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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.

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