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***Abstract*—Genetically identical cells express their genes at different labels and respond differently to changes in their environment. Large-scale microscopy-based experiments are needed to characterize the dynamics of such cell-to-cell variability as well as the phenotypic diversity in response to perturbations in growth conditions. The rich data from image-based experiments requires robust and efficient analysis. In this work, we analyze bacterial cells growing in monolayers in a microfluidic device. Individual cells are identified using a novel curvature based approach and tracked over time for several generations. The resulting tracks are thereafter assessed and sorted based on track quality to reduce errors in subsequent analysis of bacterial growth rates. The proposed method performs better than the state-of-the-art methods for segmenting phase contrast and fluorescent images, and we show a 10-fold increase in analysis speed.**

***Index Terms*—IEEEtran, journal, LaTeX, paper, template.**

I. Introduction

LIVE cell experiments pave the way to understand the complex biological functions of living organisms. Many live cell experiments require monitoring of cells under different conditions over several generations. Isogenic cells display cell-to-cell variability even when grown under similar conditions [1]. To study the origin and consequences of such variation it is necessary to monitor many individual cells for extended periods of time to reach statistically verifiable conclusions [2]. Time-lapse experiments usually generate large quantities of data, which become extremely difficult for human observers to evaluate in an unbiased way [3]. Thus, automated systems are necessary to analyze such datasets in order to to reach robust and reproducible results.

Time-lapse imaging of growing bacterial cells are important both to answer fundamental biological questions related to the bacterial cell cycle as well as to study response to changes in growth condition due to changes in nutrients or antibiotics. Based on the growth conditions and imaging modalities, various automated image segmentation and tracking packages have been created. MicrobeTracker [4] was designed to segment phase contrast images and detect fluorescent spots in a parallel fluorescent channel. Schnitzcells was specifically designed to analyze fluorescent time-lapse images of E. coli grown on agarose [5], and MAMLE [6] was also designed to analyze E. coli from phase contrast and fluorescent images.

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II. Conclusion

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Appendix A
Proof of the First Zonklar Equation

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Appendix B

Appendix two text goes here.

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