A model for the condensation of the bacterial chromosome by the partitioning protein ParB
CHASE BROEDERSZ, NED WINGREEN, Princeton University

The molecular machinery responsible for faithful segregation of the chromosome in bacteria such as Caulobacter crescentus and Bacillus subtilis includes the ParABS a.k.a. Spo0J/Soj partitioning system. In Caulobacter, prior to division, hundreds of ParB proteins bind to the DNA near the origin of replication, and localize to one pole of the cell. Subsequently, the ParB-DNA complex is translocated to the far pole by the binding and retraction of the ParA spindle-like apparatus. Remarkably, the localization of ParB proteins to specific regions of the chromosome appears to be controlled by only a few centromeric parS binding sites. Although lateral interactions between DNA-bound ParB are likely to be important for their localization, the long-range order of ParB domains on the chromosome appears to be inconsistent with a picture in which protein-protein interactions are limited to neighboring DNA-bound proteins. We developed a coarse-grained Brownian dynamics model that allows for lateral and 3D protein-protein interactions among bound ParB proteins. Our model shows how such interactions can condense and organize the DNA spatially, and can control the localization and the long-range order of the DNA-bound proteins.

Chase Broedersz
Princeton University

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