

Graph Denoising for Molecular Imaging

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Outline

- Molecular Imaging Methods
- 2 Graphs & Manifolds
- 3 GAT-Denoiser
- 4 Results on LoDoPaB-CT dataset
- 5 Summary & Future Work
- 6 Questions

Signal-to-noise-ration (SNR)

Reconstruction

SNR is a measure, which compares the power of an input signal to the power of the undesired noise.

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Cryo-Electron Microscopy (Cryo-EM)

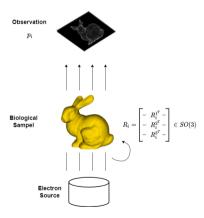
- Enables observation of molecules in near atomic resolution.
- > Major motivation for Thesis.
- During freezing, molecules rotate randomly.
- > Frozen molecules are fragile, electron microscope needs to work with low power.
- Observations can be reconstructed to 3D model.

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Only single particle cryo-EM is considered.

Cryo-EM



Cryo-EM

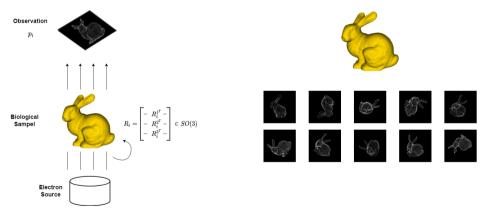


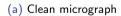
Figure: Cryo-EM overview

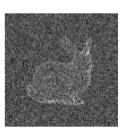
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Cryo-EM challenges

- > High-noise level
- Unknown rotation during freezing
- > (Structural variety of observations)





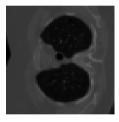


(b) Noisy micrograph

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Computed Tomography (CT)

- Related to cryo-EM
- Can be seen as a simpler version in 2D
- Good to start with towards a cryo-EM algorithm



(a) Biological sampel



(b) clean Sinogram

Observation

Observation

$$y = p + \eta$$

$$y_i = (A(x, \theta_i))$$

$$y_i[j] = p_i[j] + \eta_i[j] \quad \text{with } 1 \le i \le N, 1 \le j \le M$$

$$(1)$$

- > v: noisy observation
- > p: noiseless observation
- η : noise, assumed $\eta_i \sim \mathcal{N}(0, \sigma^2)$
- θ_i : observation angle

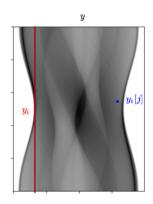
- > N: number of observations
- > M: observation dimension
- $A: L^2(\Omega) \to \mathbb{R}^M, x \mapsto A(x; \theta_i)$:
 - a non-linear operator

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Observation - Computed Tomography



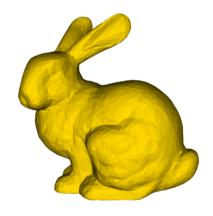
(a) Biological Sample



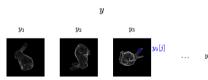
(b) CT Observation - sinogram

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Observation - Cryo-EM



(a) Biological Sample



(b) Cryo-EM Observation - micrographs

Reconstruction

Reconstruction

Recon:
$$\mathbb{R}^{M \times N} \to \mathbb{R}^{M \times M}$$

 $y \mapsto Recon(y; \theta)$ (2)





 $Recon(p, \theta) \approx x$ $Recon(p, \theta) \not\approx x$

(a) Reconstruction clean: (b) Reconstruction noisy:

Problem and Goal

Problem

p not observable directly only y is observable.

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Goal

$$denoiser: (p_i + \eta) \mapsto y_i^* \approx y_i$$

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denoiser :
$$(p_i + \eta) \mapsto y_i^* \approx y_i$$

$$Recon(denoiser(y; \theta)) \approx x$$

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Graph - Definitions

Graph Definition

A graph is defined as $G = \langle V, E \rangle$, where V is a set of nodes and E is a set of edges.

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A graph is defined as $G = \langle V, E \rangle$, where V is a set of nodes and E is a set of edges.

Nodes

 $(n_1, n_2, \dots) \in \mathbb{R}^F$, with F as node feature dimensions.

Edges

Edges are defined as a set of tuples (i, j), where i and j determine the index of the nodes.

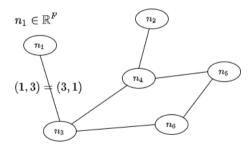


Figure: Sample graph

Graph - Definitions - Adjacency Matrix

Adjacency Matrix

The binary adjacency matrix of graph $G = \langle V, E \rangle$ is defined as:

$$A_{ij} = \begin{cases} 1 & \text{if } (i,j) \in E \\ 0, & \text{otherwise} \end{cases}$$
 (3)

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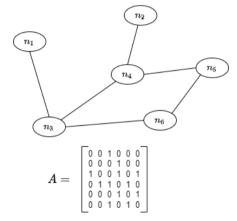


Figure: Sample graph

Graph - Definitions - Degree

Degree of a node

The *degree* of a node is defined as the number of (incoming) edges.

Degree Matrix of Graph G

Is a diagonal matrix with degree of nodes as entries.

$$D_{ii} = degree(n_i)$$

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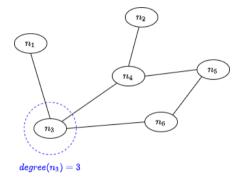


Figure: Sample graph

Graph for Molecular Imaging Observation

- > Nodes: Single observation y_i
- Edges: Use k-nearest neighbours (k-NN) to construct a graph
- > Define similarity measure:

Graph for Molecular Imaging Observation

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- Edges: Use k-nearest neighbours (k-NN) to construct a graph
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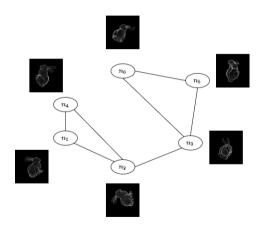


Figure: Sample graph for cryo-EM observation

Graph Laplacian (GL)

- > What can we use this graph for?
- Coifman, Shkolnisky, et al. 2008 used it to approximate angles:

Low-dimensional Embedding

- 1. Construct a k-NN graph from observations.
- 2. Calculate L = D A
- 3. Get 2nd and 3rd smallest eigenvalue with corresponding eigenvectors.

Lowdimensional Embedding

some notes and show clean embedding

Unknown angles

Show reconstruction with calculated angles

High-noise domain

Show graph Show embedding Show reconstruction

Graph Denoising

Graph denoising is the task, to estimate a denoised graph \tilde{G} from a given noisy graph G_0 , with underlying original graph G:

Definition (Graph Denoising)

$$GD: G_0 \mapsto \tilde{G} \approx G,$$

where G_0 , \tilde{G} , G denotes noisy, estimated denoised and original graph respectively.

Traditional Denoising

BM3D Non-local means

Our Approach

BM3D Non-local means

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Recap

Recap what we saw so far, define fixed angles

Big Picture

GAT-Denoiser: GNN Pipeline

Input Graph

how we defined our input graph.

Graph Attention Network - GAT

GAT, straight to the point

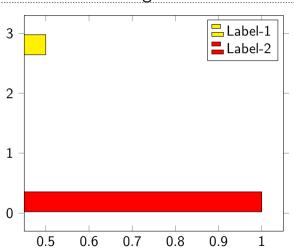
Expectation from components

expections from convolution,

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Some result testing



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