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Non-Gaussian Distribution of DNA Barcode Extension In Nanochannels Using High-throughput Imaging JULIAN SHEATS, WESLEY REINHART[1], Chemical Engineering and Materials Science, University of Minnesota, Minneapolis MN, USA, JEFF REIFENBERGER, BioNano Genomics, San Diego, CA, USA, DAMINI GUPTA, ABHIRAM MURALIDHAR, Chemical Engineering and Materials Science, University of Minnesota, Minneapolis MN, USA, HAN CAO, BioNano Genomics, San Diego, CA, USA, KEVIN DORFMAN, Chemical Engineering and Materials Science, University of Minnesota, Minneapolis MN, USA — We present experimental data for the extension of internal segments of highly confined DNA using a high-throughput experimental setup. Barcode-labeled *E. coli* genomic DNA molecules were imaged at a high areal density in square nanochannels with sizes ranging from 40 nm to 51 nm in width. Over 25,000 molecules were used to obtain more than 1,000,000 measurements for genomic distances between 2,500 bp and 100,000 bp. The distribution of extensions has positive excess kurtosis and is skew left due to weak backfolding in the channel. As a result, the two Odijk theories for the chain extension and variance bracket the experimental data. We compared to predictions of a harmonic approximation for the confinement free energy and show that it produces a substantial error in the variance. These results suggest an inherent error associated with any statistical analysis of barcoded DNA that relies on harmonic models for chain extension.

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