Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Intramolecular Fluctuation of DNA in Nanochannels via High-throughput Video Microscopy JULIAN SHEATS, Univ of Minn - Minneapolis, JEFFREY G. REIFENBERGER, HAN CAO, BioNano Genomics - San Diego, KEVIN D. DORFMAN, Univ of Minn - Minneapolis — Genome mapping is a promising technique that complements next generation sequencing. The distance between labels on barcoded DNA molecules is the main physical quantity employed by emerging nanochannel techonologies used to construct genome maps. Here we analyze time resolved data of *E. coli* DNA in a commercial nanochannel genome mapping system to obtain the probability distribution underlying the distance between labels. Improving upon a previous study of this type [1], this dynamic method avoids alignment to the reference genome, a process that is statistical in nature. The time-series analysis also allows for detection of a set of experimental artifacts present in static imaging, thereby filtering out several sources of potential systematic error. The resulting probability density remains left-skewed, supporting previous evidence. However, filtering out the artifacts resulted in a lower magnitude of skewness, which has implications for the statistical weights associated with the genome mapping algorithm.

[1]Reinhart, W. F. et al., J. Chem. Phys. **142, 064902 (2015)**

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Date submitted: 05 Nov 2015 Electronic form version 1.4