Exploring Methods for Improved Species Identification using Hyperspectral Data

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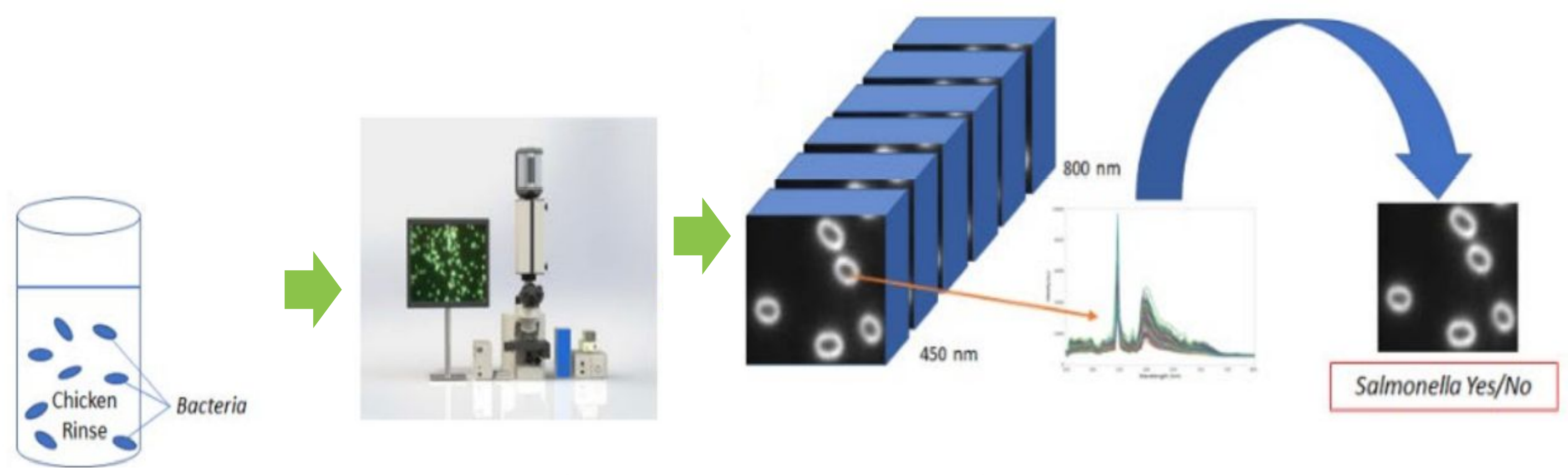
Background



Rapid Optical Detection Methods for Foodborne Pathogens
Bosoon Park, Seung-Chul Yoon, Gary Gamble, Kurt Lawrence*

Hyperspectral Microscopy Imaging (HMI) combines hyperspectral imaging (HSI) with microscopy to capture both spatial and spectral details at a microscopic level, enabling detailed chemical analysis. However, accurately identifying bacterial species remains challenging due to dataset variations and inherent biases in hyperspectral data analysis. Key steps in HMI analysis include using unbiased data, selecting optimal feature extraction techniques, and applying methods such as principal component analysis (PCA) and machine learning classifiers. This work explores compressed sensing (CS) as a sparsity-driven, regularization-based approach for image enhancement. By using sparse signal representations, CS facilitates better separation of signal and noise, while regularization ensures stability and accuracy. While CS has been widely applied in image reconstruction, its potential for feature enhancement remains underexplored. Traditional CS techniques prioritize smooth recovery by minimizing the total variation (TV) norm, which can suppress fine details. Instead, we propose minimizing the L1 norm to enhance specific image features, particularly edges, without enforcing overall smoothness. To evaluate the effectiveness of this approach, we use peak signal-to-noise ratio (PSNR) and structural similarity index (SSIM) to quantify image similarity. By successfully amplifying rough features, this method aims to improve bacterial classification accuracy in HMI data analysis.

Method

Problem Statement

$$\min_{ijk} \|X\|_1 \quad \text{subject to} \quad \|A(X)-B\|_2 \le \epsilon,$$

$A: \mathbb{R}^{n\,x\,n\,x\,n} \mapsto \mathbb{R}^{n\,x\,n\,x\,n}$ sparsifying linear transform

$B \in \mathbb{R}^{n\,x\,n\,x\,n}$ measured observations

$X: \mathbb{R}^{n\,x\,n\,x\,n}$ Image

Objective Function

$$f_{T_{ijk}} = \frac{1}{2}(\|X\|_2^2 - T_{ijk}^2), \quad i,j,k = 1,\dots,n,$$

$$f_\epsilon = \frac{1}{2}(\|A(X)-B\|_2^2 - \epsilon^2),$$

and write the problem in log-barrier form

$$F(z) := \langle c_0, z\rangle - \frac{1}{\tau}\left[\sum_{ijk}\log(-f_{T_{ijk}}(z)) + \log(-f_\epsilon(z))\right],$$

where τ is an accuracy parameter, $c_0 = \begin{bmatrix}0_{n^3}\\1_{n^3}\end{bmatrix}$ and $z = \begin{bmatrix}X(:)\\T(:)\end{bmatrix}$.

Gradient and Hessian

The gradient, g_z, and Hessian, H_z, are given by

$$g_z = c_0 + \frac{1}{\tau}\left[\sum_{ijk}\frac{1}{-f_{T_{ijk}}(z)}\nabla f_{T_{ijk}}(z) + \frac{1}{-f_\epsilon(z)}\nabla f_\epsilon(z)\right],$$

$$H_z = \frac{1}{\tau}\left[\sum_{ijk}\frac{1}{f_{T_{ijk}}(z)^2}\nabla f_{T_{ijk}}(z)(\nabla f_{T_{ijk}}(z))^T + \sum_{ijk}\frac{1}{-f_{T_{ijk}}(z)}\nabla^2 f_{T_{ijk}}(z) + \frac{1}{f_\epsilon(z)^2}\nabla f_\epsilon(z)(\nabla f_\epsilon(z))^T + \frac{1}{-f_\epsilon(z)}\nabla^2 f_\epsilon(z)\right].$$

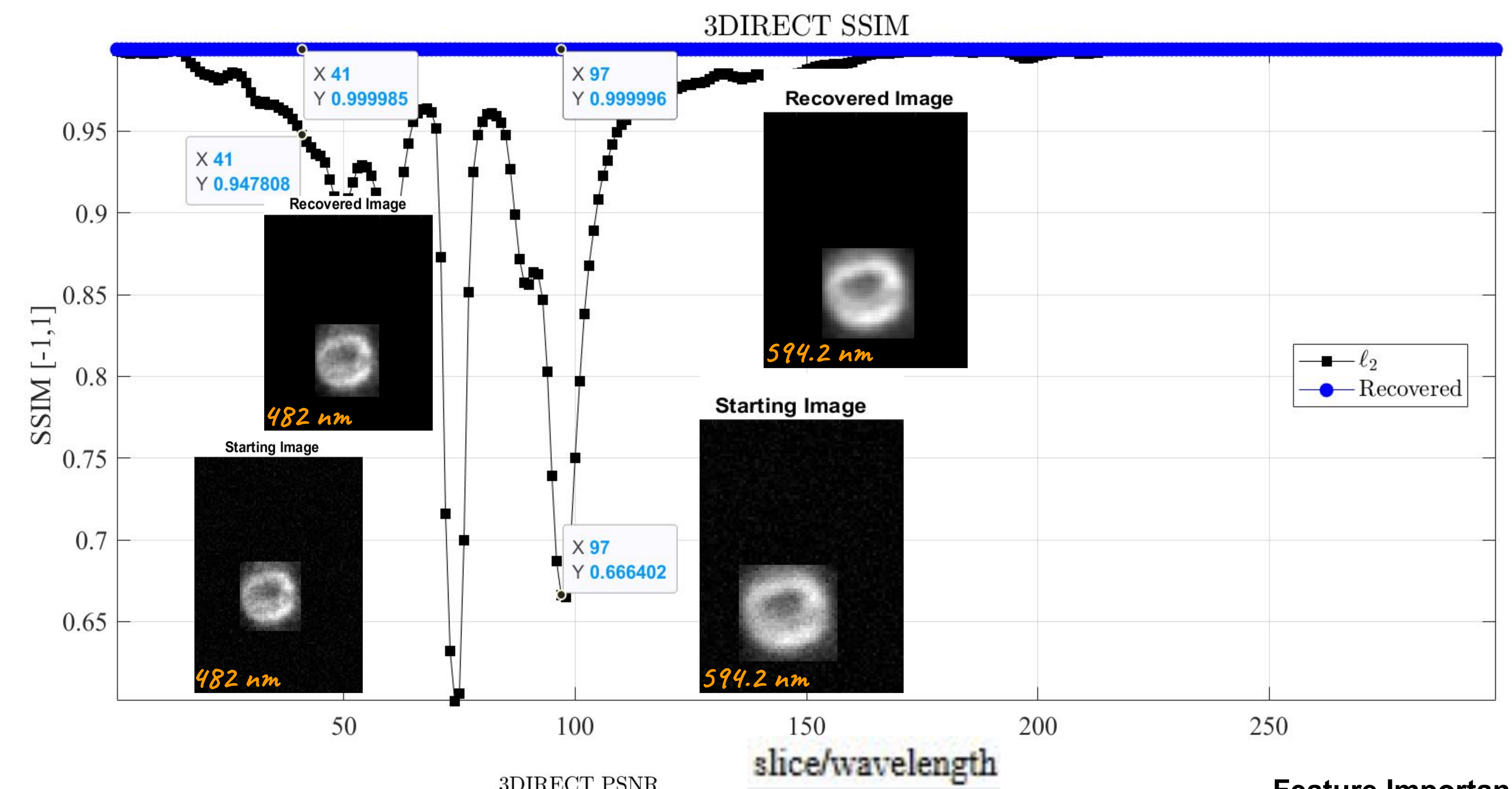
System of Equations

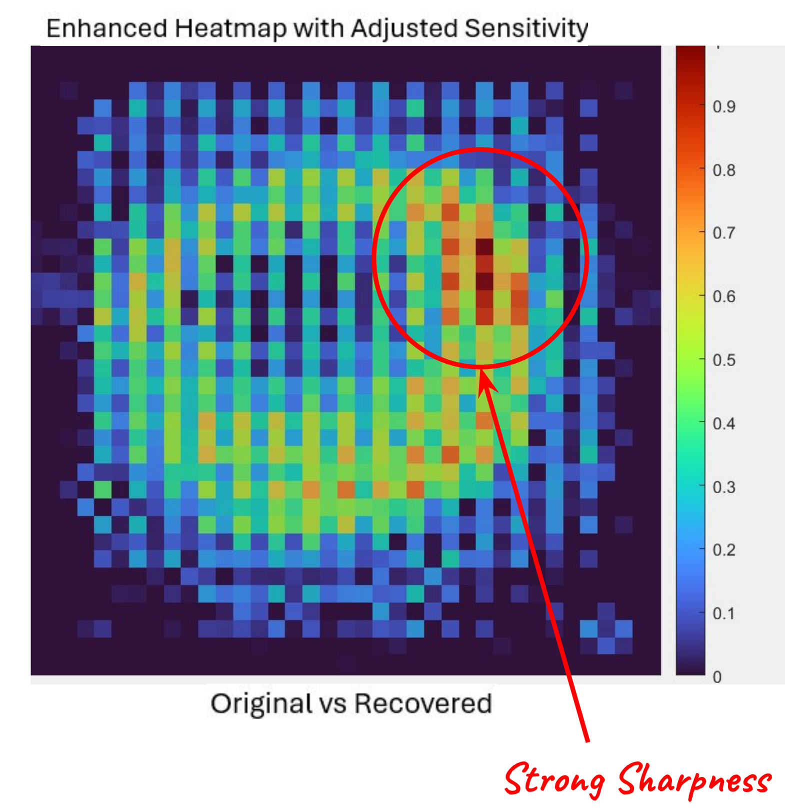
Given a feasible z,

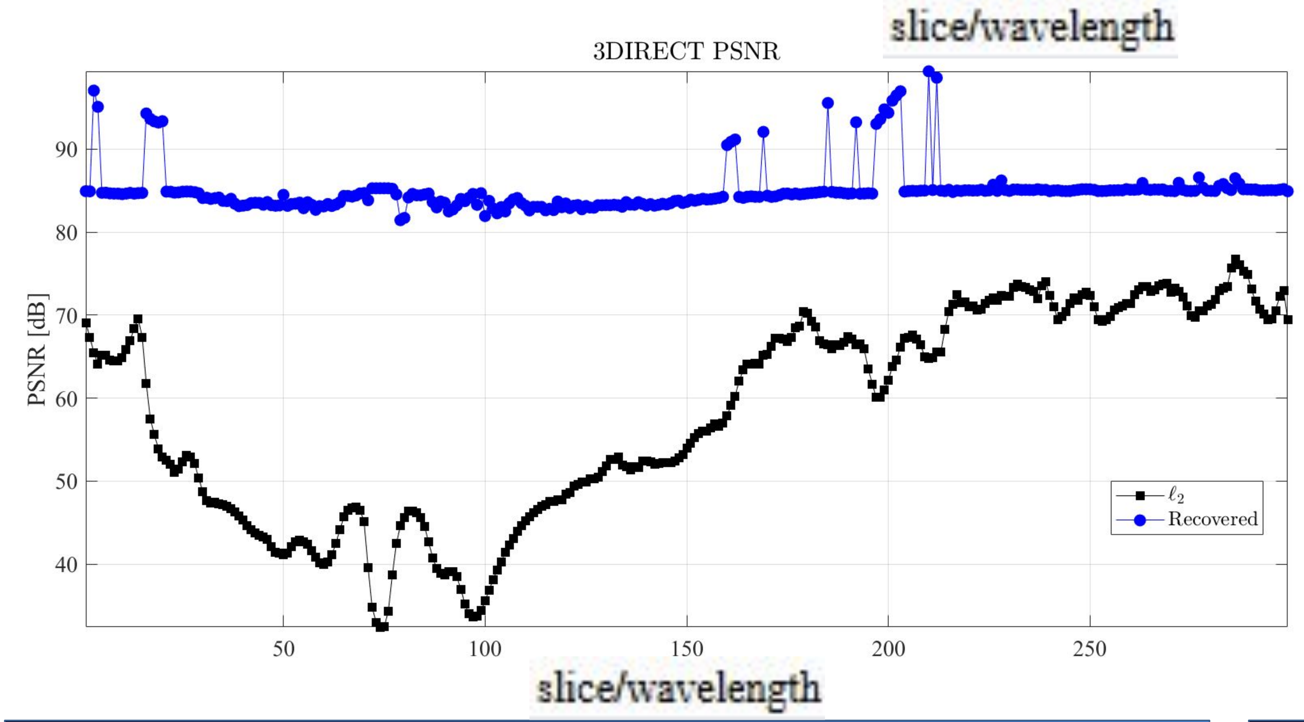
the direction Δz along which $F(z)$ is to be approximately minimized, is the solution to the system of linear equations

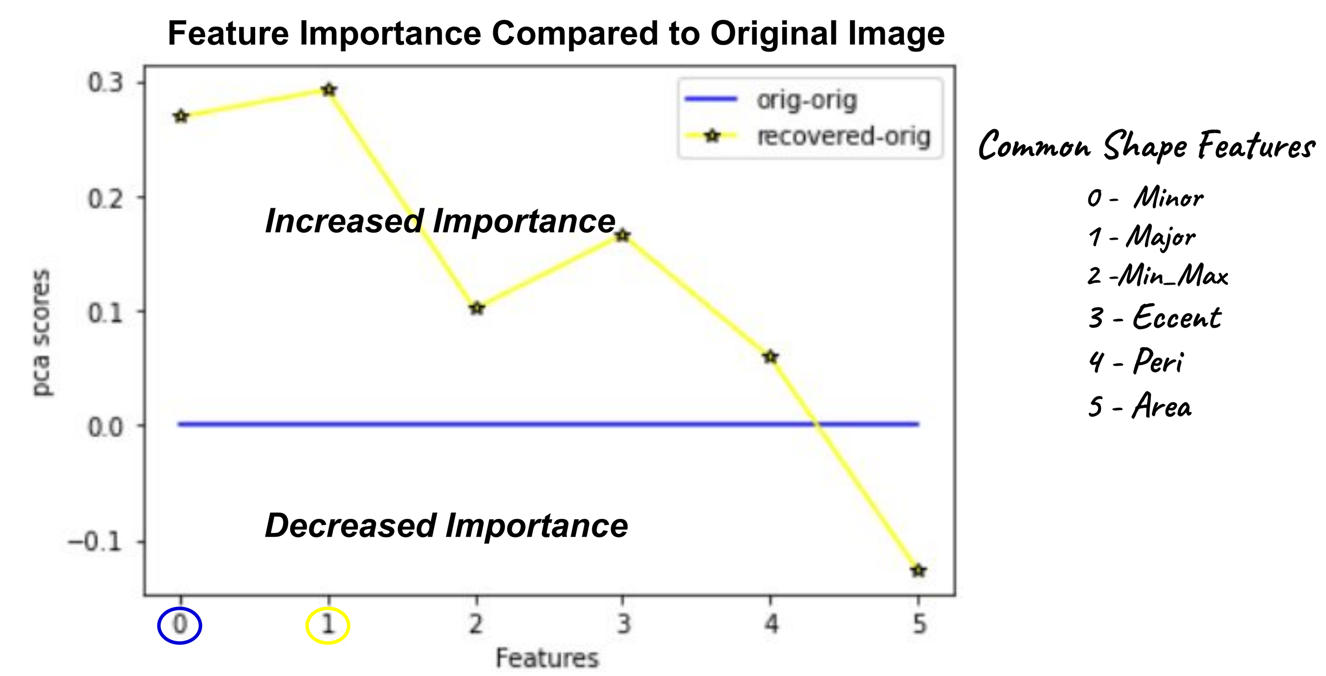
$$H_z \cdot \delta z = -g_z.$$

Data Visuals



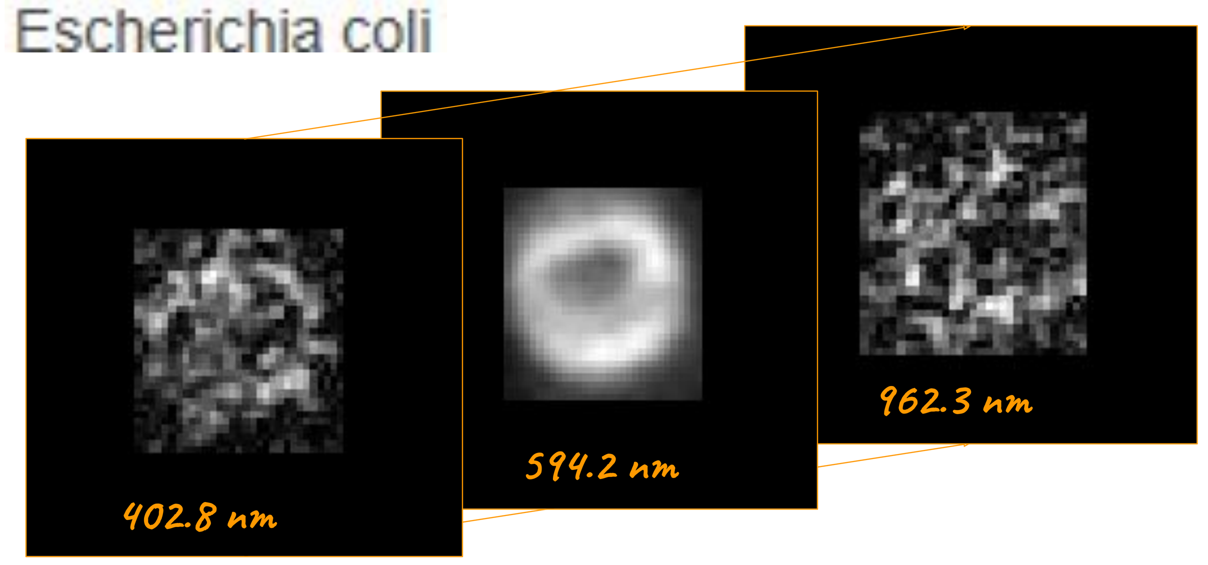


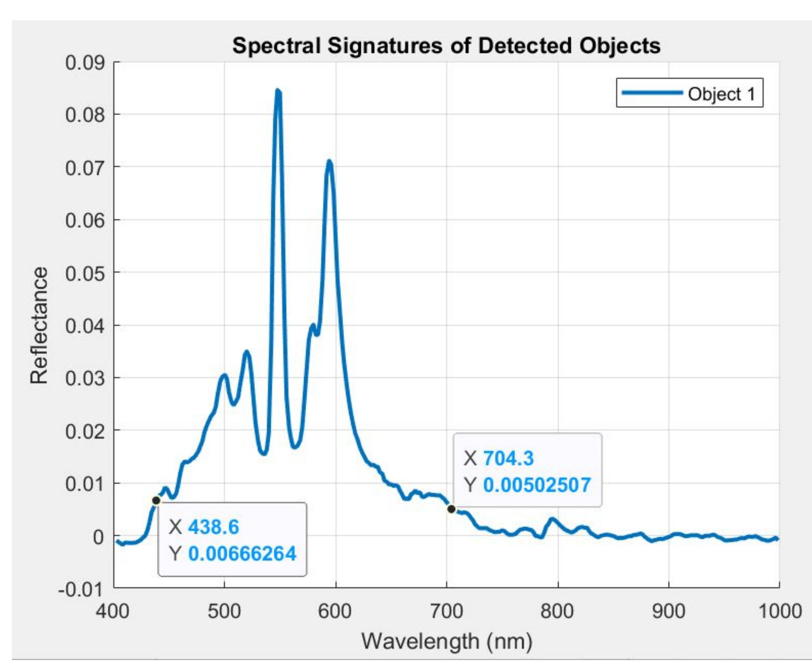




Data

Escherichia coli





Conclusion/Future Work

- SSIM & PSNR both show the l1-minimization performs well in the image enhancement.
- The heatmap shows a strong sharpness occuring in the edge. We are not looking for overall enhancement, but specific features.
- Most features had an increased importance, 1 was negatively impacted.
- Use more single cell data & different bacteria
- Show effect on classification accuracy.

Acknowledgements

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References

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