



Medical Image Super Resolution

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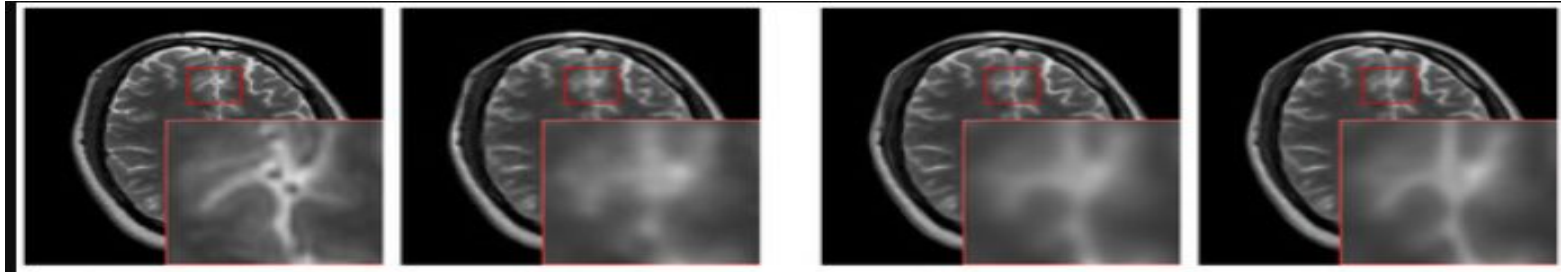


Introduction

- ❖ High resolution images desired in many applications such as medical imaging, satellite imaging, unmanned aerial vehicle (drone), video surveillance, wildlife surveillance, astronomy, oceanography etc. In medical imaging, the images are obtained for medical investigative purposes. Not only it is an important diagnosis instrument to determine the presence of certain diseases but it also significantly improve the diagnosis ability for corrective treatment.
- ❖ Super resolution algorithms are deployed in image capturing devices designed and manufactured by top companies such as Siemens and GE Healthcare.

PROBLEM STATEMENT

- ❖ Validating existing image super resolution techniques over medical images.
- ❖ Observe the impact, specifically on the diseased region in the image.
- ❖ Change in the appearance (i.e - texture, brightness etc) of the disease region due to super resolution might lead to wrong interpretation by the radiologists.



Source: [Applied Sciences | Free Full-Text | Gradient-Guided Convolutional Neural Network for MRI Image Super-Resolution | HTML \(mdpi.com\)](#)



LITERATURE REVIEW

- ❖ Up Till now, may new super resolution techniques proposed have been tested only on the normal color images. In medical, the super resolution technique has been applied on entire image. No one has at present, to our knowledge has tested and validated the effect of super resolution over diseased and non-diseased region separately. This is what we are trying to do.
- ❖ So we began with a **Null Hypothesis**: Applying Super Resolution over medical images will impact diseased (tumor) region (i.e SSIM between original image and super resolution image will not be 1)
- ❖ **Alternate Hypothesis**: Applying Super Resolution over medical images will not impact diseased (tumor) region (i.e SSIM between original image and super resolution image will be 1)



Implementations (Before Last Presentation)

- ❖ Disease Detection on Chest X-Ray images.
- ❖ Denoising Using Autoencoder on Chest X-Ray images.
- ❖ Implementing Efficient Sub-Pixel Convolution Neural Network (ESCN) on Chest X-Ray images.
- ❖ Implementation of SRGAN model. Trained the model for 220 epochs. Results were not upto mark due to lack of training and lack of resources.
- ❖ Computed Similarity Index (SSIM), Mean Absolute Error and Mean Percentage Error as evaluation metrics for entire super resolution image.
- ❖ Dataset Used - [Chest X-Ray Images \(Pneumonia\)](#) and [Brain Tumor Dataset](#)



Progress Work

- ❖ Brain tumor dataset obtained from [figshare](#) [1]. This dataset contains 3064 T1-weighted contrast-enhanced images from 233 patients with three kinds of brain tumor: meningioma (708 slices), glioma (1426 slices), and pituitary tumor (930 slices) with **mask for tumor region**. This data is in matlab format and file consists of following fields: -
 - Patient ID
 - Label
 - Image Array
 - Tumor Border (It was generated by manually delineating the tumor border)
 - Tumor Mask



Progress Work

Image: 0

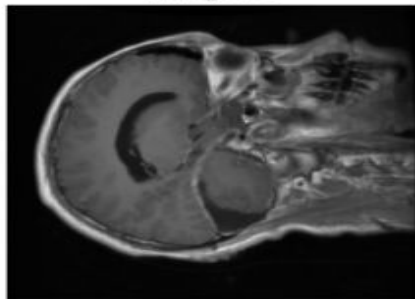


Image: 1

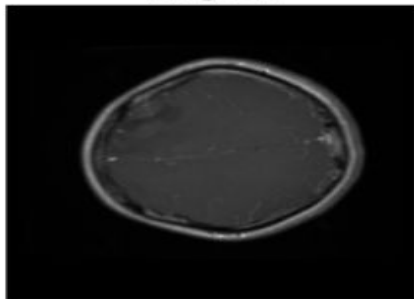


Image: 2

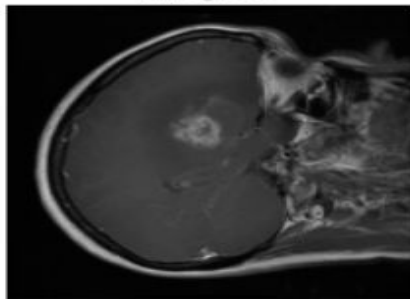


Image: 3

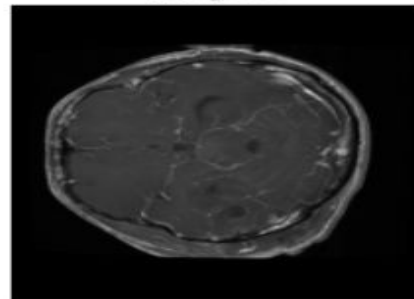


Image: 0



Image: 1



Image: 2

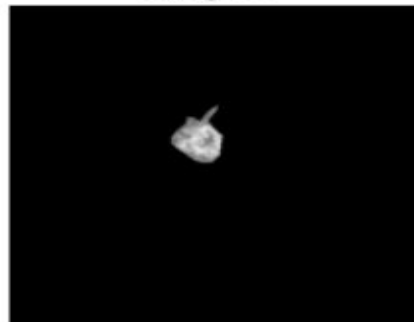
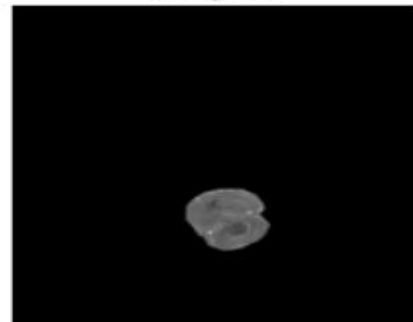
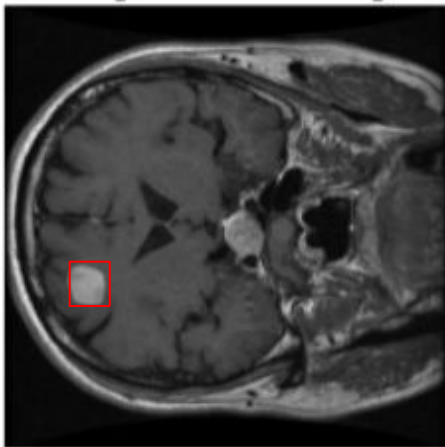


Image: 3



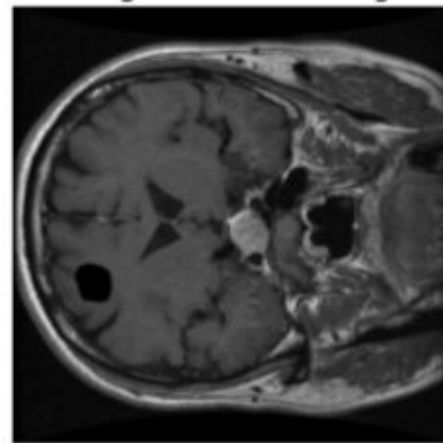
What we are trying to achieve?



Brain Image



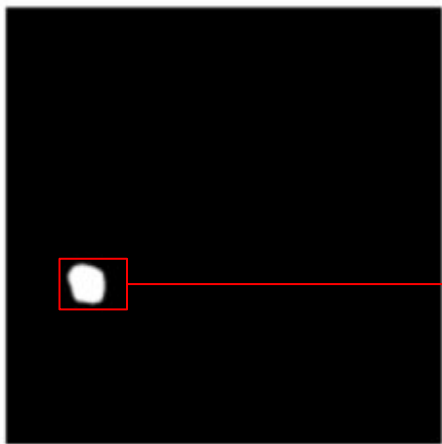
Tumor



Only Brain Region

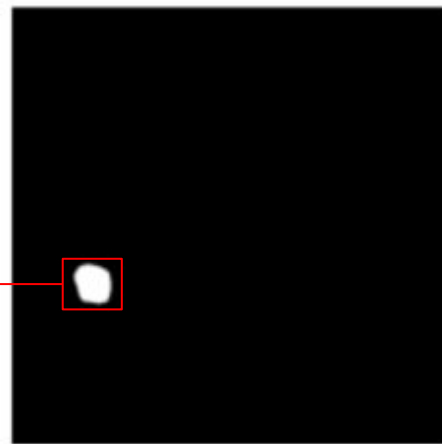


What we are trying to achieve?



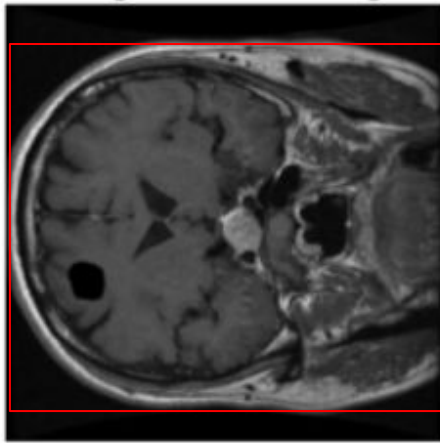
Original Image Tumor Region

SSIM



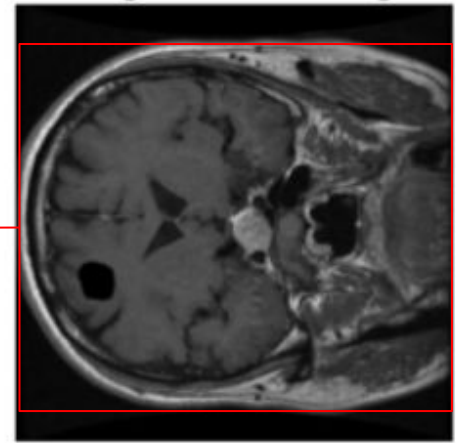
HR Image Tumor Region

What we are trying to achieve?



Original Image Brain Region

SSIM



HR Image Brain Region



How did I achieve it? (Polygon Approximation Algorithm)

Image: 1

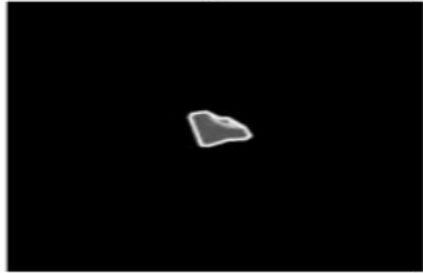


Image: 2



Image: 3



Image: 4

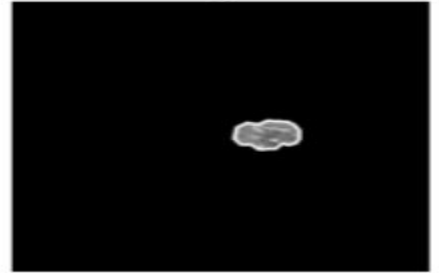


Image: 1

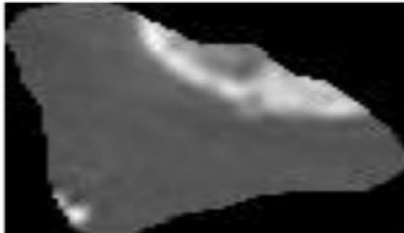


Image: 2

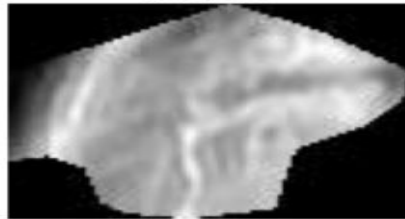


Image: 3

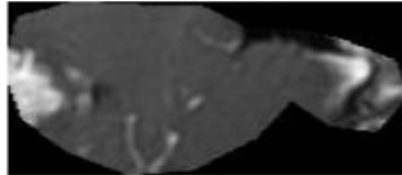
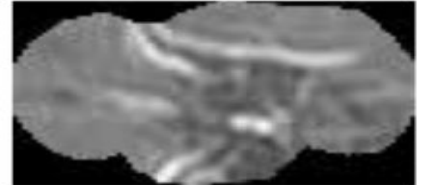
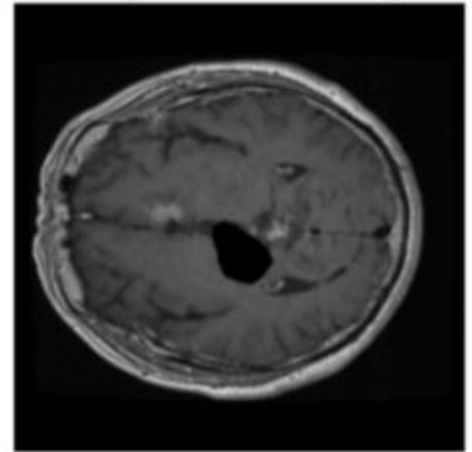
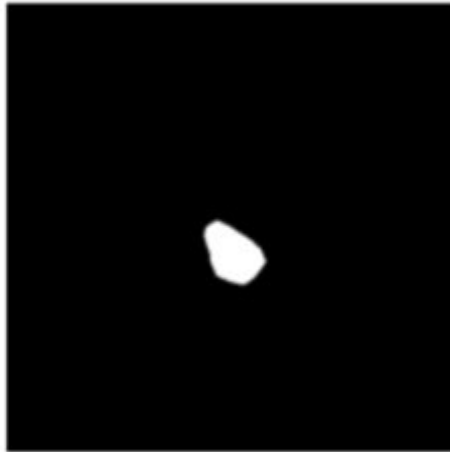
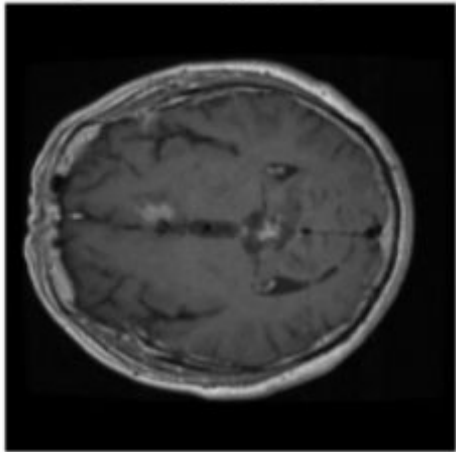


Image: 4





How did I achieve it?





Structure Similarity Index (SSIM)

- ❖ SSIM extracts three key features from an image: -
 - Luminance
 - Contrast
 - Structure
- ❖ Comparison between two images is performed on the basis of these three key metrics.



Structure Similarity Index (SSIM)

- ❖ **Luminance:** Luminance is measured by averaging over all the pixel values. Its denoted by μ (Mu) and the formula is given below,

$$\mu_x = \frac{1}{N} \sum_{i=1}^N x_i. \quad (2)$$

The luminance comparison function $l(\mathbf{x}, \mathbf{y})$ is then a function of μ_x and μ_y .

where x_i is the i th pixel value of the image x . N is the total number of pixel values.

Source: <https://www.cns.nyu.edu/pub/eero/wang03-reprint.pdf>



Structure Similarity Index (SSIM)

- ❖ **Luminance Comparison Function:** It is defined by function, $l(x,y)$ which is shown below, μ (mu) represents mean of given image, x and y are two images being compared.

$$l(\mathbf{x}, \mathbf{y}) = \frac{2\mu_x\mu_y + C_1}{\mu_x^2 + \mu_y^2 + C_1}$$

where C_1 is a constant to ensure stability when the denominator becomes 0. C_1 is given by,

$$C_1 = (K_1L)^2$$



Structure Similarity Index (SSIM)

- ❖ **Contrast:** It is measured by taking the *standard deviation (square root of variance)* of all the pixel values. It is denoted by σ (sigma) and represented by the formula below,

$$\sigma_x = \left(\frac{1}{N-1} \sum_{i=1}^N (x_i - \mu_x)^2 \right)^{\frac{1}{2}}. \quad (4)$$

The contrast comparison $c(\mathbf{x}, \mathbf{y})$ is then the comparison of σ_x and σ_y .

Where x and y are the two images and μ is the mean of the pixel values of the image. Source: <https://www.cns.nyu.edu/pub/eero/wang03-reprint.pdf>



Structure Similarity Index (SSIM)

- ❖ **Contrast Comparison Function:** It is defined by function, $c(x,y)$ which is shown below, σ (sigma) represents standard deviation of the given image, x and y are two images being compared.

$$c(\mathbf{x}, \mathbf{y}) = \frac{2\sigma_x\sigma_y + C_2}{\sigma_x^2 + \sigma_y^2 + C_2}$$

where C_2 is given by,

$$C_2 = (K_2L)^2$$



Structure Similarity Index (SSIM)

- ❖ **Structure:** The structural comparison is done by using a consolidated formula represented in next slide, but in essence what we do is, we divide the input image with its *standard deviation* so that the result has unit standard deviation which allows for a more robust comparison

$$(\mathbf{x} - \mu_x) / \sigma_x$$

where x is the Input Image



Structure Similarity Index (SSIM)

- ❖ **Structure Comparison Function:** It is defined by function, $s(x,y)$ which is shown below, σ (sigma) represents standard deviation of the given image, x and y are two images being compared.

$$s(\mathbf{x}, \mathbf{y}) = \frac{\sigma_{xy} + C_3}{\sigma_x \sigma_y + C_3}.$$

where $\sigma(xy)$ is given by,

$$\sigma_{xy} = \frac{1}{N-1} \sum_{i=1}^N (x_i - \mu_x)(y_i - \mu_y).$$



Structure Similarity Index (SSIM): Constant Parameters Explained

- ❖ For computation of SSIM, there are few constants involved C_1, C_2 and C_3 , given below,

$$C_1 = (K_1 L)^2 \quad C_2 = (K_2 L)^2 \quad C_3 = C_2/2$$

Here we took $K_1 = 0.01$, $K_2 = 0.03$ and $L = 65535$

L is defined as dynamic range for pixel values and it depends on the bit size of the image. More details on how to select the value of L can be found [scikit-image/image data_types](https://scikit-image.org/docs/stable/user_guide/image_data_types.html)



Structure Similarity Index (SSIM)

❖ Finally, SSIM score is given by,

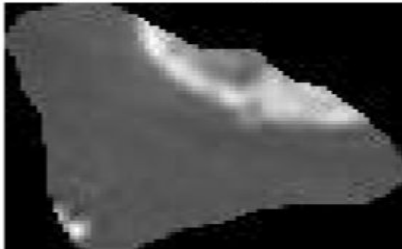
$$\text{SSIM}(\mathbf{x}, \mathbf{y}) = [l(\mathbf{x}, \mathbf{y})]^\alpha \cdot [c(\mathbf{x}, \mathbf{y})]^\beta \cdot [s(\mathbf{x}, \mathbf{y})]^\gamma$$

where $\alpha > 0$, $\beta > 0$, $\gamma > 0$ denote the relative importance of each of the metrics. To simplify the expression, if we assume, $\alpha = \beta = \gamma = 1$ and $C_3 = C_2/2$, we can get,

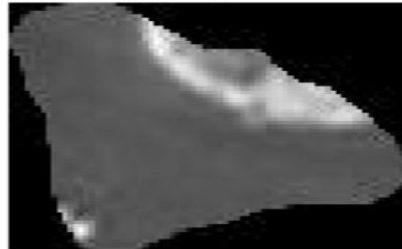
$$\text{SSIM}(\mathbf{x}, \mathbf{y}) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_2)}{(\mu_x^2 + \mu_y^2 + C_1)(\sigma_x^2 + \sigma_y^2 + C_2)}.$$

SSIM Results for Tumor Region

Super Resolution Image Tumor 1

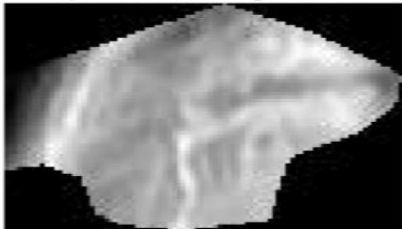


Original Image Tumor 1

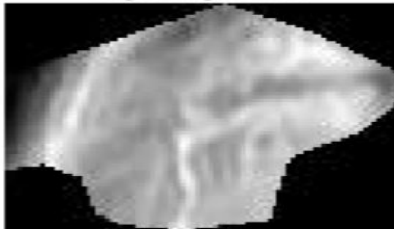


SSIM 0.961471018306179

Super Resolution Image Tumor 2



Original Image Tumor 2

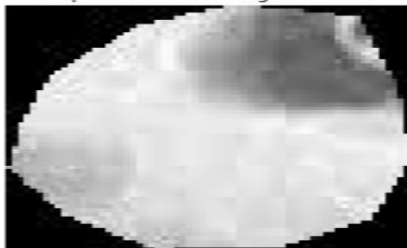


SSIM 0.9060500579130395

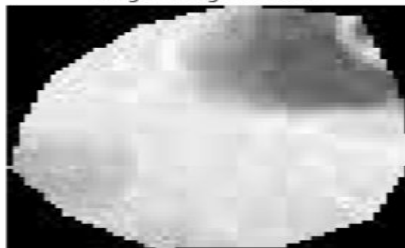


SSIM Results for Tumor Region

Super Resolution Image Tumor 5

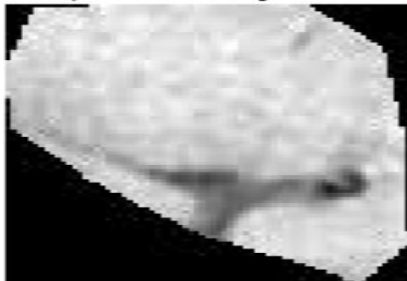


Original Image Tumor 5

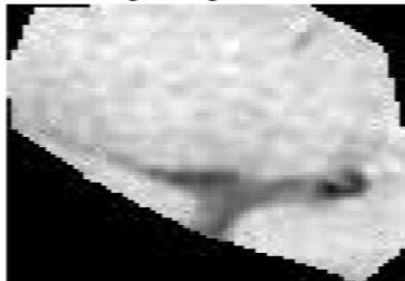


SSIM 0.8736712943010898

Super Resolution Image Tumor 6



Original Image Tumor 6

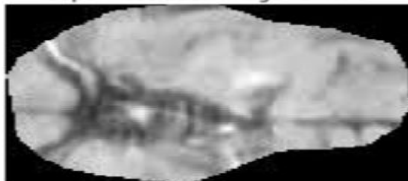


SSIM 0.8724159347023605

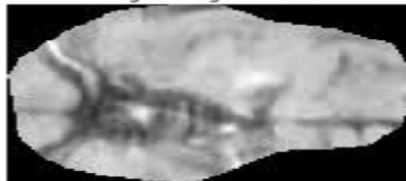


SSIM Results for Tumor Region

Super Resolution Image Tumor 9



Original Image Tumor 9



SSIM 0.9015596438558307

Super Resolution Image Tumor 10



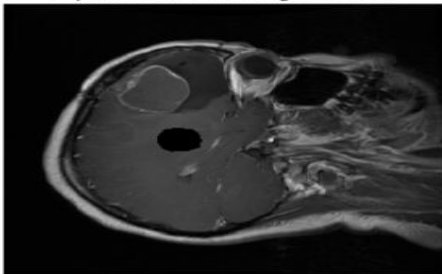
Original Image Tumor 10



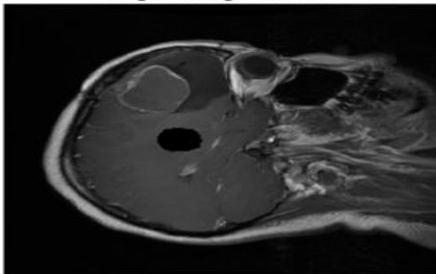
SSIM 0.8829544493765127

SSIM Results for Brain Region

Super Resolution Image Tumor 1

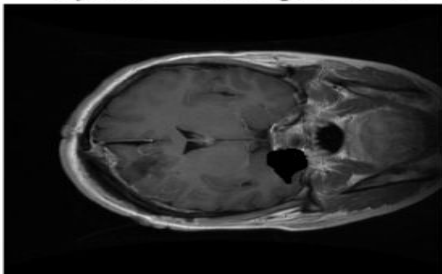


Original Image Tumor 1

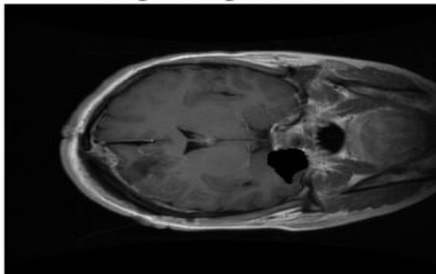


SSIM 0.9918605406208175

Super Resolution Image Tumor 2



Original Image Tumor 2

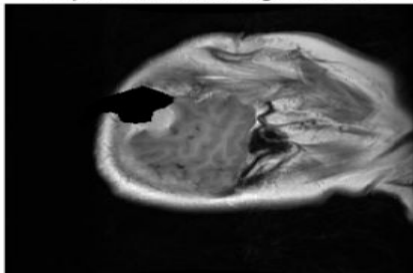


SSIM 0.9898840710782558

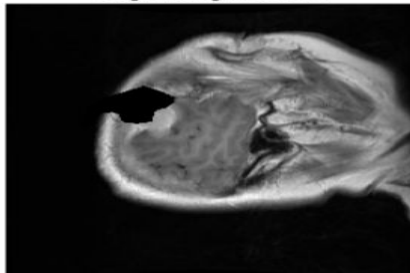


SSIM Results for Brain Region

Super Resolution Image Tumor 6

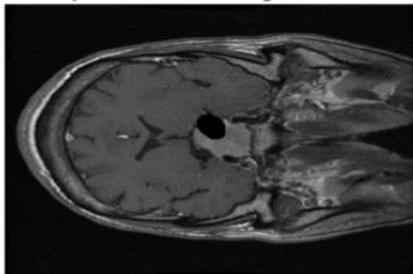


Original Image Tumor 6

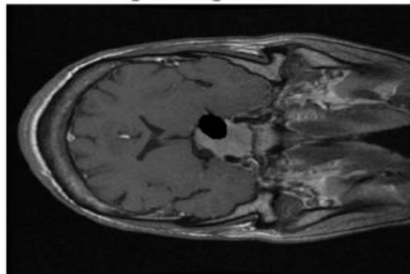


SSIM 0.9823550091213183

Super Resolution Image Tumor 7



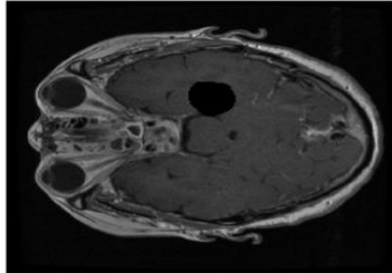
Original Image Tumor 7



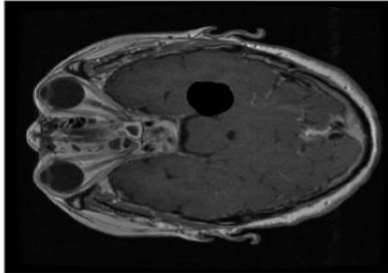
SSIM 0.9882826763831886

SSIM Results for Brain Region

Super Resolution Image Tumor 13

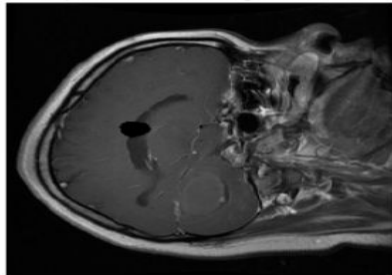


Original Image Tumor 13

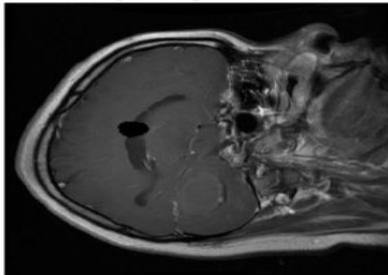


SSIM 0.9902937508190963

Super Resolution Image Tumor 14



Original Image Tumor 14



SSIM 0.9866380114324615

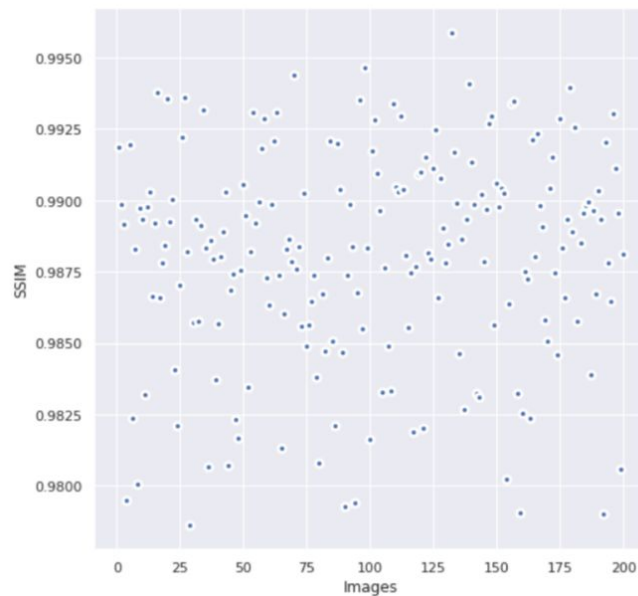


SSIM Metric Plots (Brain Region)

Error Barplot



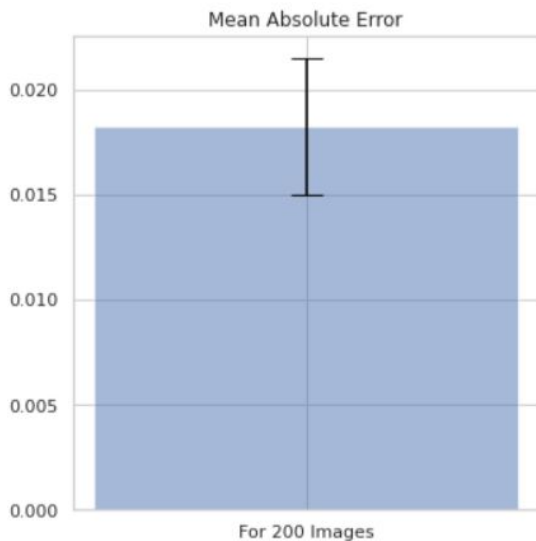
Scatter Plot



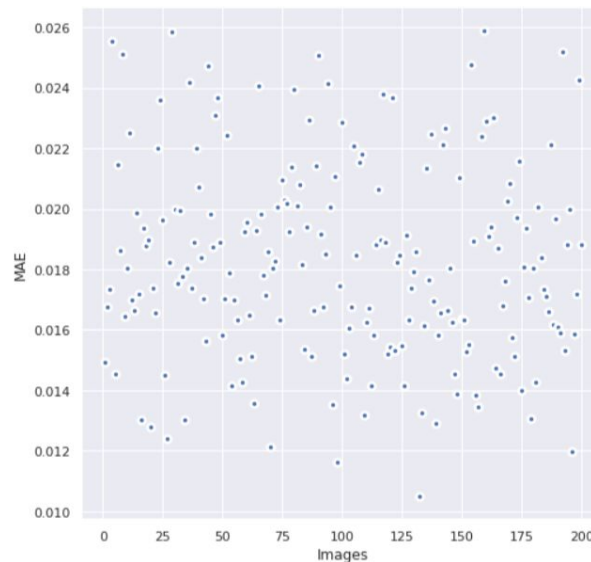


Mean Absolute Error (MAE) Metric Plots (Brain Region)

Error Barplot



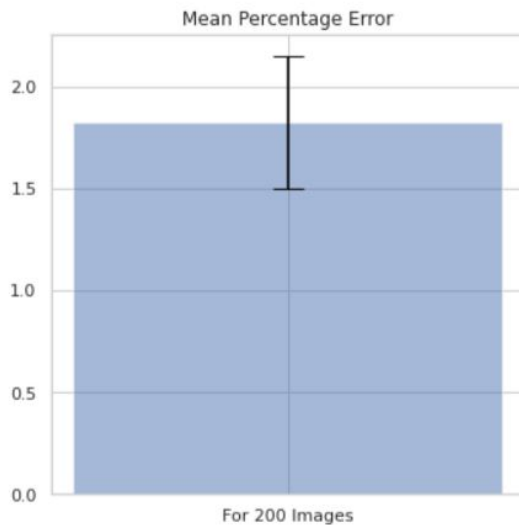
Scatter Plot



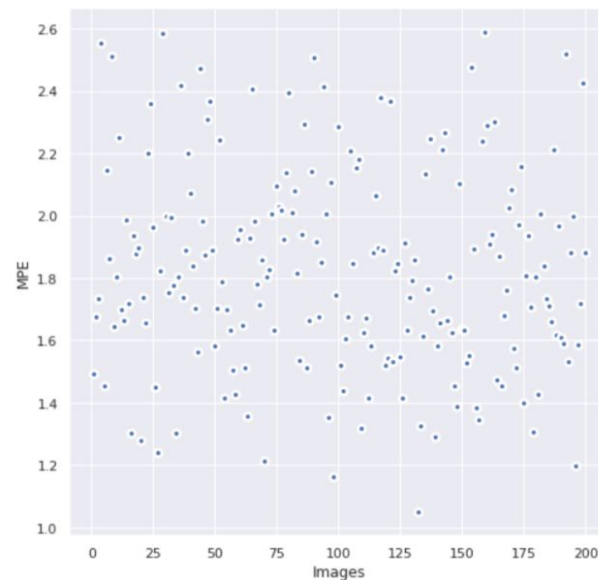


Mean Percentage Error (MPE) Metric Plots (Brain Region)

Error Barplot



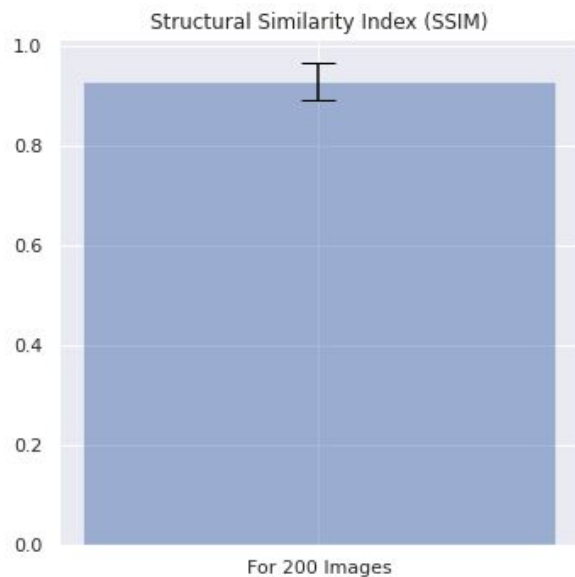
Scatter Plot



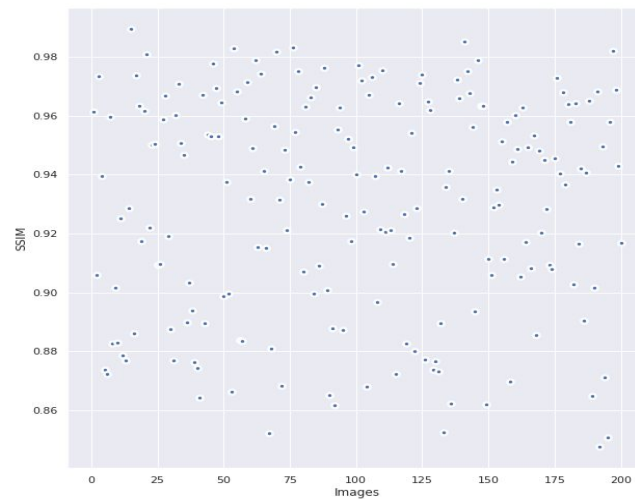


SSIM Metric Plots (Tumor Region)

Error Barplot



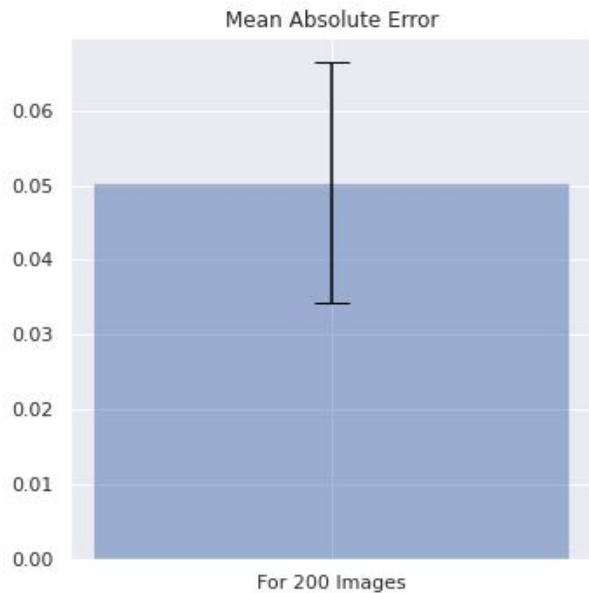
Scatter Plot



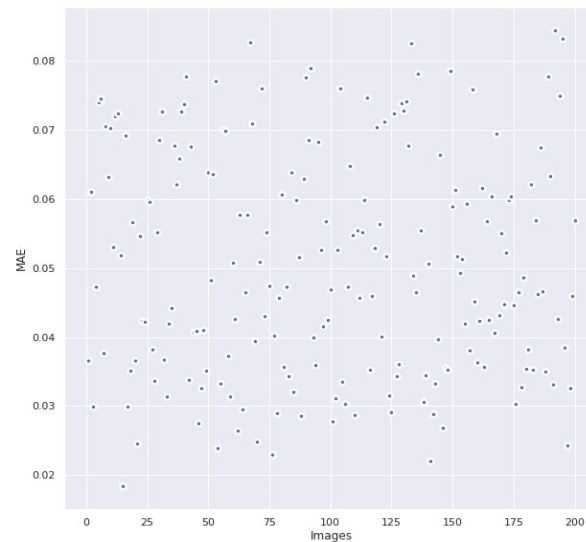


Mean Absolute Error (MAE) Metric Plots (Tumor Region)

Error Barplot



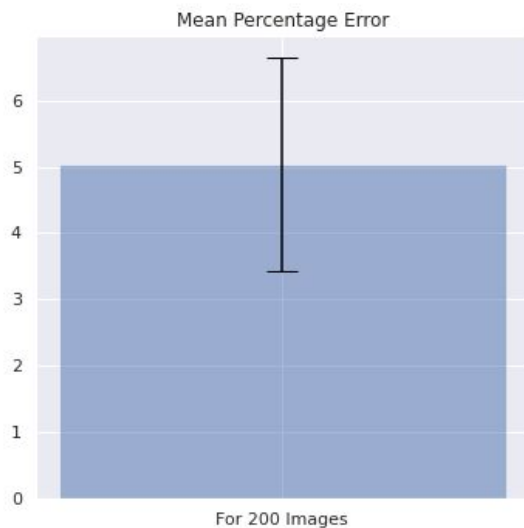
Scatter Plot



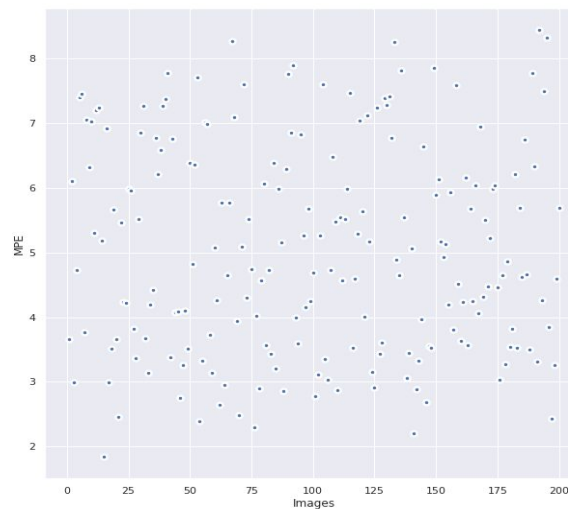


Mean Percentage Error (MPE) Metric Plots (Tumor Region)

Error Barplot



Scatter Plot





Brain Tissue Metric Table

Model : ESPCN
Dataset - Brain Tumor
Dataset
Images - 200 Super
Resolution Images

	Mean	Standard Deviation
SSIM	0.9880	0.0037
MAE	0.0182	0.0032
MPE	1.8237	0.3246



Tumor Metric Table

Model : ESPCN
Dataset - Brain Tumor
Dataset
Images - 200 Super
Resolution Images

	Mean	Standard Deviation
SSIM	0.9294	0.0365
MAE	0.0503	0.0161
MPE	5.0374	1.6115



Universal Quality Index (UQI)

- ❖ UQI is a special case of ssim, where $C1=0$ and $C2=0$. It produces unstable results when when either $(\mu_x^2 + \mu_y^2)$ or $(\sigma_x^2 + \sigma_y^2)$ is very close to zero [2].
- ❖ I have computed UQI separately for tumor and brain regions, but, since the results are unstable we are not hence we have not included QUI in our final metric evaluation results.



Future Work

- ❖ Evaluate metrics for tumor and brain regions of SRGAN model generated super resolution images, currently facing issues while running SRGAN on High Performance Computing (HPC) device.
- ❖ Compute and evaluate model performance over for X-Ray Pneumonia Dataset.
- ❖ Compute SSIM, MAE, and MPE for entire X-Ray Image.



References

- ❖ [1] Cheng, Jun (2017): brain tumor dataset. figshare. Dataset.
<https://doi.org/10.6084/m9.figshare.1512427.v5>
- ❖ [2] Zhou Wang, Member, IEEE, Alan Conrad Bovik, Fellow, IEEE, Hamid Rahim Sheikh, Student Member, IEEE, and Eero P. Simoncelli, Senior Member, IEEE “Image Quality Assessment: From Error Visibility to Structural Similarity”.
- ❖ [3] Christian Ledig, Lucas Theis, Ferenc Huszar, Jose Caballero, Andrew Cunningham, Alejandro Acosta, Andrew Aitken, Alykhan Tejani, Johannes Totz, Zehan Wang, Wenzhe Shi “Photo-Realistic Single Image Super-Resolution Using a Generative Adversarial Network” (2017).
- ❖ [4] Wenzhe Shi¹, Jose Caballero¹, Ferenc Huszar, Johannes Totz¹, Andrew P. Aitken¹, Rob Bishop¹, Daniel Rueckert¹, Zehan Wang¹ “Real-Time Single Image and Video Super-Resolution Using an Efficient Sub-Pixel Convolutional Neural Network” (2016)

