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Correlating cell morphology and stochastic gene expression using fluorescence spectroscopy and GPU-enabled image analysis DOUGLAS SHEPHERD, EVAN SHAPIRO, Department of Physics, University of Colorado Denver, Denver, CO 80217, EVAN PERILLO, Department of Biomedical Engineering, University of Texas at Austin, Austin, TX 78712, JAMES WERNER, Center for Integrated Nanotechnologies, Los Alamos National Laboratory, Los Alamos, NM 87544 — Biological processes at the microscopic level appear stochastic, requiring precise measurement and analytical techniques to determine the nature of the underlying regulatory networks. Single-molecule, single-cell studies of gene expression have provided insights into how cells respond to external stimuli. Recent work has suggested that macroscopic cell properties, such as cell morphology, are correlated with gene expression. Here we present single-cell studies of a signal-activated gene network: Interleukin 4 (IL4) RNA production in rat basophil leukemia (RBL) cells during the allergic response. We fluorescently label individual IL4 RNA transcripts in populations of RBL cells, subject to varying external stimuli. A custom super-resolution microscope is used to measure the number of fluorescent labeled IL4 transcripts in populations of RBL cells on a cell-by-cell basis. To test the hypothesis that cell morphology is connected genotype, we analyze white light images of RBL cells and cross-reference cell morphology with IL4 RNA levels. We find that the activation of RBL cells, determined by white-light imaging, is well correlated with IL4 mRNA expression.

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