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Elucidating the role of transcription in shaping the 3D structure of the bacterial genome¹ HUGO B. BRANDAO, Graduate Program in Biophysics, Harvard University, XINDAN WANG, Harvard Medical School, DAVID Z. RUDNER, Department of Microbiology and Immunobiology, Harvard Medical School, LEONID MIRNY, Institute for Medical Engineering and Science, Massachusetts Institute of Technology — Active transcription has been linked to several genome conformation changes in bacteria, including the recruitment of chromosomal DNA to the cell membrane and formation of nucleoid clusters. Using genomic and imaging data as input into mathematical models and polymer simulations, we sought to explore the extent to which bacterial 3D genome structure could be explained by 1D transcription tracks. Using B. subtilis as a model organism, we investigated via polymer simulations the role of loop extrusion and DNA super-coiling on the formation of interaction domains and other fine-scale features that are visible in chromosome conformation capture (Hi-C) data. We then explored the role of the condensin structural maintenance of chromosome complex on the alignment of chromosomal arms. A parameter-free transcription traffic model demonstrated that mean chromosomal arm alignment can be quantitatively explained, and the effects on arm alignment in genomically rearranged strains of B. subtilis were accurately predicted.

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