Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Mapping DNA methylation by transverse current sequencing: Reduction of noise from neighboring nucleotides JOSE ALVAREZ, Department of Physics, University of Puerto Rico, San Juan, PR 00931-3344, USA, STEVEN MASSEY, Department of Biology, University of Puerto Rico, San Juan, PR 00631-3360, USA, ALAN KALITSOV, JULIAN VELEV, Department of Physics, University of Puerto Rico, San Juan, PR 00931-3344, USA — Nanopore sequencing via transverse current has emerged as a competitive candidate for mapping DNA methylation without needed bisulfite-treatment, fluorescent tag, or PCR amplification. By eliminating the error producing amplification step, long read lengths become feasible, which greatly simplifies the assembly process and reduces the time and the cost inherent in current technologies. However, due to the large error rates of nanopore sequencing, single base resolution has not been reached. A very important source of noise is the intrinsic structural noise in the electric signature of the nucleotide arising from the influence of neighboring nucleotides. In this work we perform calculations of the tunneling current through DNA molecules in nanopores using the non-equilibrium electron transport method within an effective multi-orbital tight-binding model derived from first-principles calculations. We develop a base-calling algorithm accounting for the correlations of the current through neighboring bases, which in principle can reduce the error rate below any desired precision. Using this method we show that we can clearly distinguish DNA methylation and other base modifications based on the reading of the tunneling current.

Julian Velev
Department of Physics, University of Puerto Rico, San Juan, PR 00931-3344, USA

Date submitted: 06 Nov 2015 Electronic form version 1.4