Saliency-guided compressive fluorescence microscopy

Shimon Schwartz, Alexander Wong, and David Clausi
Department of Systems Design Engineering
University of Waterloo

UNIVERSITY OF Waterloo

Vision and Image Processing Group
Systems Design Engineering

Abstract:

A novel saliency-guided approach is proposed for improving the acquisition speed of compressive fluorescence microscopy systems. By adaptively optimizing the sampling probability density based on regions of interest instead of the traditional unguided random sampling approach, the proposed saliency-guided compressive fluorescence microscopy approach can achieve high-quality microscopy images using less than half of the number of fluorescence microscopy data measurements required by existing compressive fluorescence microscopy systems to achieve the same level of quality.

Introduction:

Fluorescence microscopy has broad applications in molecular studies of individual proteins and living cells. A key benefit of fluorescence microscopy over those based on optical density changes and chemiluminescent emission is its greater sensitivity and range. A popular fluorescence microscopy approach is scanning confocal microscopy, where samples are scanned by a laser to reconstruct an image. However, such an approach has been traditionally limiting in terms of acquisition speed due to the image being acquired pixel by pixel.

Problem:

- To address acquisition speed limitation, the concept of compressive fluorescence microscopy (CFM) was proposed to greatly increase acquisition speed while preserving high reconstruction quality. CFM is based around compressive sensing (CS), which allows for greatly reduced fluorescence microscopy acquisition times by accurately recovering the image from sparse, sub-Nyquist measurements.
- Much of the research in CFM systems focuses on hardware design and reconstruction design, thus leaving the design of the sampling procedure largely unexplored. However, given that many applications of fluorescence microscopy involve regions of interest with structured characteristics, the design of the sampling procedure can have a tremendous effect on acquisition speed and reconstruction quality.

Objective:

Motivated by the importance of the sampling procedure on CFM performance, the main contribution of this paper is the introduction of a saliency-guided compressive fluorescent microscopy system, which incorporates a saliency-guided sparse measurement model that was developed to significantly improves reconstruction quality and acquisition speed for situations where regions of interest have structured characteristics.

Saliency-guided CFM framework :

- Existing CFM systems employs a traditional sampling scheme that sample the entire scene in the same manner regardless of the underlying data. However, such an approach is limited for many practical applications of fluorescence microscopy, which involve distinct regions of interest with highly salient structural characteristics. Given that such regions are of greater interest for analysis purposes, one is motivated to obtain higher quality reconstructions for these regions than the background regions.
- Let the scene being imaged via fluorescence microscopy contain M x N sampling locations organized in a finite, rectangular lattice.
- Given such a lattice, let us partition it into three complementary sets Ω_D, Ω_S and Ω^C_{DS} (Ω_D represents highly salient locations, Ω_S represents sparse sampling, and Ω^C_{DS} represent non-sampled locations) such that
- Ω_D represents highly salient locations, Ω_D is defined based on a function $\Gamma(m,n)$ that quantifies saliency at a given location (m,n). Since regions of interest in many CFM applications are characterized by large spatial intensity variations (which relates to structural characteristics), one can define a saliency function $\Gamma(m,n)$ as:

$$\Gamma(m,n) \rightarrow \Omega_D \ \ if \ \ S(m,n) > t_a, \forall(m,n)$$

where

$$S(m,n) = \left|\left| I_\mu - I(m,n) \right|\right|$$

and where I_μ is the mean, I(m,n) is the corresponding vector of the Laplacian of the Gaussian filtered data, and t_a is the threshold value (set at two times the mean saliency S(m,n) of a given data.

Given a collection of K ≤ N x M, the linear measurements of f can be expressed as:

$$y_k = \phi_k\, f + \varepsilon_k = \sum_{i=1}^{N} f(i)\phi_k\,(i) + \varepsilon_k$$

where y_k is the kth measurement, Φ_k is the kth sampling function and ε represents the combined effect of measurement and quantization noises.

In the proposed saliency-guided CFM framework, since there are no measurements in Ω^C_{DS} and the sampling distributions of Ω_D and Ω_S are different, the sampling function at each location. where $\Phi^D_k(m,n)$ are realizations of a Gaussian distributed random variable with variance 1 and mean 0, and where $\Phi^S_k(m,n)$ are realizations of a Gauss-Bernoulli distributed random variable x:

$$P_S(x|\Pi,\sigma) = \Pi\ \delta(x) + (1-\Pi)\ \mathcal{N}(x|0,\sigma^2)$$

where P_S=0 with probability Π and P_S is Gaussian distributed with probability Π. In this implementation, mean is zero and variance is one, and Π was selected to be 0.9 (represents 90% compression rate or 10% sampling) as the maximum compression rate where CFM can still produce reasonably reconstructed images.

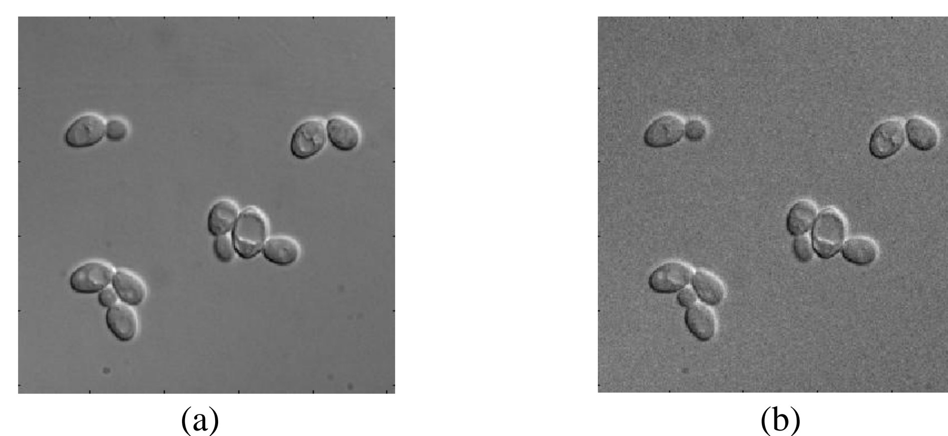
Implementation :

- Based on the above theory, the saliency-guided CFM framework can be implemented in two phases. In the first phase, a traditional sampling procedure is employed where f is sampled sparsely via $\Phi^S_k(m,n)$ with the pdf P_S using only 10\% of the sampling locations. The saliency function $\Gamma(m,n)$ is then employed to determine subset Ω_D based on the fluorescence microscopy image reconstructed from these samples.
- In the second phase, f is sampled by $\Phi^D_k(m,n)$ with pdf that sample highly salient regions of interest with greater density. The samples from the two subsets Ω_D and Ω_S are then combined and used to reconstruct the fluorescence microscopy image at a higher accuracy than that achieved in the first phase.
- To reconstruct the fluorescence microscopy image from the acquired samples, a l1-based total variation minimization approach was employed:

$$\text{argmin}_f \left\{ \lambda |f|_{TV_{l_1}} + \frac{1}{2}|\Phi f - y|_2^2 \right\}$$

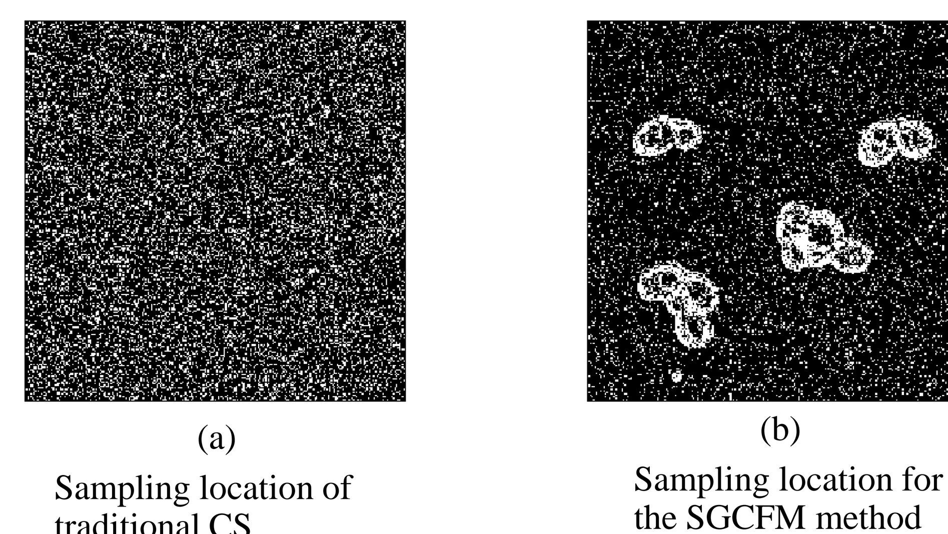
where $|\cdot|_{TVl1}$ denotes the l1-based anisotropic total variation norm, and can be solved using Fast Iterative Shrinkage-Thresholding Algorithm (FISTA) approach.

Experimental Results:



(a) (b)

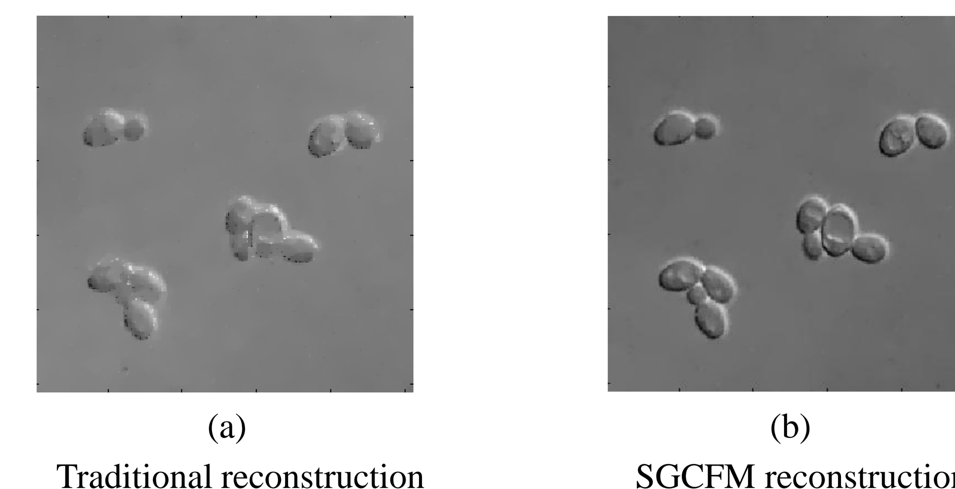
Figure 1. Example of (a) fully sampled fluorescence microscopy image, and (b) the corresponding noise contaminated version (standard deviation = 3%) used in the first set of experiments.



(a) Sampling location of traditional CS

(b) Sampling location for the SGCFM method

Figure 2. Sampling locations of 75% compression rate fluorescence microscopy image (Figure 1.), where "white" represents sampling location (25% in this case) and "black" is a non-sampling location (75% in this case). In the traditional CS (a) the sampling locations are distributed uniformly, and in SGCFM method (b), the same amount of sampling locations distribution is guided by region of interest .



(a) Traditional reconstruction

(b) SGCFM reconstruction

Figure 3. Example reconstruction results for first set of experiments at 75% compression rate and 3% noise level.

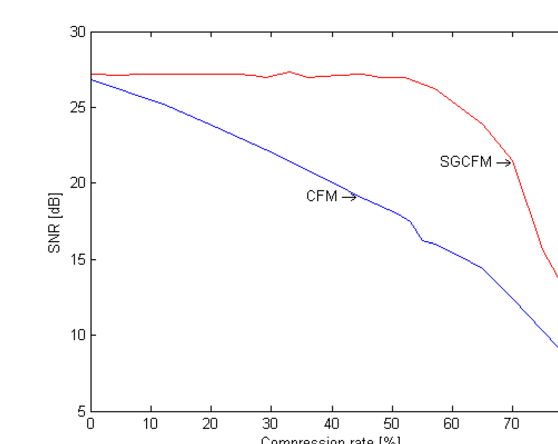


Figure 4. SNR vs. compression rate for reconstruction results of fluorescence microscopy images contaminated by Gaussian noise with noise with a standard deviation that is 3% of the dynamic range.

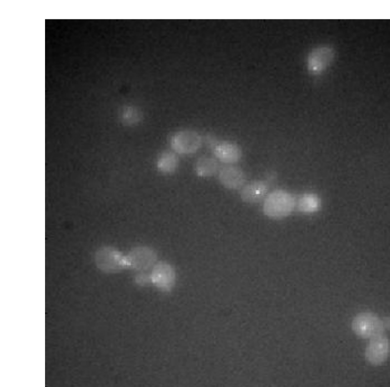
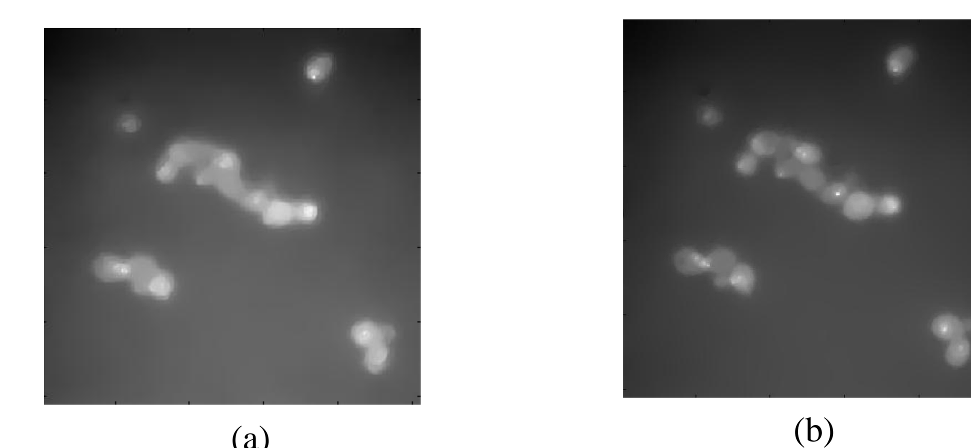


Figure 5. Example of fully sampled noisy fluorescence microscopy image (real noise)



(a) Traditional reconstruction

(b) SGCFM reconstruction

Figure 6. Example reconstruction results for real noisy set of experiments at 80% compression rate from real noise-contaminated measurements.

Acknowledgements:

This research has been sponsored by the Natural Sciences and Engineering Research Council of Canada (NSERC) and Geomatics for Informed Decisions (GEOIDE). The authors would also like to thank Yeast Resource Center for the test fluorescence microscopy data.