Pre-class assignment 5: CryoEM

Read the following two papers and answer relevant questions.

1. 《RECONSTRUCTING CONTINUOUS DISTRIBUTIONS OF 3D PROTEIN STRUCTURE FROM CRYO-EM IMAGES》

   a. **Image Formation Model**

   Cryo-EM aims to recover a structure of interest $V : \mathbb{R}^3 \to \mathbb{R}$, consisting of an electron density at each point in space based on a collection of noisy image $X_1, \ldots, X_n$ produced by projecting (i.e. integrating) the volume in an unknown orientation along the imaging axis.

   The noisy image X can be formed by the process described by the equation

   $$X(r_x, r_y) = g * \int_{\mathbb{R}} V(R^T \mathbf{r} + t) dr_z + \mathcal{N} \qquad \mathbf{r} = (r_x, r_y, r_z)^T$$

   - Please briefly explain the forward formation process corresponding to the above equation. (Explain symbol notions at first)

   b. **Pose Inference**

   - Pose estimation for Cryo-EM is critical and not trivial. How does this paper handle such problems, please briefly explain it.

2. 《Topaz-Denoise: general deep denoising models for cryoEM and cryoET》

   - Topaz divides frames into **odd/even** two parts (A/B) of equal amount. considering the following two alternatives:

     ○ How about dividing them evenly but **randomly**?

     ○ How about **taking the first half as part A and the second half as part B**?

   What are potential drawbacks if doing so? (Hint: You may not find perfectly matching lines in the paper. You can consider perspectives from dose and sampling intervals.)