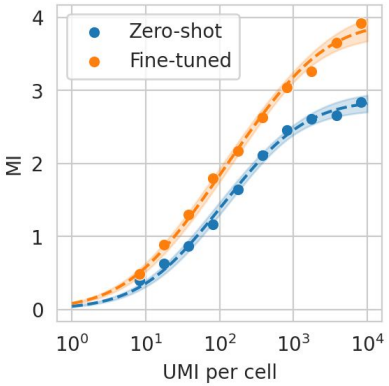
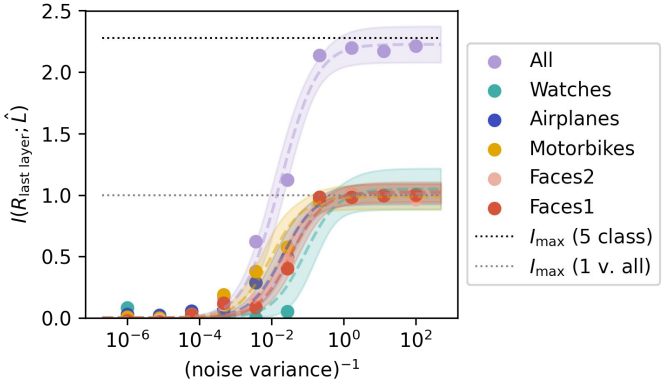
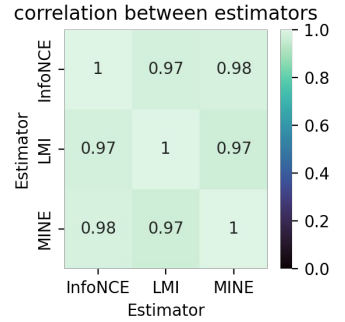


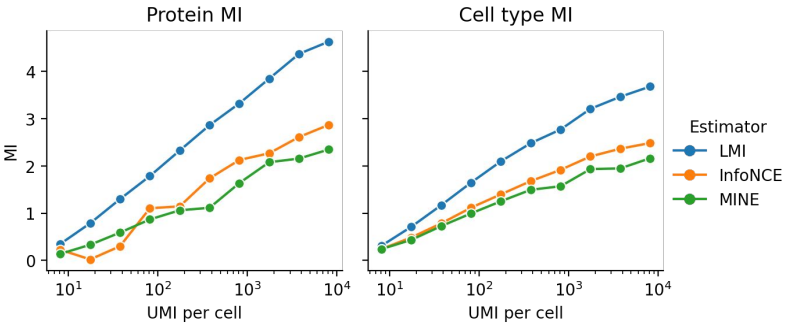
Rebuttal Figure 1. Noise-scaling of pretrained Geneformer's protein MI with UMI per cell in PBMC CITE-seq data, in the fine-tuned and zero-shot setting. The model is fine-tuned with respect to cell type annotations. Fine-tuning is done using the Helical API (Helical, 2024). Dotted line shows fit to Eqn. 2.



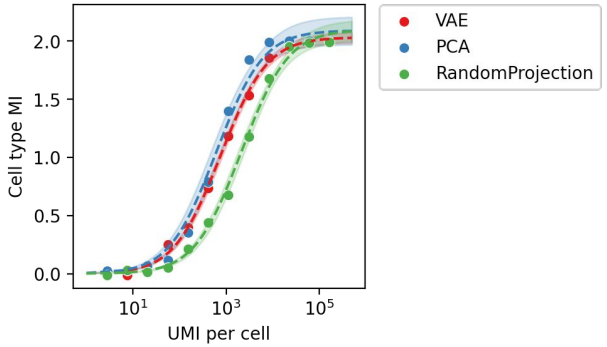
RF2. Noise-scaling of 90M parameter ViT's label MI, with additive Gaussian noise. The model is pretrained on ImageNet1k (weights distributed by PyTorch) and fine-tuned on (noisy) Caltech101. Dotted line shows fit to Eqn. 2.



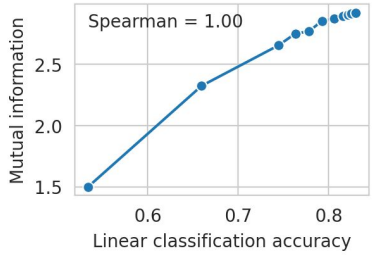
RF3. Pearson correlation between MI estimators for VAE noise-scaling on PBMC CITE-seq dataset.



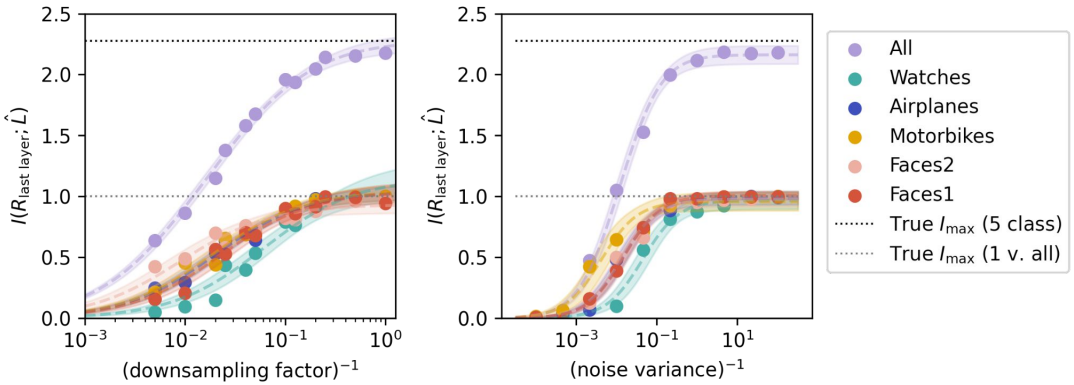
RF4. MI estimates from different estimators for VAE noise-scaling experiments on PBMC CITE-seq datasets.



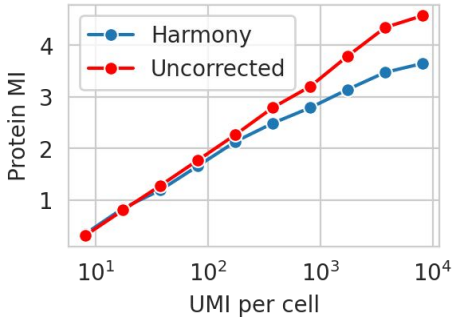
RF5. Noise scaling analysis on Splatter-generated data where cells are sampled uniformly from 4 distinct ground-truth cell type with maximal information of 2 bits.



RF6. Relationship between MNIST autoencoder representation label MI and classification accuracy. Model is sampled at 10 different points during training.



RF7. Re-analysis of Mobilenetv2 models trained in Figure 5. Here, MI is estimated using last layer representations from the model rather than the quantized predicted label. Dotted curves show fit to Eqn. 2.



RF8. Noise scaling curves for VAEs trained on PBMC CITE-seq dataset, with and without Harmony batch correction. Original dataset consists of 8 distinct donors.