B \approx 0.7$ nm the Bjerrum length, $k_B T$ the thermal energy, and α the ionization fraction (negative for DNA). The mean field is:

$$u(z)/k_B T = \chi_{PS}\phi(z) + \tfrac{1}{2}\phi^2(z) - \alpha\psi(z), \tag{2}$$

with Flory-Huggins parameter $\chi_{PS} = 0$ for good solvent. The dimensionless surface charge ratio

$$\gamma = \sigma_{\text{surface}}/(\alpha N \sigma_P), \tag{3}$$

represents electrode charge relative to brush charge. For anionic DNA ($\alpha < 0$), $\gamma < 0$ corresponds to an attractive (collapsing) field and $\gamma > 0$ to a repulsive (stretching) field.

B. Hybridization Kinetics

The kinetic landscape is governed by two competing energy contributions [7], [9]: the electrophoretic work ΔG_{ep}, which becomes favorable as the surface potential $\psi(0)$ increases, and the electrostatic brush penalty, which scales inversely with H [9], with $r_D = \kappa^{-1}$ the Debye screening length:

$$\Gamma = 8\pi N \sigma_P \ell_B r_D^2 / H. \tag{4}$$

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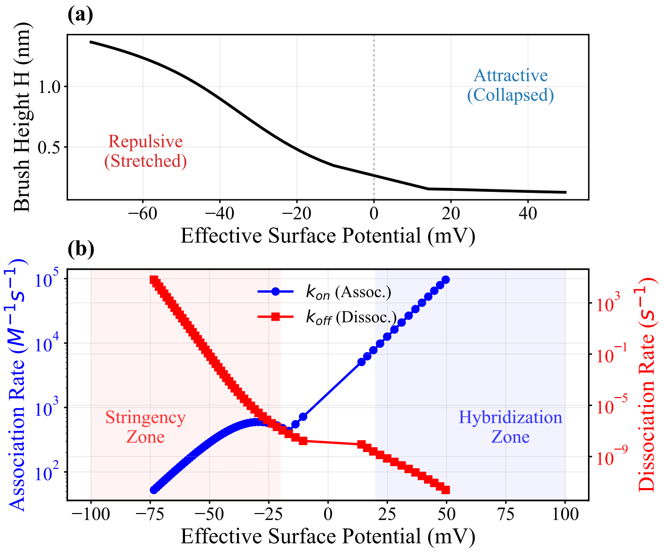

Fig. 1. (a) Brush height vs. surface potential showing conformational change. (b) Voltage-controlled k_{on} and k_{off}; the single crossover separates the Hybridization and Stringency regimes.

This creates a contradiction: attractive bias lowers ΔG_{ep} but simultaneously collapses the brush, sharply increasing Γ. The total brush penalty also includes a steric contribution:

$$\Delta G_{\text{steric}}/k_BT = N_t\left[(\tfrac{1}{2}-\chi_{PS})\bar{\phi}^2 + \tfrac{1}{3}\bar{\phi}^3\right], \quad (5)$$

where N_t is the target strand length and $\bar{\phi} = N\sigma_P a^3/H$ the average volume fraction.

We model association as a *nucleation-limited* process [10], requiring only a seed of $N_{nuc} \approx 4$ monomers to penetrate the brush. The effective association rate thus becomes:

$$k_{\text{on}} = k_{\text{react}} \exp\left[-\frac{N_{nuc}}{N}(\Gamma + \Delta G_{\text{steric}} + \Delta G_{\text{ep}})/k_BT\right], \quad (6)$$

with an intrinsic rate $k_{\text{react}} \sim 10^5\ \text{M}^{-1}\text{s}^{-1}$.

Dissociation is governed by the stability of the full helix under load. We apply the Bell–Evans model [11] using the effective charge of the entire target strand (N_t) driven by the local field $E = -d\psi/dz$ [7], such that the off-rate is given by $k_{\text{off}} = k_0 \exp(Fx_\beta/k_BT)$, where $k_0 \sim 4\times 10^{-4}\ \text{s}^{-1}$ represents the thermal breathing of the duplex, and $x_\beta \approx 0.7$ nm is the transition-state distance.

III. RESULTS AND DISCUSSION

Figure 1 shows results for 20-mer ssDNA at $I \approx 0.1$ M and $\sigma_P = 3\times 10^{12}\ \text{cm}^{-2}$. Panel (a) demonstrates conformational response: the brush extends to ∼1.4 nm under repulsive bias ($\psi(0) < 0$) and collapses below 0.2 nm under attractive bias. The gap between -12 mV and $+20$ mV corresponds to a first-order-like phase transition where stretched and collapsed conformations coexist as two free energy minima of comparable depth, preventing the self-consistent solver from settling on either state. Below $H \approx 0.43$ nm (monomer size), the continuum model breaks down, indicating a pancake regime where DNA lies flat on the electrode.

Panel (b) shows the crossover of the k_{on} and k_{off} curves, outlining two distinct operating regimes. In the *Hybridization Zone*, k_{on} approaches the diffusion limit ($\sim 10^5\ \text{M}^{-1}\text{s}^{-1}$) while dissociation is negligible ($< 10^{-10}\ \text{s}^{-1}$). In the *Stringency Zone*, the dissociation rate increases to $\sim 10^5\ \text{s}^{-1}$, enabling rapid clearing of bound targets.

This dual-regime kinetic landscape enables adaptive MC receiver operation. The orders-of-magnitude separation between k_{on} and k_{off} in each regime ensures high contrast between capture and reset states, allowing the receiver to switch between them via applied voltage. This directly targets the key performance bottlenecks in MC systems: reducing ISI and bit error rate (BER), preventing receptor saturation, and improving signal-to-interference-plus-noise ratio (SINR) relative to passive receivers with fixed binding kinetics.

IV. CONCLUSION

We presented an SF-SCF framework for voltage-controlled DNA hybridization that predicts sharp kinetic transitions consistent with experimental observations at high grafting density. The resulting dual-regime kinetic landscape provides a theoretical basis for adaptive MC receivers that mitigate ISI by alternating between capture and reset modes under time-varying channel conditions, such as varying flow rates, bit rates, or background interference. Future work will integrate this model with MC channel models for end-to-end BER analysis and validate the brush response through particle-based simulations and experimental characterization.

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