GrapHiC: Graph-Based Hierarchical Clustering for SMLM

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Single-Molecule Localization Microscopy (SMLM)

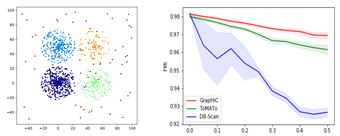
- Popular technique in super-resolution microscopy (10-20 nm)
- SMLM data:
  - A list of localized points $\mathbf{p}_m = (x_m, y_m), m = 1, \dots, M$
  - (optional) uncertainty σ_m and photon count N_m
- Common limitations of the existing clustering methods for SMLM:
  - Shape prior: e.g. objects of the same size.
  - Noise prior: e.g. uniform noise
- Hierarchical clustering: Obtaining information at different scales.

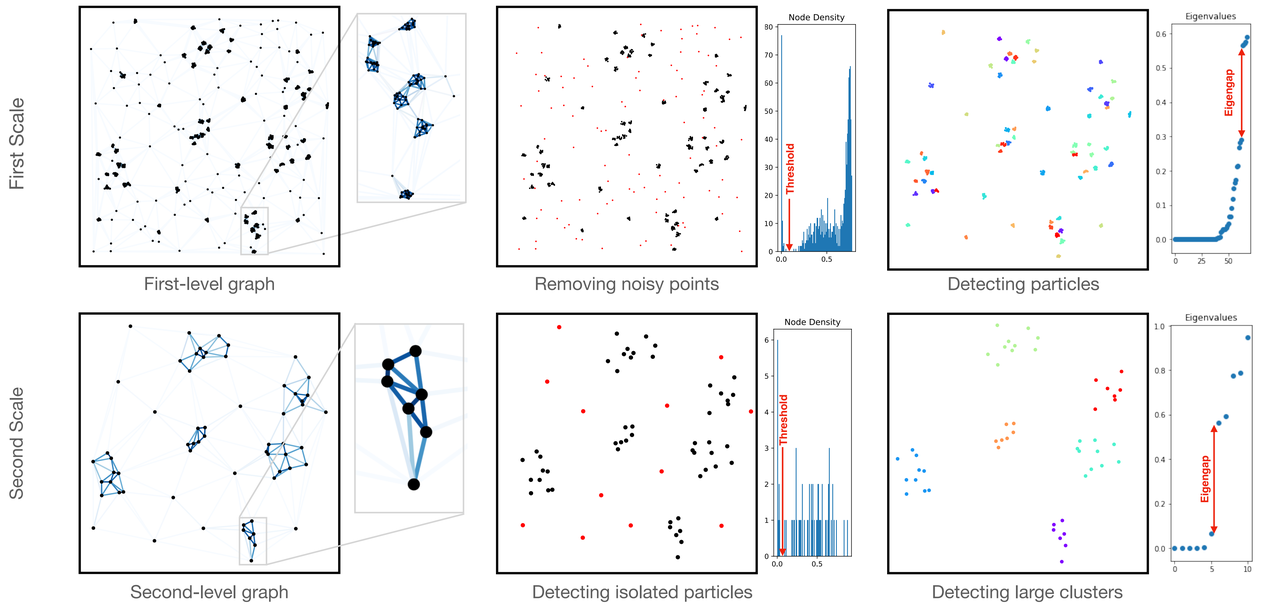
Method Summary

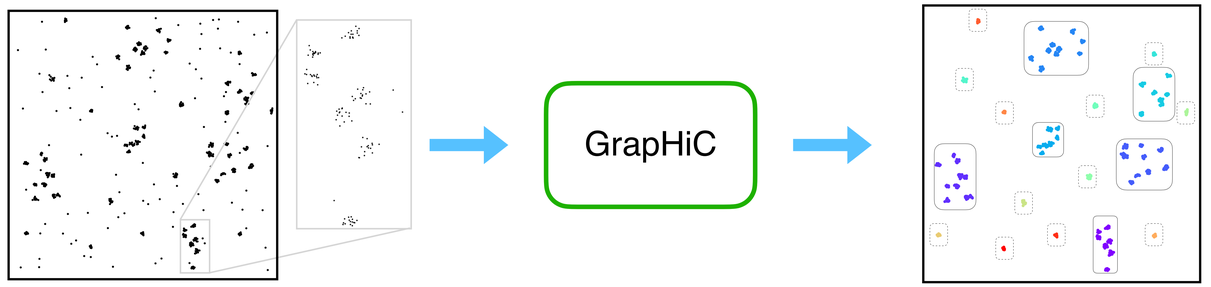
1. Graph construction
   - Vertices: $v_m = (\mathcal{N}(\mathbf{p}_m, \mathbf{\Sigma}_m), N_m)$
   - Connectivity pattern: Delaunay triangulation
   - Weights: $w(v_m, v_n) = \exp\left(-\frac{d(v_m, v_n)}{2\sigma_s^2}\right)$
     - $d(\cdot, \cdot)$: metric between probability distributions
     - σ_s: costumized parameter
2. Preprocessing: detection of the isolated nodes
   - Density associated to node v_m: $\rho_m = \frac{\sum_n w_{m,n}}{|\{n: w_{m,n} \neq 0\}|}$
   - Removing isolated nodes by applying a threshold on ρ_m
3. Spectral clustering
   - Estimating the number of clusters
     $\Rightarrow$ Finding the eigengap of the Laplacian matrix
   - Applying K-means on the first K eigenvectors.
4. Assign to each cluster C, a pair $(\mathcal{N}(\mathbf{p}_C, \mathbf{\Sigma}_C), N_C)$ and go to step 1.

Quantitative Comparison

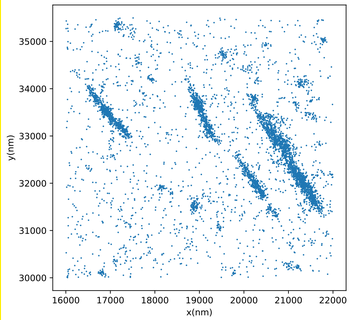
- Synthetic data
- $n_k = 500 \times (1-q)^{k-1}$
- q: varying parameter.
- Comparison metric
  $\text{FMI} = \frac{\text{TP}}{\sqrt{(\text{TP}+\text{FP}) \times (\text{TP}+\text{FN})}}$

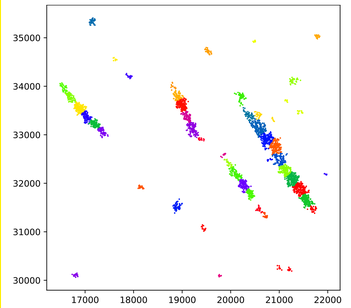


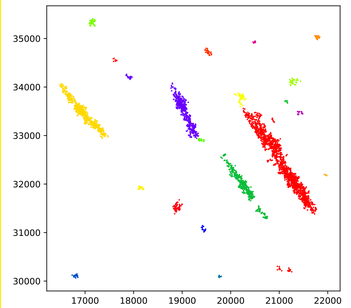




Real Data







Source: H. Deschout, I. Platzman, D. Sage, L. Feletti, J. P. Spatz, and A. Radenovic, "Investigating focal adhesion substructures by localization microscopy," *Biophysical Journal*, vol. 113, no. 11, pp. 2508–2518, 2017.