

CryoSphere: SO(3)-equivariant method for cryo-EM pose estimation

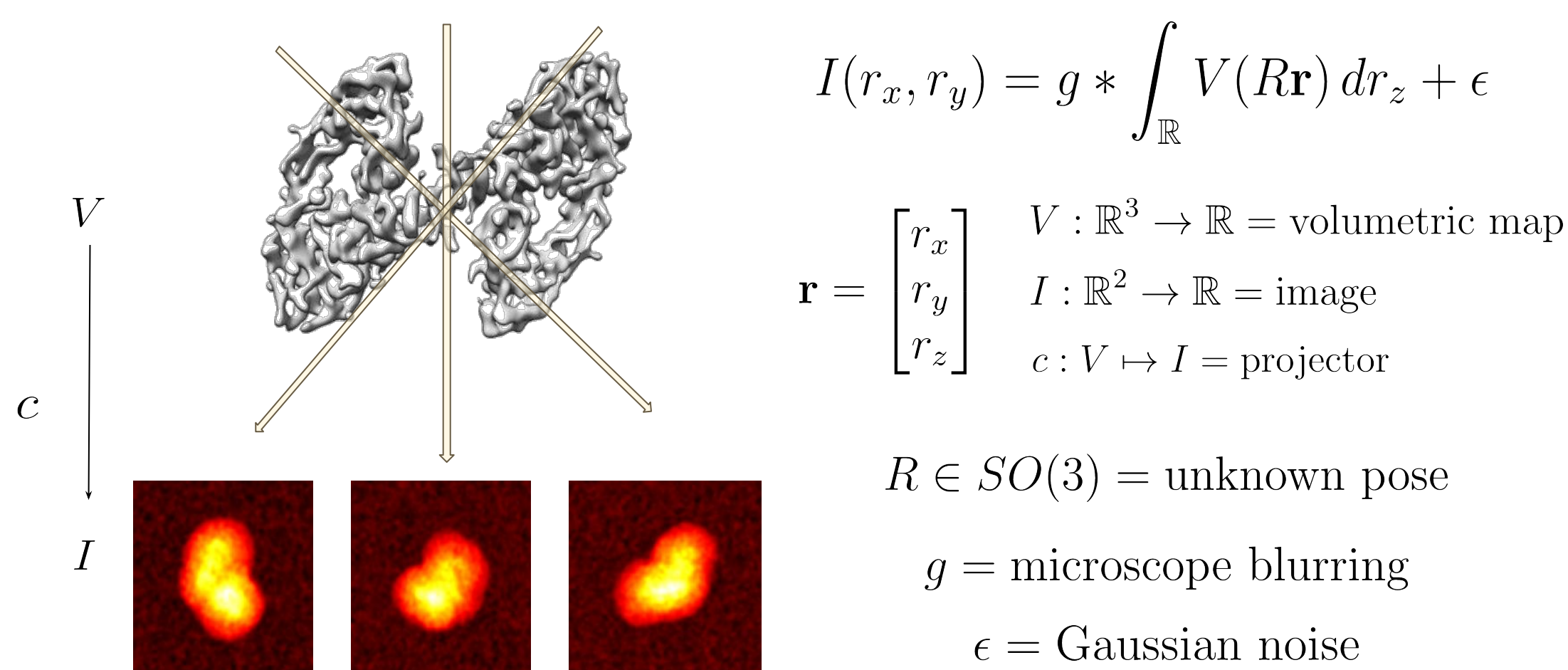
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Introduction

- Cryo-EM is the state-of-the-art technique to determine the 3D structure of proteins at high resolution
- The output of a single cryo-EM run is 10^4 to 10^7 noisy projection images, all taken from unknown random orientations
- Here, we focus on the task of **3D pose estimation of protein electron density volume from projection images** to investigate the following:

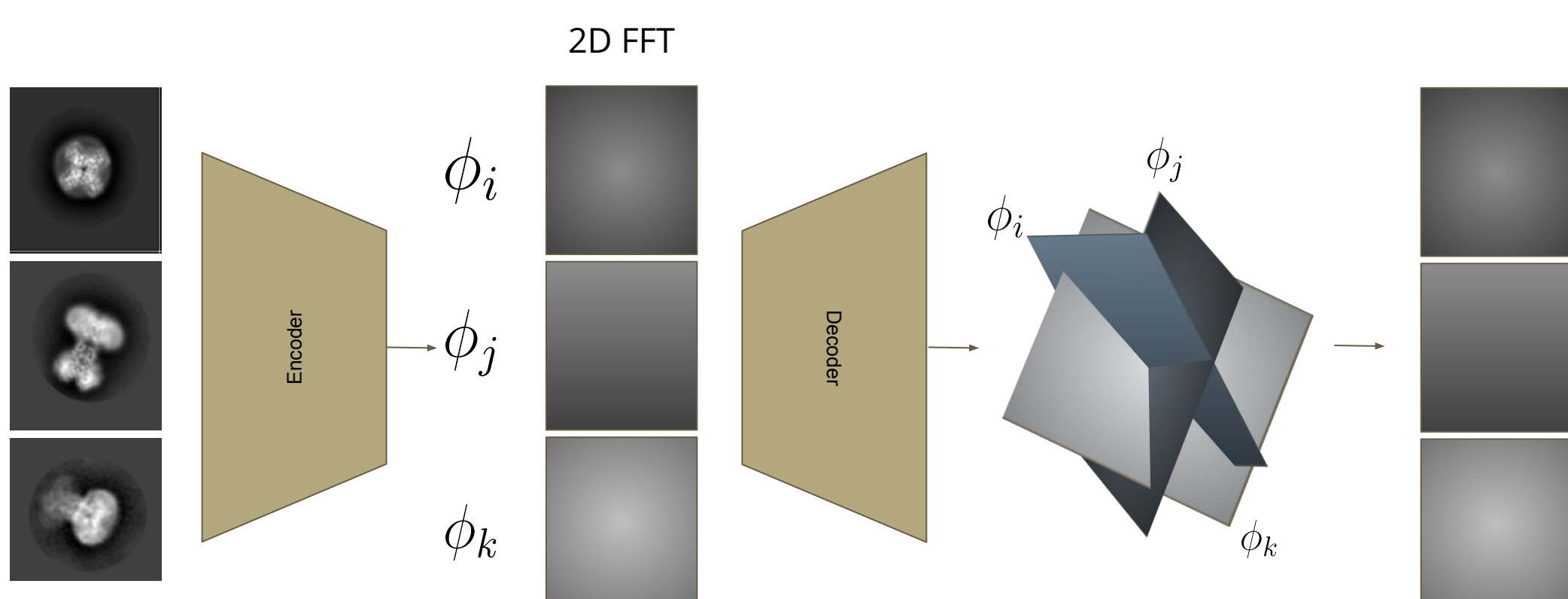
Can we reconstruct protein structure using fewer projection images by exploiting symmetries?

- The homogenous, single-particle setting treats a protein as volumetric map V , and projection operator c maps V to image I



Related Work

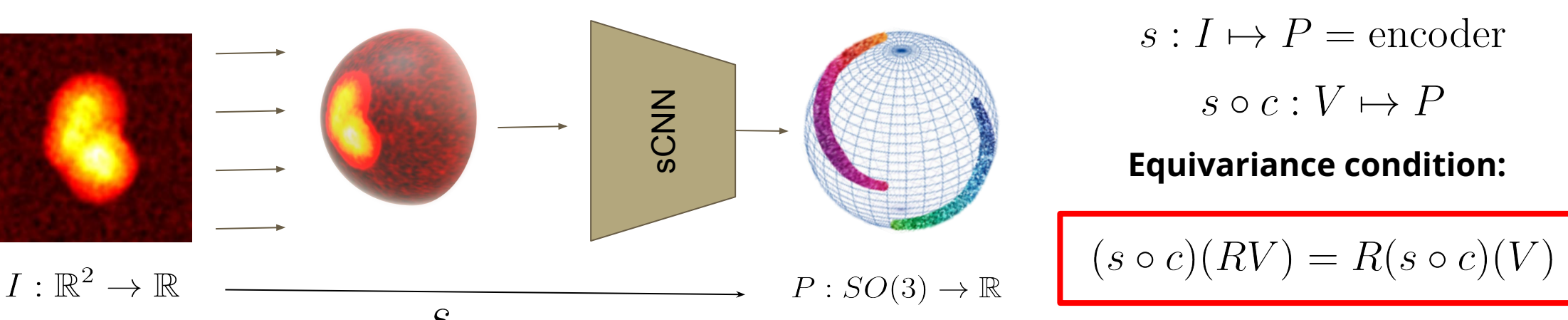
- Current state-of-the-art is **CryoFIRE** which employs an image-to-pose encoder and pose-to-slice decoder, reconstructing the 3D volume using Fourier Slice Theorem
- The model is trained using a symmetric loss between projections of the 3D model at predicted orientations and ground truth projections



- Notably, CryoFIRE predicts a single orientation for every projection image, but we aim to instead learn a more complex representation of pose from each image
- The representation we learn is a probability distribution over orientations in $SO(3)$, as done in prior work **Image2Sphere**
- Image2Sphere exploits 3D object symmetry for pose prediction by projecting images onto a half-sphere and performing spherical convolutions
- The model is trained in a supervised manner using cross entropy loss, inspiring our training protocol

Background & Workflow

- Our general workflow involves projecting input images onto a half-sphere and training a spherical convolutional neural network to predict a probability distribution over $SO(3)$
- Similar to previous work, our encoder is **approximately SO(3) equivariant**



- At inference time, the sCNN encoder is used to predict a probability distribution for each input image which can be used for reconstruction with Fourier Slice Theorem
- Fundamentally, cryo-EM images are highly noisy and the proteins we aim to learn symmetries on are complex, requiring specific modifications to the training regime

Methods

Data & Label Generation

Model Building

Model Training

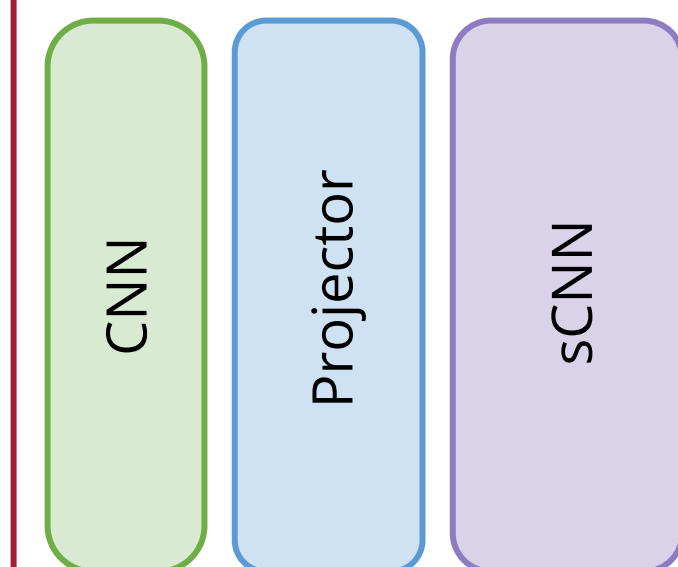
Synthetic Images

- Using ground truth 3D electron density map (from PDB), performed orthographic projection from n orientations
- Added Gaussian noise and blur

Training Labels

- For each data point, initialized a grid over $SO(3)$ with bin width 15 degrees
- Each grid cell contains MSE with respect to ground truth image from that pose
- Generated binary mask over spherical grid where 1 represents the largest 5% of $1/\text{MSE}$ values

Architecture



- Featurized 2D projection image with 2 Conv2d layers and ReLU activation
- Project featurization onto half-sphere using depthwise convolution
- Learned spherical signal over $SO(3)$ with S2 convolution, $SO(3)$ activation, and $SO(3)$ convolution

Loss Function

- Used a Binary Cross Entropy Loss between the predicted probability map and ground truth
- Ground truth probability mask generated by

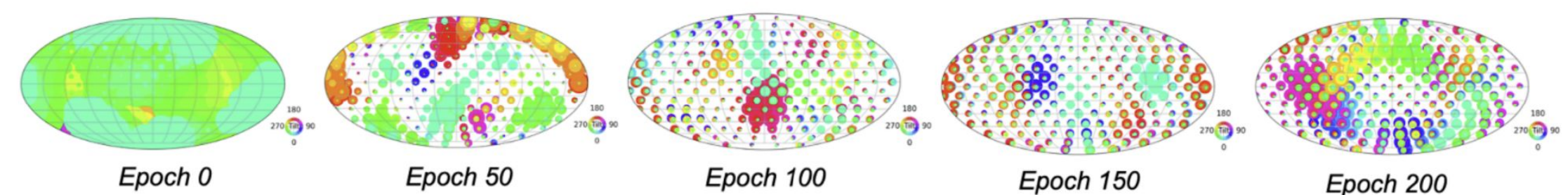
$$\Pr[R | I] = e^{-\lambda \text{MSE}(I, c(RV))}^2$$

- before bitmasking
- λ tuned to produce separation between similar and dissimilar poses to encourage learning of symmetries

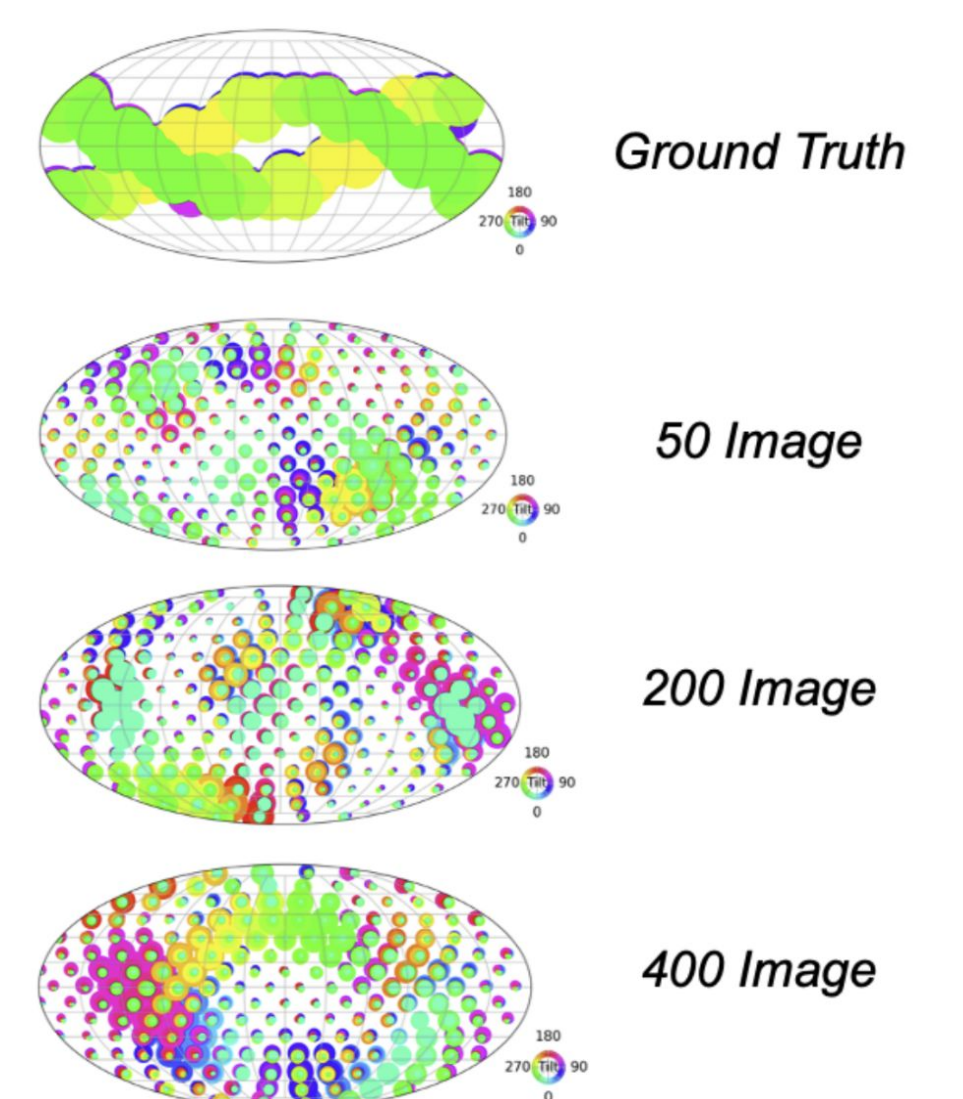
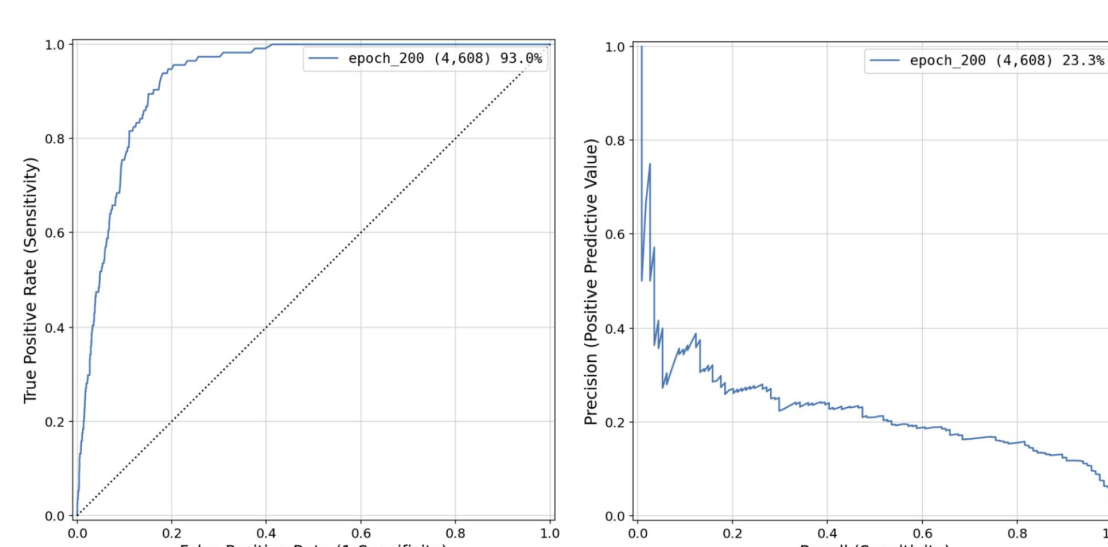
Hyperparameters

- Model trained for 200 epochs with learning rate of 0.001
- Spherical equivariant layers use $\text{Imax} = 4$

Experiments



- We trained the model using different numbers of projections (50 to 400)
- The model trained on 400 images for 200 epochs learns the training data and generalizes best
- We quantitatively tested for equivariance, and given that both mean and maximum MSE is considerably lower with our model predictions, our model learns an approximately equivariant function



	Mean	Min	Max
Our Model	.0050	.0024	.0075
Random Baseline	.0074	.0025	.0144

MSE on equivariance tests

Conclusions

- Equivariant methods can be used to learn protein symmetries from 2D images, as captured by the relation between rotations before imaging and rotations across the probability map
- Although learning against a ground truth probability map is unstable, this can be rectified by using binary masks with carefully chosen thresholds

Limitations & Future Work

- Synthetic projection images may provide biased benchmarks; difficult to test on real cryo-EM data (petabytes of storage)
- May not generalize to proteins with symmetries not seen during training
- Integrate pose model with reconstruction using Fourier Slice Theorem
- Increase the resolution used for both images and the spherical CNN to improve the granularity of predicted probability maps and (eventually) reconstruction

References

- [1] **CryoFIRE**: Levy, A. & Wetzstein, G. & Martel, J. & Poitevin, F. & Zhong, E. (2022). Amortized Inference for Heterogeneous Reconstruction in Cryo-EM. *Neural Information Processing Systems*.
- [2] **Image2Sphere**: Klee, D. & Biza, O. & Platt, R. & Walters, R. (2023). Image to Sphere: Learning Equivariant Features for Efficient Pose Prediction. *International Conference on Learning Representations*.