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Forward convolution approach to reconstructing 3D bacterial cell shape reveals MreB localizes based on geometric cues BENJAMIN BRATTON, RANDY MORGENSTEIN, ZEMER GITAI, JOSHUA SHAEVITZ, Princeton Univ — Over the past few years we have developed an image-processing framework that allows us to extract precise 3D shapes of bacterial cells from fluorescence microscopy data. This approach, using active meshes, minimizes the difference between an observed Z-stack and model shapes that have been convolved with the experimental point spread function. From these xyz coordinates, we calculate geometric parameters such as local curvatures, surface areas, and the relative enrichment of fluorescent signals. This method generates reconstructions for a variety of bacterial sizes and shapes including rods, vibriods and spiral bacteria. As one example case for a particular fluorescent signal, we have been studying the localization of the bacterial actin homolog, MreB. Along with our previous work on the cell shape role of MreB polymers [Ouzounov et al., BiophysJ 2016] and MreB rotation [Morgenstein et al., PNAS 2015], here we show in straight and curved rod bacteria that MreB localizes based on local Gaussian curvature. This curvature localizing mechanism helps ensure rod-like growth of the cell and helps prevent branching. Gaussian curvature is the product of the two principal curvatures, something which can only be measured using a fully three dimensional notion of cell shape. Using MreB point mutants that have altered curvature sensitivities, we are testing the hypothesis that cells straighten deformations by patterning growth at the proper geometry.

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