Detecting and Tracking Hard-to-Detect Bacteria in Dense Porous Backgrounds

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JUNE 18-22, 2023 CVPR VANCOUVER, CANADA

KGML Knowledge-guided Machine Learning

Overview

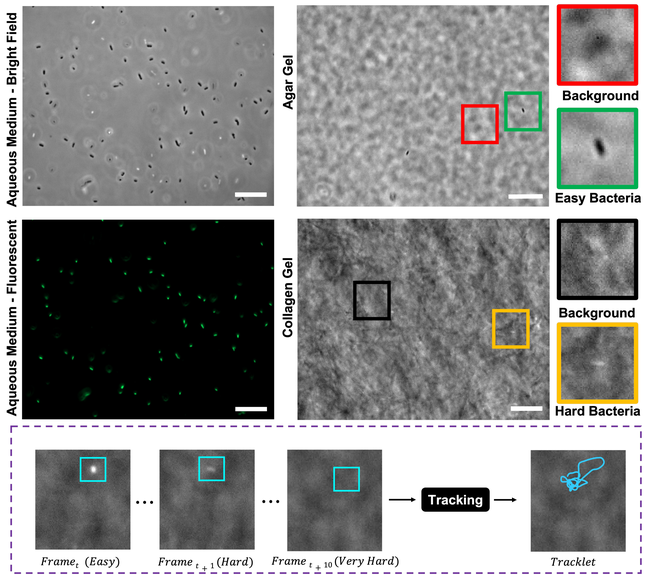
Goal: To track bacteria in complex environments such as polysaccharides (agar) or protein (collagen) hydrogels.

Motivation

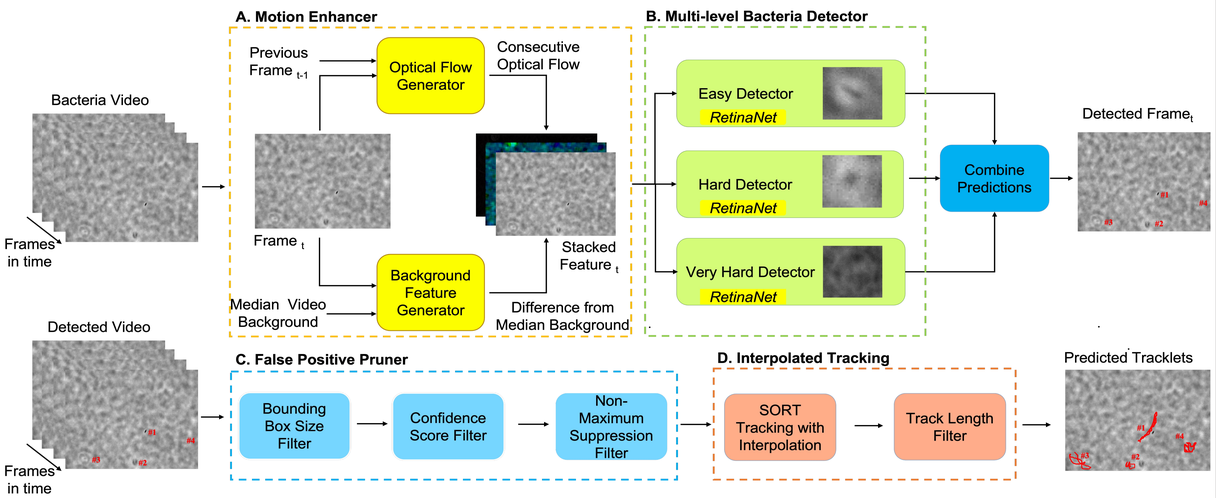
- Bacteria tracking is crucial for understanding the motile behavior of bacteria in ecological and biomedical settings
- Previous works have performed bacteria tracking using fluorescent images or in aqueous medium
- High motility speed of bacteria (10s μm/s) necessitates high frame rate imaging that is not possible with fluorescent images and only feasible using bright-field imaging
- Agar and collagen resemble more realistic settings inside the human body than aqueous media

Challenges

- Bacteria and hydrogel background look very similar and are hard to distinguish from each other
- 2D imaging misses out-of-plane motion of bacteria, resulting in some bacteria getting out of focus.
- Bacteria move as random walk, making it difficult to extract predictive motion features



Proposed Approach: Multi-level Motion Enhanced Tracker (MMET)



A: Motion Enhancer

- **Optical Flow Features:** Adds an estimate of motion of objects in video
- Lucas-Kanade method for Optical Flow computation:

$$\partial I_x u + \partial I_y v + \partial I_t = 0$$

where u and v are the optical flow vectors

- **Median Deviation Features:** Represents the difference between the pixel intensity and the typical background intensity.
- We define MDF as follows:

$$\Delta I = |I^t - \text{median}(I^{1:T})|$$

we assume that the median intensity corresponds to the background media

B: Multi-level Bacteria Detector

- Visibility patterns and detection requirements change with bacteria category, making single-level methods fail
- We train multi-level bacteria detectors for each bacteria category

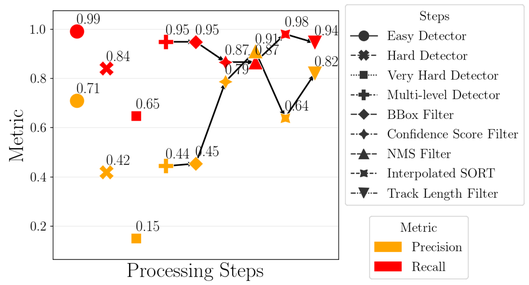
D: Interpolated Tracking

- We improve the SORT algorithm by interpolating for missing detections using predictions from the Kalman-filters of SORT algorithm
- It improves overall recall of our proposed pipeline

C: False Positive Pruner

- The Bounding Box Size filter removes all bacteria predictions having an area bigger than 30x30 pixels. Average bacteria size is 22x22 pixels
- The Confidence Score filter only considers predictions with a confidence score greater than 30%
- The NMS filter only keeps only the prediction with the highest confidence score. A duplicate prediction has an IOU match of 70% or more.

Results



Model	Task	Agar		Collagen	
		Precision	Recall	Precision	Recall
NM-MT	Detection	0.17	0.90	0.17	0.66
MMT	Detection	0.14	**0.98**	0.24	0.80
MMET (ours)	Detection	**0.45**	0.95	**0.27**	**0.82**
MMT	Tracking	0.05	**1.0**	0.14	**0.88**
MMT + FPP	Tracking	0.63	0.94	0.35	0.80
MMET (ours)	Tracking	**0.82**	0.94	**0.51**	0.81

- Precision significantly increases after the FPP module with a marginal drop in recall
- The Interpolated SORT module further boosts the recall

We compare our approach against two single model object detectors:

(1) No Motion Monolithic Tracker (NM-MT) - trained only on images

(2) Motion-based Monolithic Tracker (MMT) - trained on our motion enhanced features.

Conclusion

- We present a pipeline for detecting and tracking bacteria in complex environments such as agar and collagen hydrogels
- Our results demonstrate that the proposed pipeline can predict even hard-to-detect bacteria. Specifically, we achieve a precision of 0.82 and recall of 0.94 on Agar

Future Work

- Ground truth bacteria moving close by are restricted by the NMS Filter to be predicted correctly. Hence, the False Positive Pruner can be further improved to group duplicate tracks in crowded settings
- Deep learning-based tracking methods can be explored for improved tracking instead of using SORT
- Learning fine-grained labels of bacteria (easy/medium/hard) without additional supervision can be explored since generating fine grained annotations is manually tedious
- Detected bacteria trajectories can be used to train trajectory forecasting algorithms that predict bacteria movement based on bacteria characteristics, environment textures, and time.

Acknowledgement: We acknowledge the support of the National Science Foundation (NSF) under Grants IIS-2107332, CBET CAREER-1454226 and CBET-2133739, and the 4-VA Grant at Virginia Tech which provided funding for this research.