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Stacks of Gold: Utilizing GANs to Enhance 3D Microscopy Imaging Data

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Abstract: Confocal microscopy, a pivotal tool in biomedical research, offers detailed 3D visualizations of living cells, providing insights into their spatial morphology, interactions, and life cycle progression. Fluorescence (FL) microscopy images are of high quality; however, they require expensive and toxic FL labeling to be captured. We focus on extracting detailed 3D information from easy-to-perform but low-quality bright-field (BF) images via BF-to-FL translation and enhancing the quality of 3D FL microscopy images through deconvolution, denoising, and deblurring.

Bright-field to Fluorescence Translation

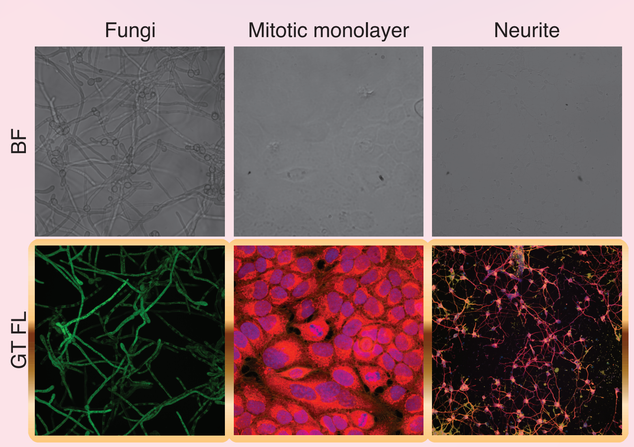

Figure 2. Mean and max projections of the corresponding BF and ground-truth (GT) FL images from three datasets.

Fungi, Mitotic monolayer, and Neurite datasets

We tested CycleGAN, Pix2Pix, and Vox2Vox GANs on the fungi data, revealing that the **Vox2Vox** model is best-suited for the task.

The mitotic monolayer and neurite datasets featured multi-channel FL signals, which were combined into a single FL image for model training.

We adopted a two-stage training approach for processing the neurite data.

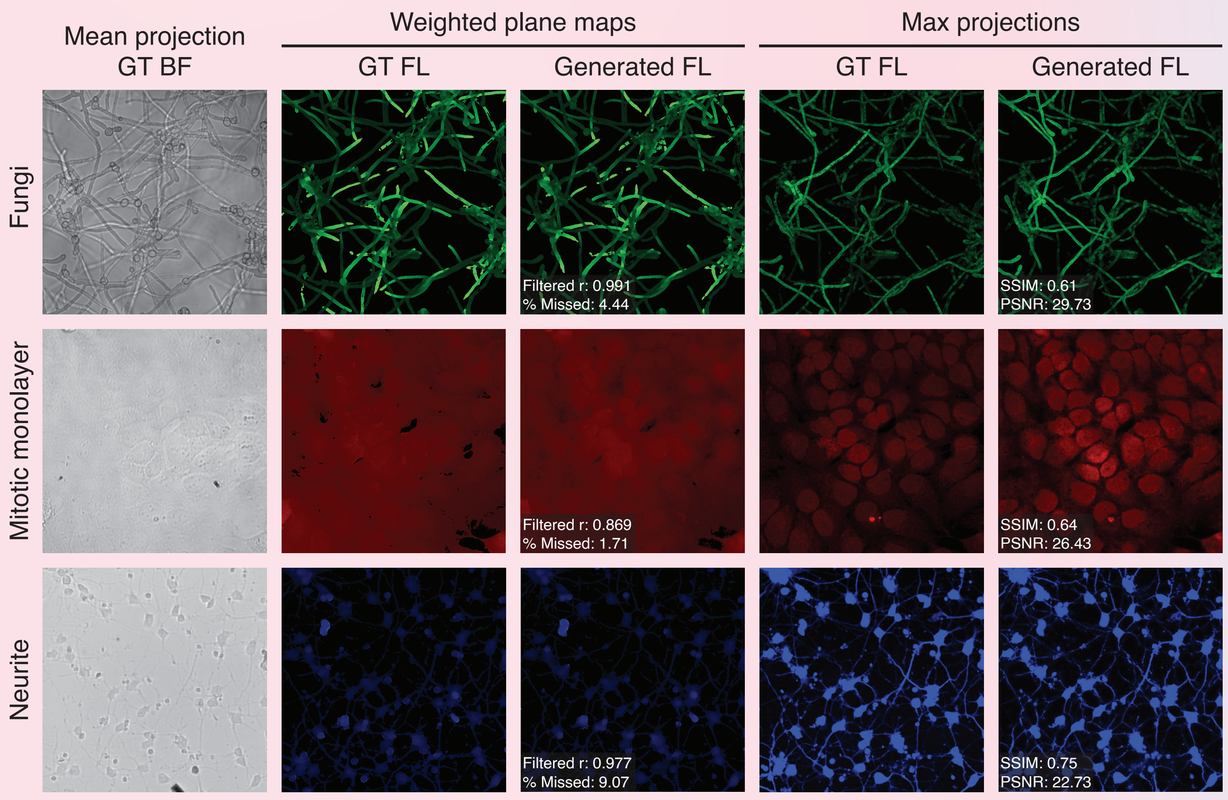

Figure 3. Projections and weighted plane maps of the GT FL and generated samples across three datasets. The plane maps provide insight into the FL signal distribution in the depth dimension. The model performs well in all cases, generaing images highly similar to the GT FL images.

Tumor dataset

Tumor data required significant preprocessing: segmentation-based cropping, registration, and the FL deblurring model application. These steps were essential for achieving satisfactory BF-to-FL translation performance.

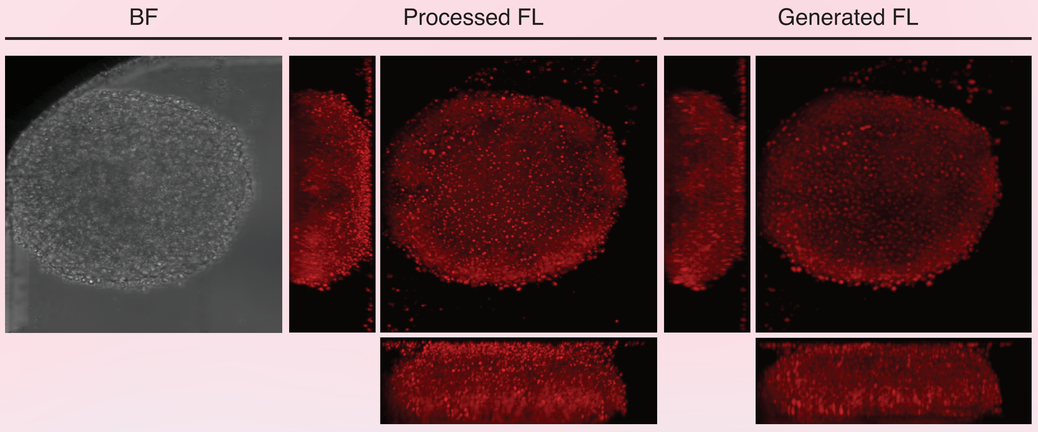

Figure 4. *xy*, *zy*, and *xz* projections of the tumor data. The generated FL signal appears similar to the processed FL data.

Acknowledgement

I am grateful to the Biomedical Computer Vision research group and all its members for their support and valuable insights. Special thanks to my supervisor, Dmytro Fishman, and Kaupo Palo from Revvity for their invaluable expertise and our fruitful discussions. I also thank Revvity for providing the data and continuing their involvement in the project, as well as the Institute of Computer Science High-Performance Computing Center for providing the computing resources.
This work would not be possible without them.

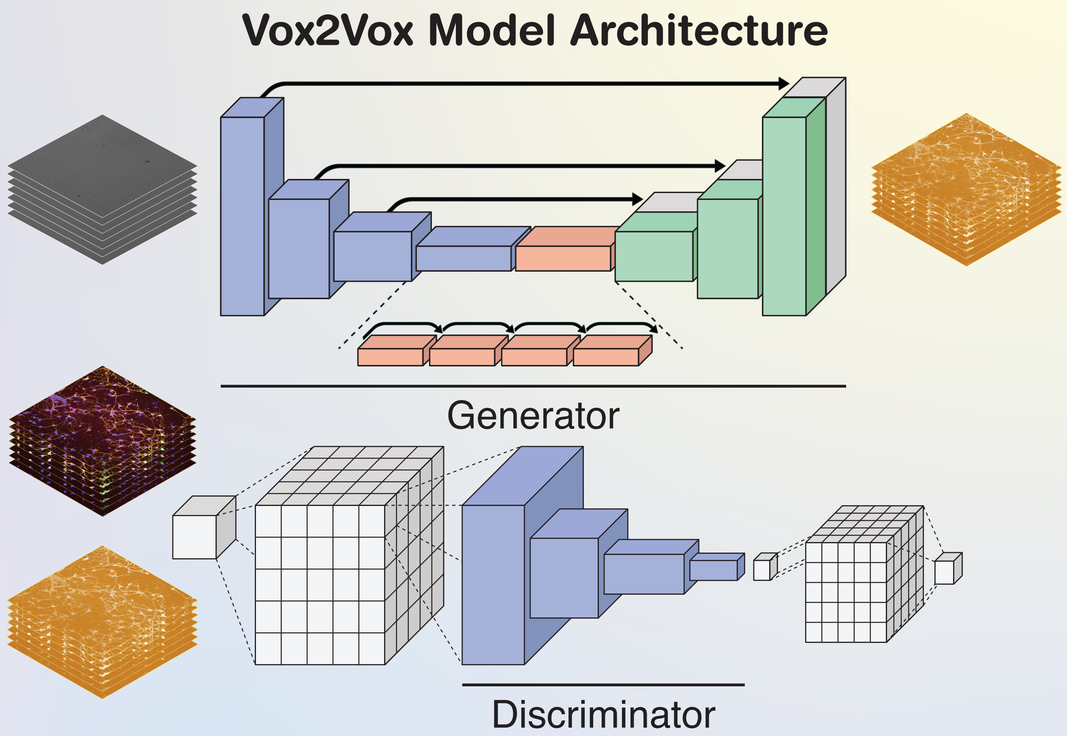

Figure 1. Vox2Vox model has proven to work best in the biomedical image translation setting. It features a 3D U-Net-based generator and a 3D PatchGAN discriminator.

Fluorescence Image Enhancement

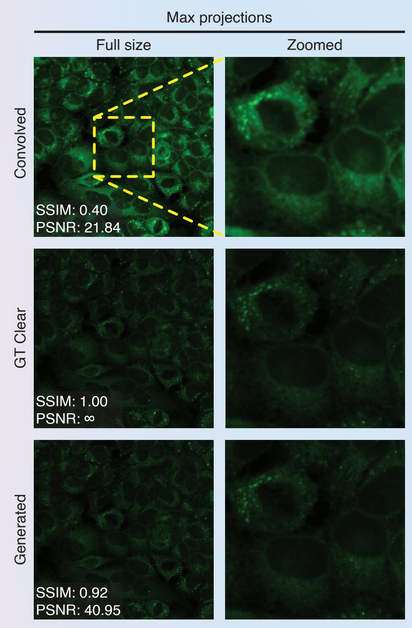

Figure 5. Mitotic monolayer deconvolution.

Mitotic monolayer dataset

We created a synthetic deconvolution dataset using a single FL channel from the mitotic monolayer dataset. Input images were convolved with a point spread function (PSF) to emulate the naturally occurring blurring. Aslo, we added a combination of Gaussian and salt-and-pepper noise to the images.

Cyst and Tumor datasets

We were provided with two small supervised deblurring datasets of cyst and tumor data. These datasets were cleaned using a proprietary semi-automated algorithm.

We observed that the trained deblurring models are high-performing and robust. We used the tumor deblurring model during the downstream preprocessing of the tumor dataset for the BF-to-FL translation task.

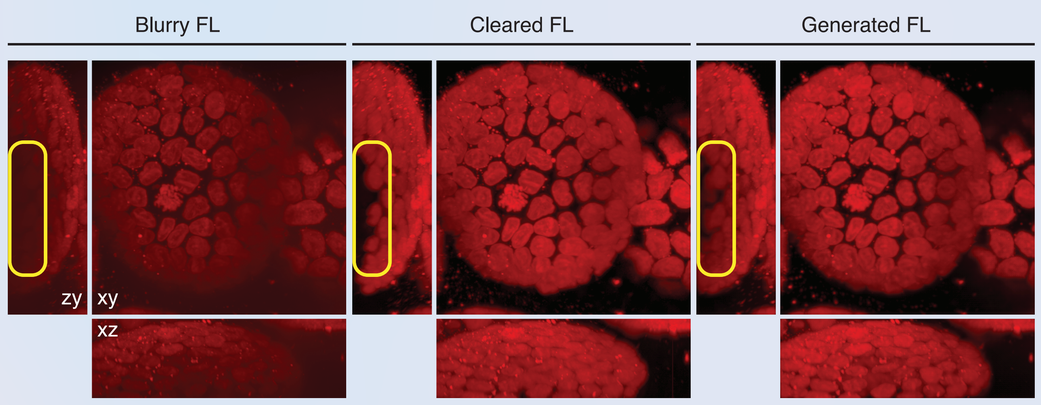

Figure 6. *xy*, *zy*, and *xz* projections of the cyst data. We can observe that the model recovered cells that were missed during the preparation of the supervised dataset, proving its robustness.

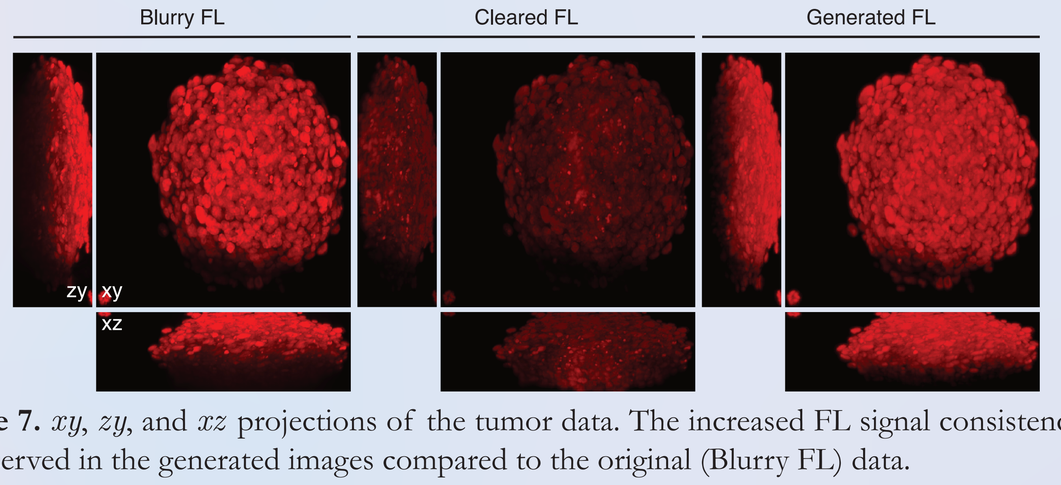

Figure 7. *xy*, *zy*, and *xz* projections of the tumor data. The increased FL signal consistency can be observed in the generated images compared to the original (Blurry FL) data.

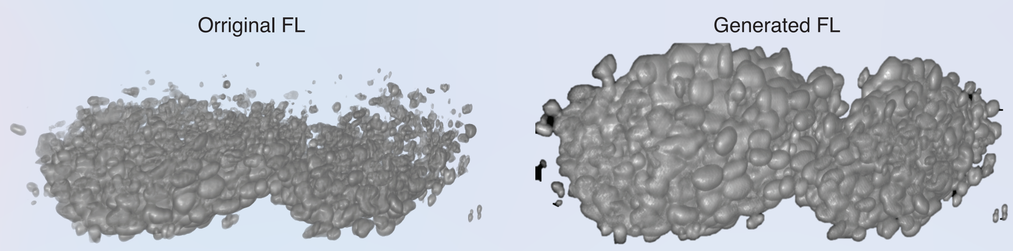

Figure 8. 3D reconstructions of the tumor data. We can observe significant signal recovery in the top layers of the generated images compared to the original data.

Conclusion

We demonstrated significant potential for GAN incorporation into a microscopy image processing workflow. The selected Vox2Vox model was proven to be robust and capable of generating high-quality images in both BF-to-FL translation and FL enhancement tasks. Furthermore, we showed that Vox2Vox can outperform the current state-of-the-art proprietary FL deblurring algorithm. Additionally, we presented a case of downstream application, using the *in silico* enhanced FL images to improve BF-to-FL translation performance.