

**NATIONAL AND KAPODISTRIAN UNIVERSITY OF ATHENS
SCHOOL OF SCIENCES
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Athanasios D. Balomenos

Bacterial image analysis based on time-lapse microscopy

Abstract

Time-lapse microscopy technologies now enable detailed data generation on dynamic cellular processes at the single cell level. Recent studies have highlighted the use and importance of this technology for investigating biological noise in the dynamics of gene regulation, competence pathways, and aspects of cell growth and proliferation, among other areas. Mathematical and statistical models are of growing interest in describing and testing hypothesis for such systems and rely on extraction of data from time-lapse microscopy imaging techniques that generate sequences of individual, pixel based image frames. It is undeniable fact that time-lapse microscopy is an essential tool enables systems and synthetic biologists to analyze single cell features and gene expressions dynamics of single cells. However, the analysis of such data is very time-consuming and prone to errors since it is essentially performed by human-user. Here, we address the problem in a multi-resolution image analysis framework.

In this Master's thesis, we developed a methodology identifying the boundaries of cells and tracking them over time (bacterial segmentation and lineage construction) even in formed microbial communities where there is great difficulty in identifying individual cells. The automated pipeline combines from image processing to machine learning techniques for bacterial segmentation and frame to frame cell tracking.

The proposed pipeline was tested and evaluated with two different image datasets and several still images. The results seem to be very promising. Great effort was given so as to evaluate thoroughly the proposed method and expand its capability to deal with as many as possible kinds of imaging modalities, i.e. phase contrast, bright field, and fluorescent and microscopy types, i.e. optical and confocal. We illustrate the robustness and the reliability of the proposed pipeline regardless of the image modality. The developed methodology is fully automated and matches the high-throughput prerequisites.

SUBJECT AREA: Image Processing and Machine Learning

KEYWORDS: bacterial image segmentation, cell counting, cell lineage construction, cell feature extraction and visualization, expectation maximization.