LCuts: Linear Clustering of Bacteria using Recursive Graph Cuts

Jie Wang, Tamal Batabyal, Mingxing Zhang, Ji Zhang, Arslan Aziz, Andreas Gahlmann, Scott T. Acton

Department of Electrical and Computer Engineering & Department of Chemistry, University of Virginia, Charlottesville, USA

Introduction

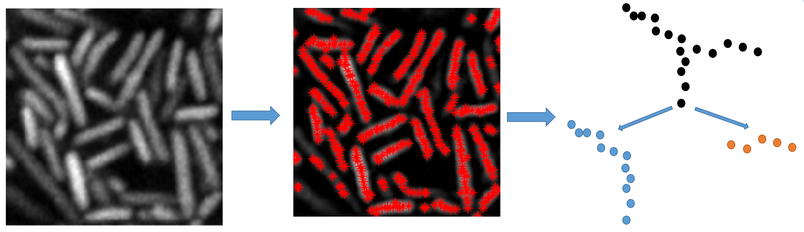
Challenges: Bacterial biofilm segmentation poses significant challenges due to lack of apparent structure, poor imaging resolution, limited contrast between conterminous cells and high density of cells that overlap.

Proposed method: A graph-based data clustering method, LCuts, is presented with the application on bacterial cell segmentation. The method assists in the assessment of several facets, such as bacterium tracking, cluster growth, and mapping of migration patterns of bacterial biofilms.

Highlights

Our approach is built on the following insight:

- Even though the raw image data does not show distinct boundaries in intensity between densely packed cells…
- We are still able to reliably compute local intensity maxima that delineate the central axis of each cell.
- Then we partition based on the approximate co-linearity of points.



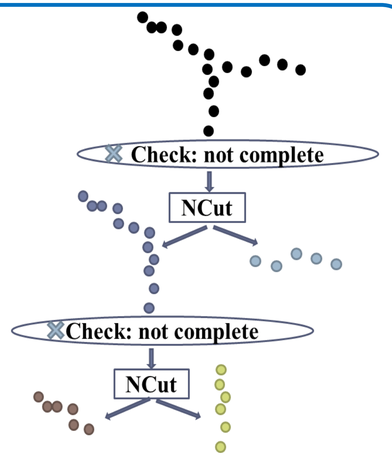
Original image | Find local maxima | Recursive partition

LCuts

Part 1: Graph Construction

Part 2: Compute the bi-partition solution

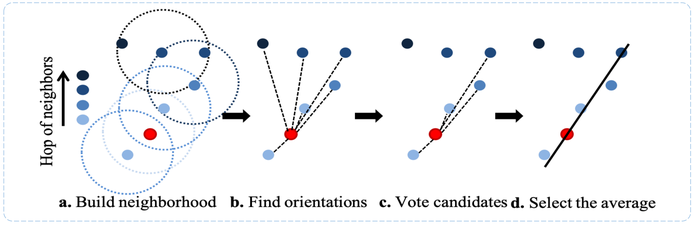
Part 3: Recursively re-partition until the stopping criterion is satisfied



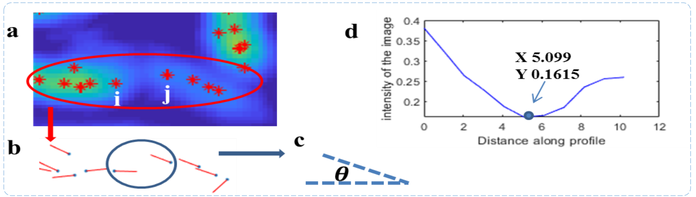
- ***Graph Construction***

Graph = node + edges + weights

- Node features: location & direction (via majority voting)



- Edges with weights: adjacency matrix

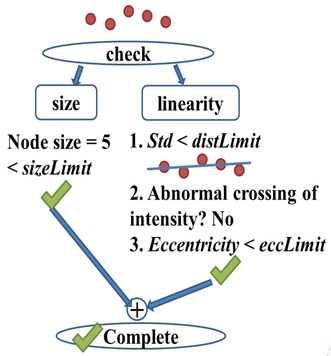


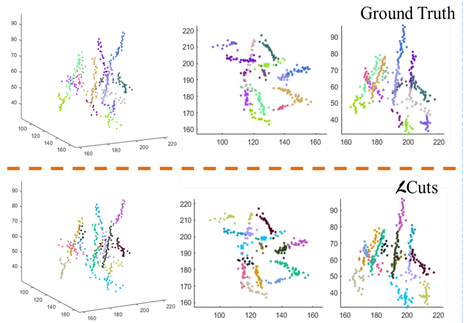
$$w_{ij} = w_{distance} \cdot w_{direction} \cdot w_{intensity}$$

$$w_{distance} = e^{-D_{ij}^2/\sigma_D^2} \qquad w_{direction} = e^{-(\cos(\theta)-1)^2/\sigma_T^2}$$

$$w_{intensity} = \min I_{i \to j} \quad \text{(if less than thresh)}$$

- ***Stopping Criterion***

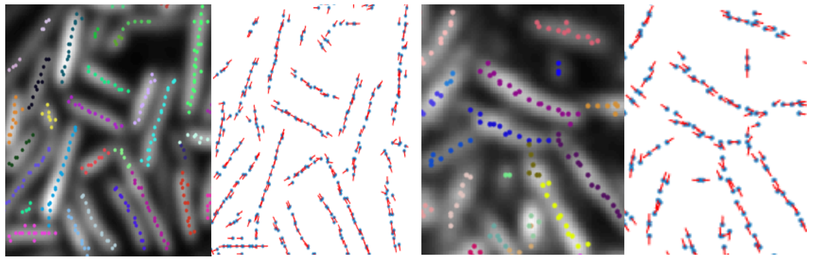




- Preliminary 3D results

Results

- 2D results with corresponding node direction feature



Conclusion

A graph-based solution, LCuts, is introduced to find the linear structures that identify individual bacteria in the biofilm, which is:

- Automated
- Adaptive to multi-dimensional spaces
- Independent of the number of bacteria present
- Provide informatics: positions, orientations, …

Advanced 3D version of LCuts will be available soon. Thanks!