Introduction

- Multiplexed Ion Beam Imaging (MBI, shown below) is a novel imaging platform that allows biologists to image up to 40 proteins simultaneously in tissue.
- Images have far more channels than traditional RGB biological images (shown left).
- Increasing data acquisition increases quality, but at the cost of efficiency.

Our Goal: Employ deep learning to upsample data collected at low scan times to higher quality, noise free MBI images.

SuperMIBI: A convolutional neural network for prediction of upsampled multiplexed imaging data from short acquisition times

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SuperMIBI Baseline & Network Architecture

Baseline: Non-local means denoising (NLM)
NLM denoising works by coloring pixels based on the signal of similar pixels. Here we use the efficient ALM implementation.
NLM denoising to act as a baseline to evaluate our model's quality. It is used to modify upsampled data, but sufficiently reduces noise and smooth signal.

SuperMIBI
SuperMIBI is built around the SRCNN architecture.
1. Layer 1: 128 filters of size 5 x 5, ‘same’ padding, stride of 1, batch norm, and ReLU activation.
2. Layer 2: 64 filters of size 1 x 1, ‘same’ padding, stride of 1, batch norm, and ReLU activation.
3. Layer 3: 8 filters of size 5 x 5, stride of 1, batch norm, and ReLU activation.

Implemented with Keras and Tensorflow

Data Description

- Data Overview
  - Three A x B pairs, each with size 1024 x 1024 x 2.
  - Each channel with various spatial distribution and dynamic range.
  - Datasets are the same as seen in the previous section.

- Dataset
  - Train: 95% of data, Test: 5% of data.

Hyperparameter Tuning and Model Training

Loss: Mean-squared Error

\[ \text{Loss} = \sum \left( y_i - \hat{y}_i \right)^2 \]

Parameter Initialization

- Xavier

Filter number and sizes
- SRCNN uses a 9-1-5 structure for filter sizes across layers.
- Performance for SuperMIBI Improved by increasing filter sizes.
- Basic SRCNN uses 64 and 32 filters in layers 1 and 2, respectively.
- Performance for SuperMIBI Improved by using 128 and 64 filters for layers 1 and 2, respectively.

Data Normalization

\[ X_{\text{norm}} = \frac{X - \mu}{\sigma} \]

- Performed on a per-channel basis.
- Improved model performance significantly.

Results

Example 1: Single channel (KBB), 14 epochs, MSE = 1.76

Example 2: Single channel (CD45), 14 epochs, MSE = 2.63

Example 3: Multi-channel (KBB+CD45), 14 epochs, MSE = 1.96

Discussion and Future Directions

- Normalizing the data set resulted in improved performance of the model.
- Larger filters better capture global features, but decrease the spatial accuracy of the predicted output, while smaller filter sizes result in upsampled noise, but better preservation of granular features.
- More training data and utilizing additional image channels may improve training.
- More complex architecture, such as those in the CARE-CNN may improve network performance.

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