Development and Application of an Improved Model for Microfluidic Transport in Protein and DNA Separation

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The separation of DNA (deoxyribonucleic acid) and protein samples is a key step in many genomic and proteomic studies required in biology, biomedicine, disease diagnosis, drug discovery, forensic analyses and other applications. An essential process in biology of living cells is to analyze DNA, protein and RNA samples which require complicated, time consuming and labour-intensive processes in conventional labs. Traditional technologies (gel and capillary electrophoresis) are time consuming, have limited capacity, and are difficult to control the initial sample shape and volume which are influencing the separation resolution. To achieve high-resolution separation of DNA and protein sample, the use of microchips are proposed. One geometry for sample injection is a cross-linked microchannel where the sample is first focused by the carrier stream in the intersection and then pinched off with a controllable plug shape. Many parameters influence the sample plug shape and size such as channel geometry, fluid properties and operating conditions such as applied potential. Experimentally exploring controlling parameters is very expensive, therefore, modelling and numerical simulation are excellent tools for optimizing chip design and predicting effective operating conditions to precisely control the sample to ideal shape for improving separation. Moreover, there is a gap in theoretical microfluidics, although the advent of microfluidics goes back to decades ago. There has been little research done on derivation of Poisson-Boltzmann equation as a fundamental governing equation in literature. Some references covered part of the derivation of Poisson equation, but no one looked at the Boltzmann part from statistical thermodynamics approach. Therefore, derivation of Poisson-Boltzmann equation has been covered in this research in detail and a comprehensive understanding of sample transport is achieved. Then numerical simulations are conducted with the view to predicting the optimal plug shape to maximize sample separation and its resolution.