Denoising High Density Gene Expression in Whole Mouse Brain Images

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Highlights

- Image Analysis of gene expression data in model animals is key to understanding the distribution of cell types in their brains.
- High density cellular/nuclear gene expression affects registration accuracy via the pixel intensity of the anatomical features in downsampled images.
- We propose to use a deep neural network with adversarial loss for denoising the gene expression to improve the registration accuracy.

Background

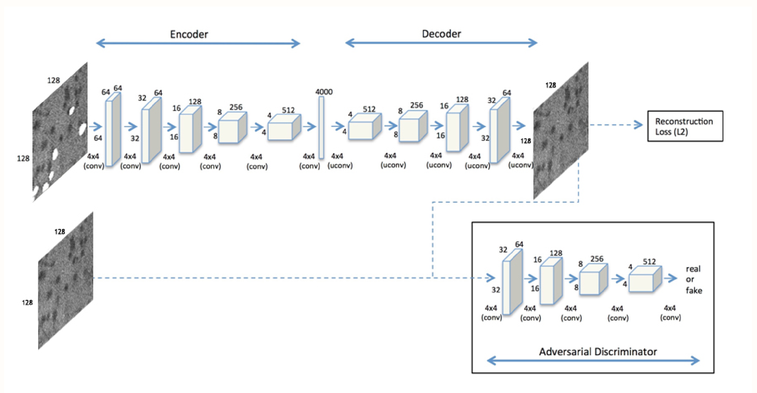


Figure 1: Context encoder [1] by Pathak et al., uses adversarial training for block image inpainting.

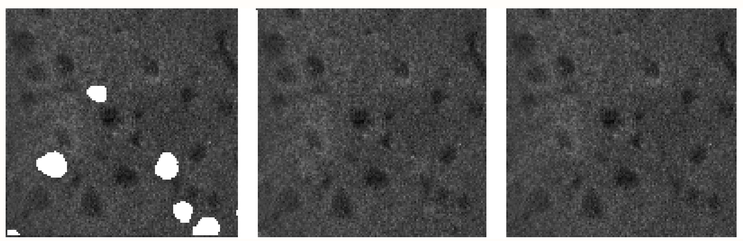


Figure 2: From left: input image with expression masked, network output and groundtruth

Pipeline

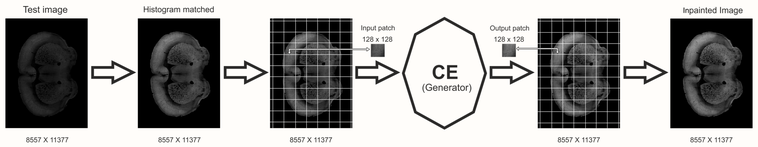


Figure 3: Pipeline with context encoder for expressiong denoising

- During training we use 128*128 image patches from zero expression dataset and 128*128 masks from high expression dataset
- During testing we use image and its correponding masks, inpaint patchwise and restitch back to get full resolution image.

Results

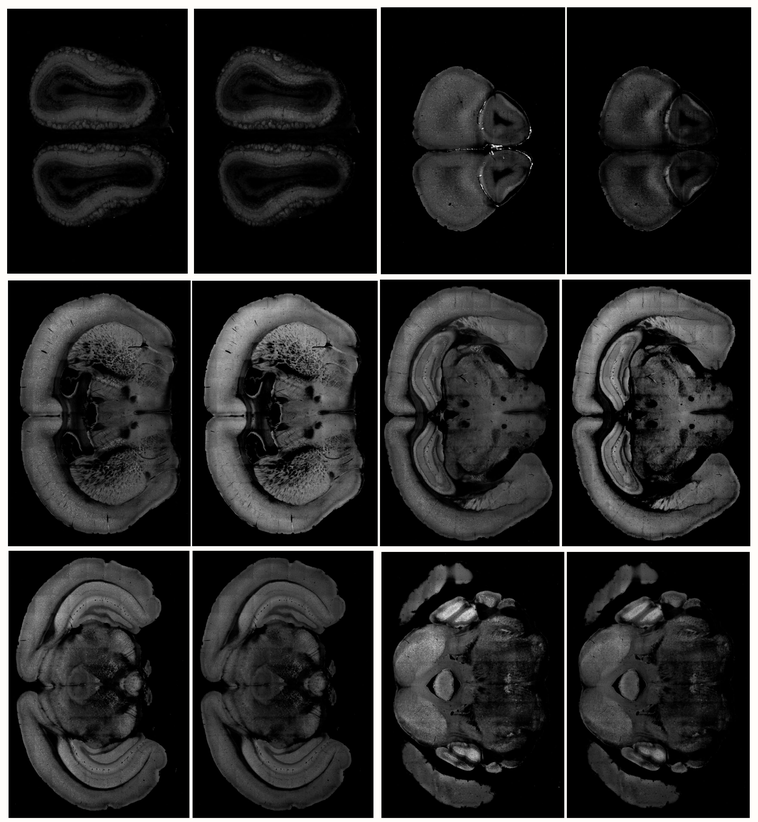
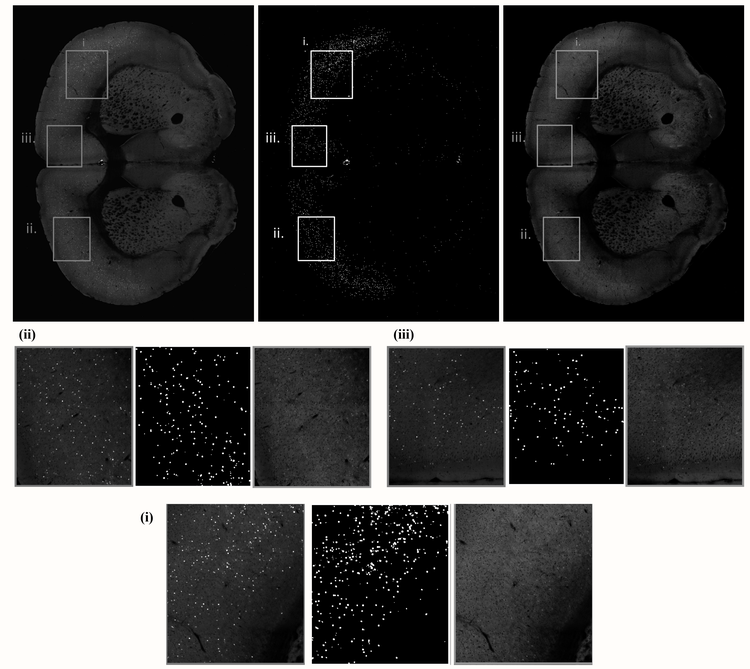


Figure 4: Inpainting slices at different depth. In every pair, left is input image and right is the output from network.



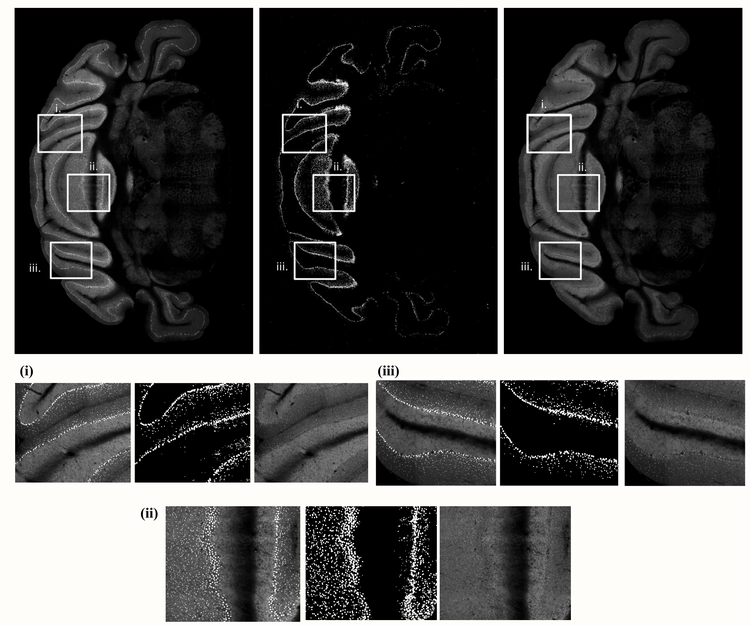


Figure 5: Inpainting slices, from left, input with expression, mask, inpainted output

References

[1] Pathak, Deepak et al. "Context encoders: Feature learning by inpainting", *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition*. 2016.

Society for Neuroscience, 11-15 Nov 2017,Washington, USA