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Fluorescence Lifetime Imaging Microscopy (FLIM) Data Analysis by Inverse Modelling

Fluorescence lifetime imaging microscopy (FLIM) provides important information and high-quality images about inter-cellular activity, metabolic state, cellular morphology, etc. [1]. It is a sophisticated imaging approach that relies on the complex curve fitting method by extraction of lifetime parameters. The 'fit-free' deep learning (DL) based lifetime estimation method, which serves as an inverse modelling tool, is the major emphasis of this research. The DL training has been done in two steps: autoencoder and convolutional neural network (CNN). We have carried out our experiments with three datasets to train the autoencoder: (1) noisy data as input and denoised data as output (2) noisy data as input and denoised data as output (without convolution with system response function/IRF) (3) noisy data as input and noisy data as output. After training all, we used the bottleneck features from all three trained autoencoders and used their bottleneck features as input to a CNN to predict lifetime parameters. The last step is the performance analysis of the trained DL model by comparing it with 'FLIMview'[2].

In this study, we also showed our denoising model stability based on different system response functions/ IRF and noise levels. Here, we can see the model performance is quite stable, which represents by the mean square error (MSE) and it is low for all combinations.

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