Medical Image Super Resolution

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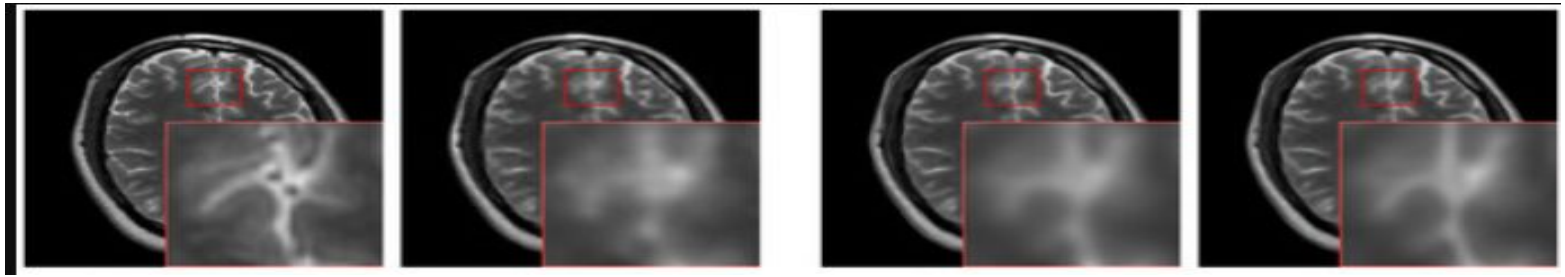
Introduction

- 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)

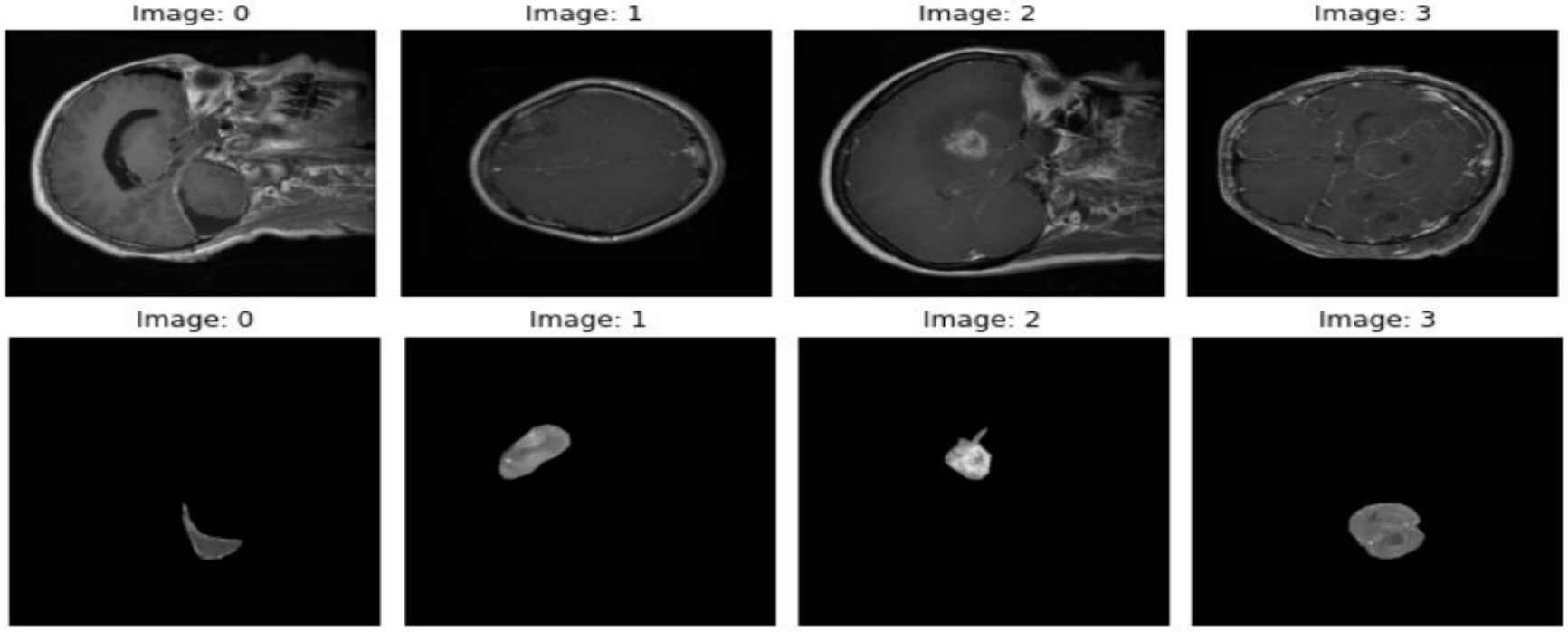
Implementations (Before Last Presentation)

- 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**

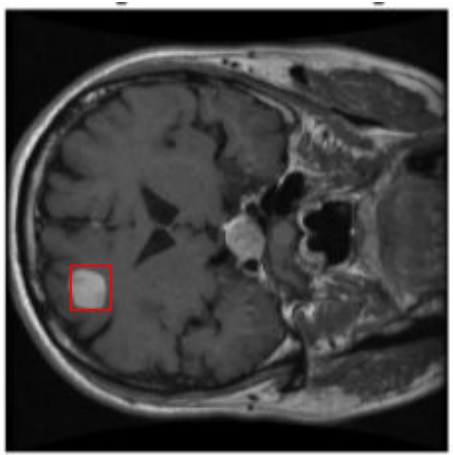
Progress Work

- Brain tumor dataset obtained from figshare. 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

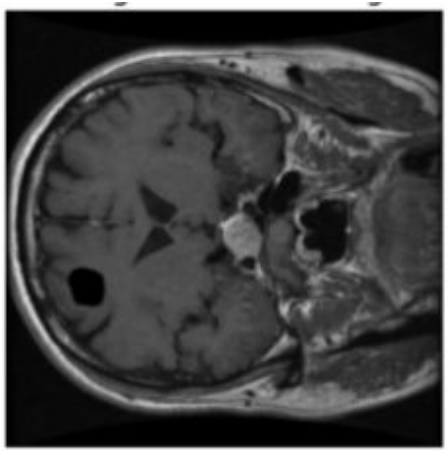


What we are trying to achieve?



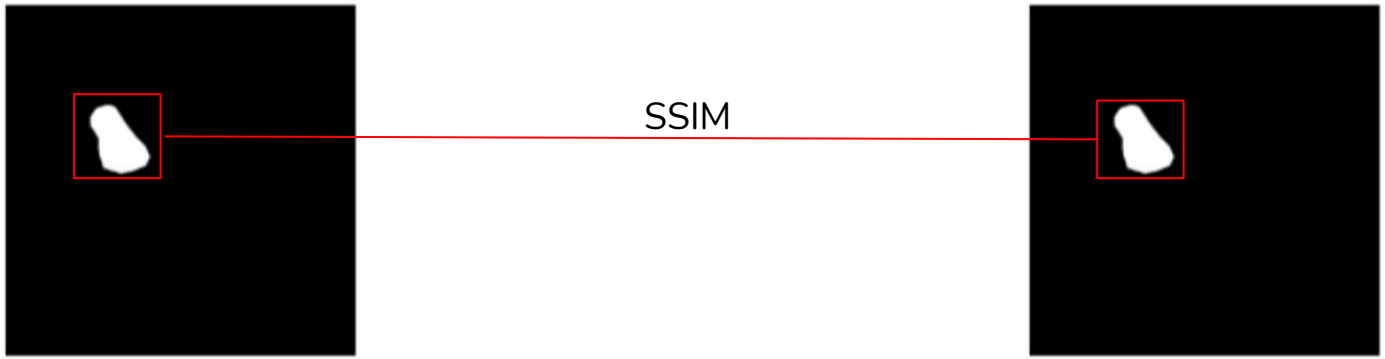
Brain Image

Tumor



Only Brain Region

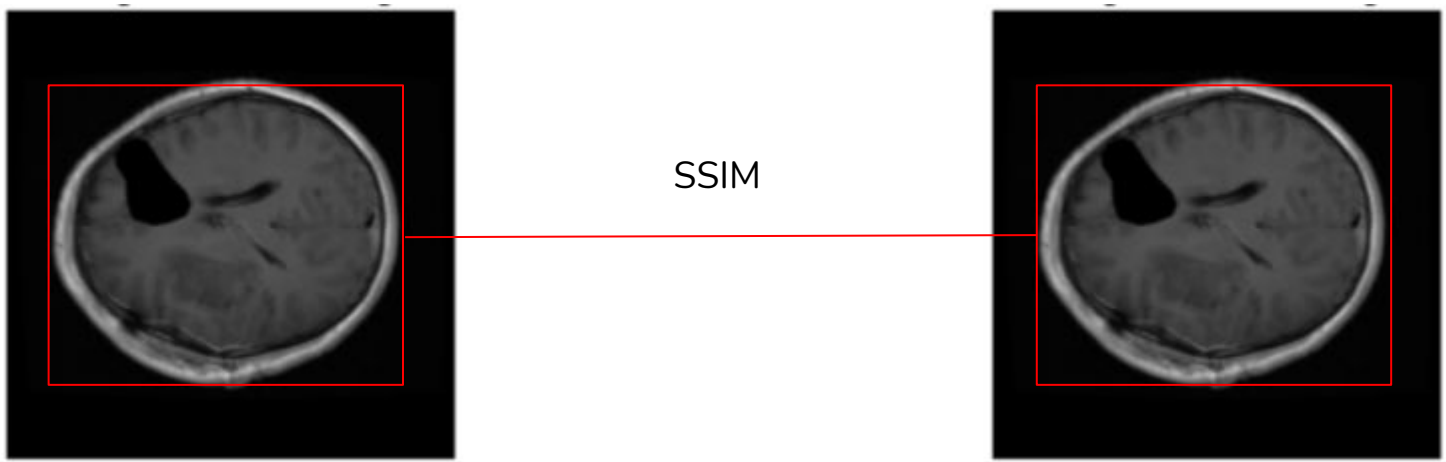
What we are trying to achieve?



Original Image Tumor Region

HR Image Tumor Region

What we are trying to achieve?

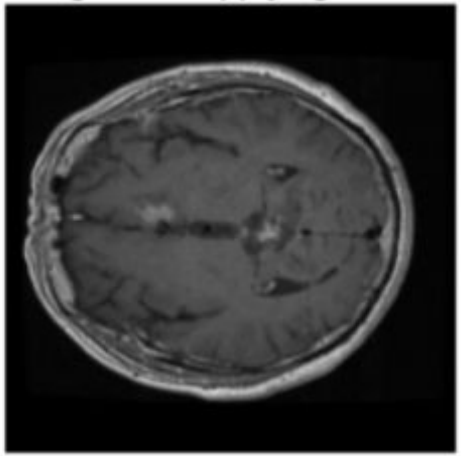


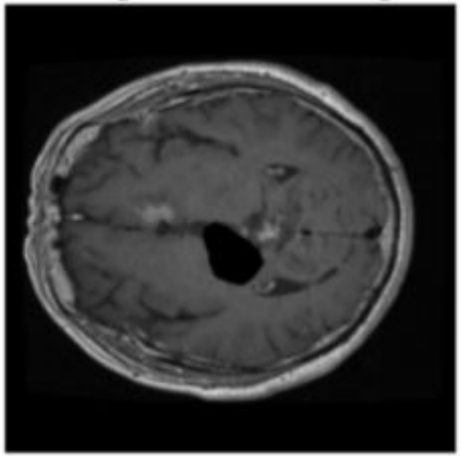
Original Image Brain Region

HR Image Brain Region

How did I achieve it?

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,

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

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

where xi is the ith 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 C1 is a constant to ensure stability when the denominator becomes 0. C1 is given by,

$$C_1 = (K_1 L)^2$$

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,

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

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 mu 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 C2 is given by,

$$C_2 = (K_2 L)^2$$

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 σ(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)

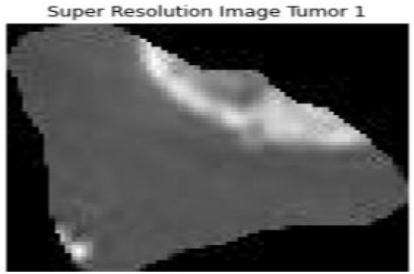
- Finally, SSIM score is given by,

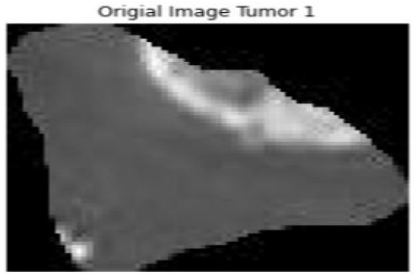
$$\mathrm{SSIM}(\mathbf{x},\mathbf{y}) = [l(\mathbf{x},\mathbf{y})]^{\alpha} \cdot [c(\mathbf{x},\mathbf{y})]^{\beta} \cdot [s(\mathbf{x},\mathbf{y})]^{\gamma}$$

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 C3 = C2/2, we can get,

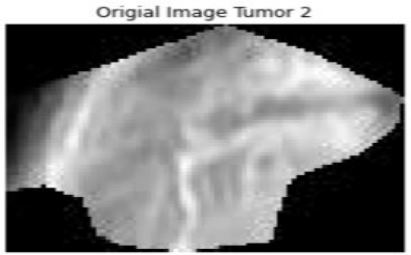
$$\mathrm{SSIM}(\mathbf{x},\mathbf{y}) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_2)}{\left(\mu_x^2 + \mu_y^2 + C_1\right)\left(\sigma_x^2 + \sigma_y^2 + C_2\right)}.$$

SSIM Results for Tumor Region





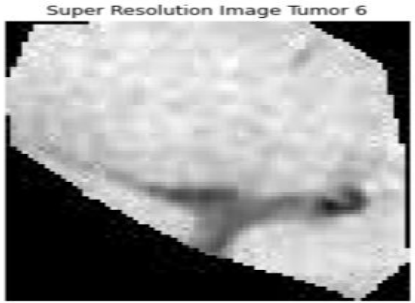
SSIM 0.961471018306179

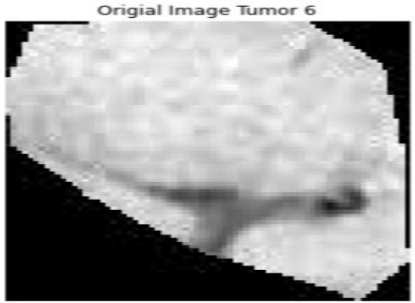


SSIM 0.9060500579130395

SSIM Results for Tumor Region

SSIM 0.8736712943010898

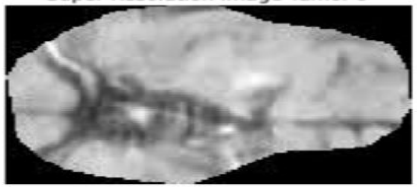




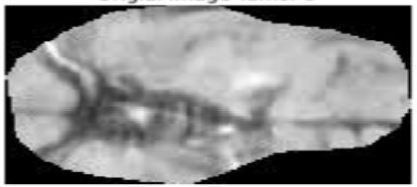
SSIM 0.8724159347023605

SSIM Results for Tumor Region

Super Resolution Image Tumor 9



Origial Image Tumor 9



SSIM 0.9015596438558307

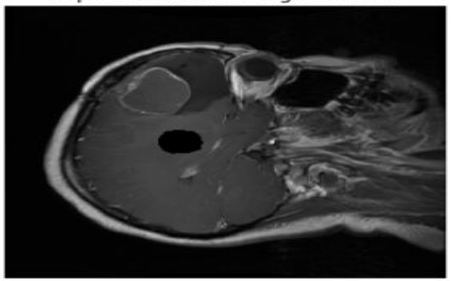
Super Resolution Image Tumor 10

Origial Image Tumor 10

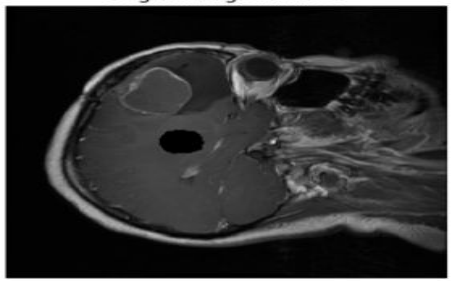
SSIM 0.8829544493765127

SSIM Results for Brain Region

Super Resolution Image Tumor 1

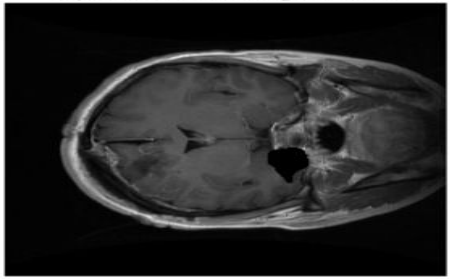


Origial Image Tumor 1

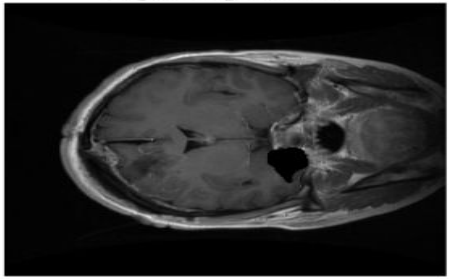


SSIM 0.9918605406208175

Super Resolution Image Tumor 2

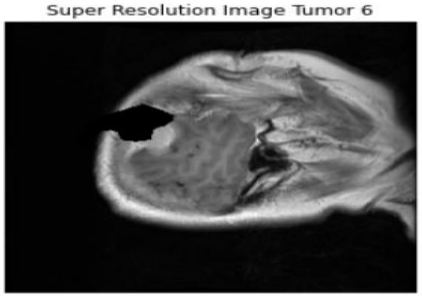


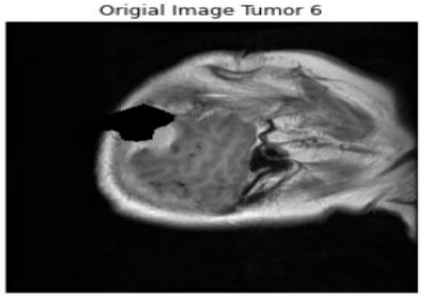
Origial Image Tumor 2



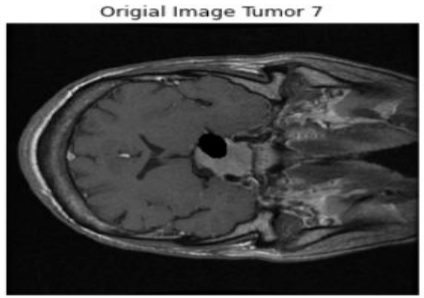
SSIM 0.9898840710782558

SSIM Results for Brain Region



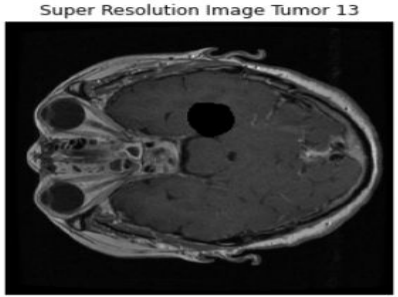


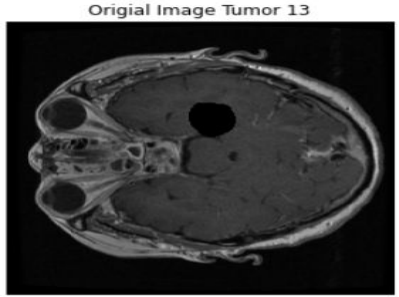
SSIM 0.9823550091213183



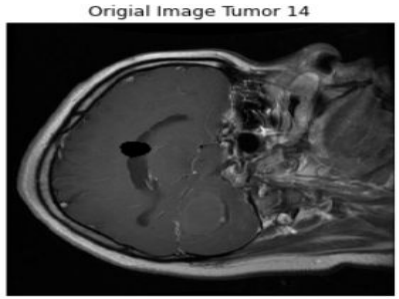
SSIM 0.9882826763831886

SSIM Results for Brain Region





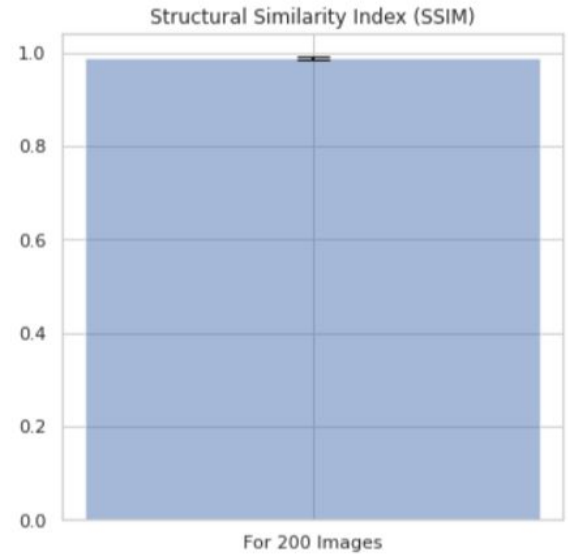
SSIM 0.9902937508190963



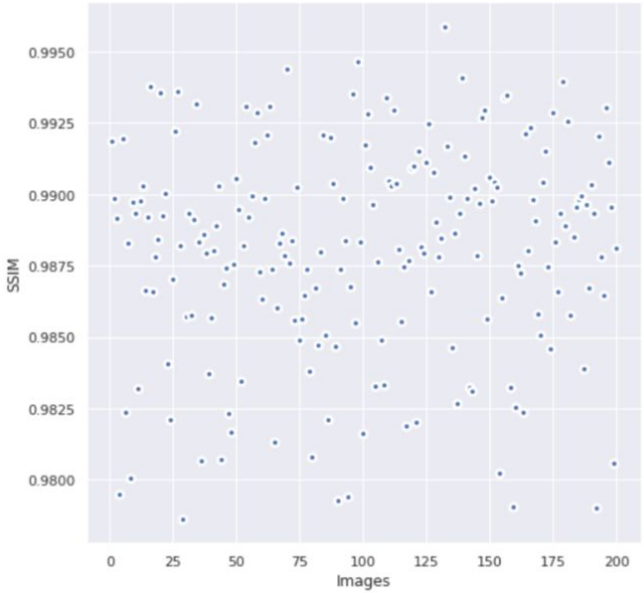
SSIM 0.9866380114324615

SSIM Metric Plots (Brain Region)

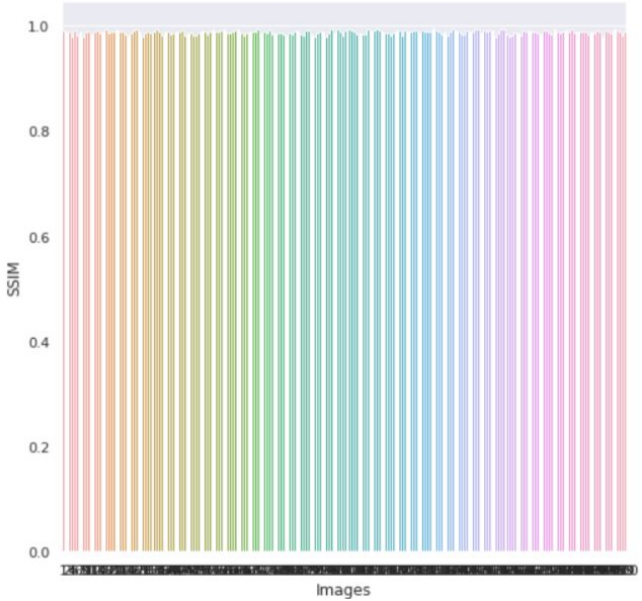
Error Barplot



Scatter Plot

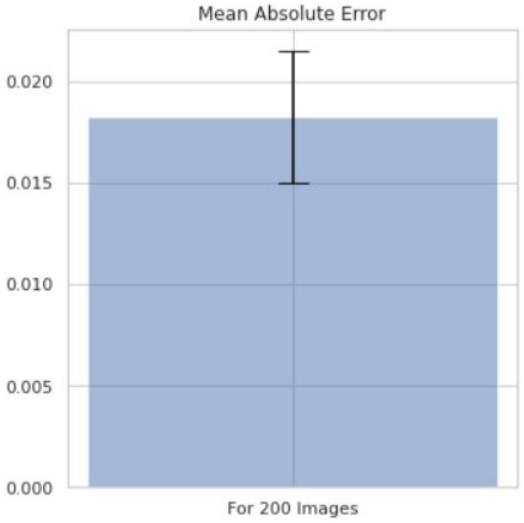


Barplot

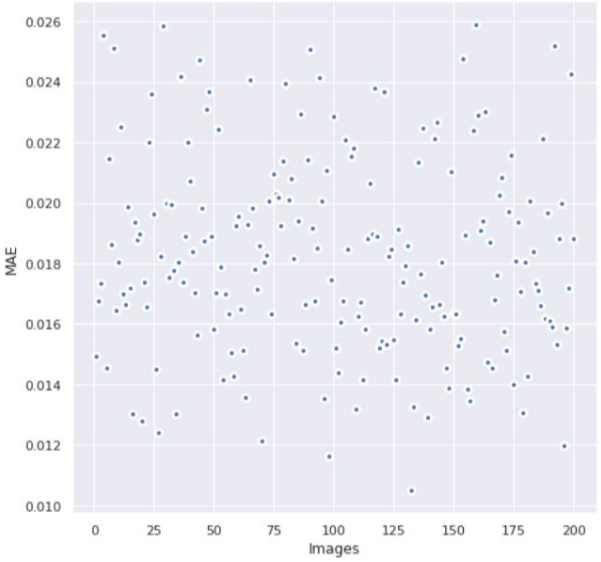


Mean Absolute Error (MAE) Metric Plots (Brain Region)

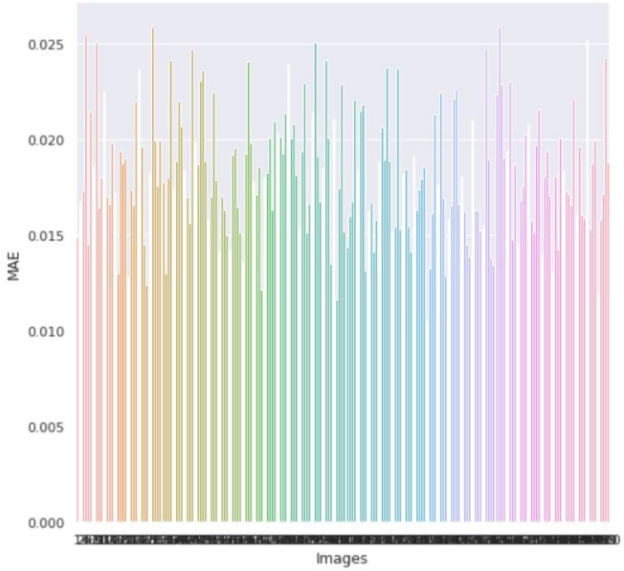
Error Barplot



Scatter Plot

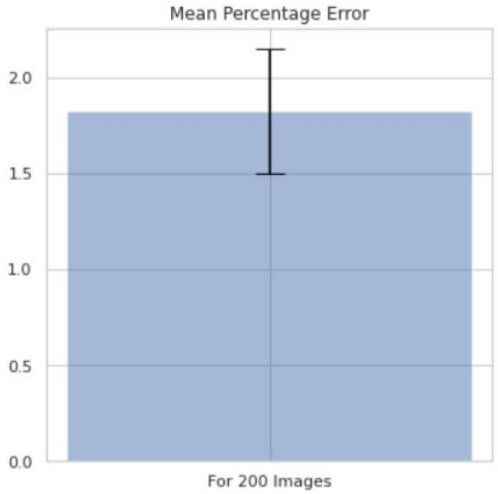


Barplot

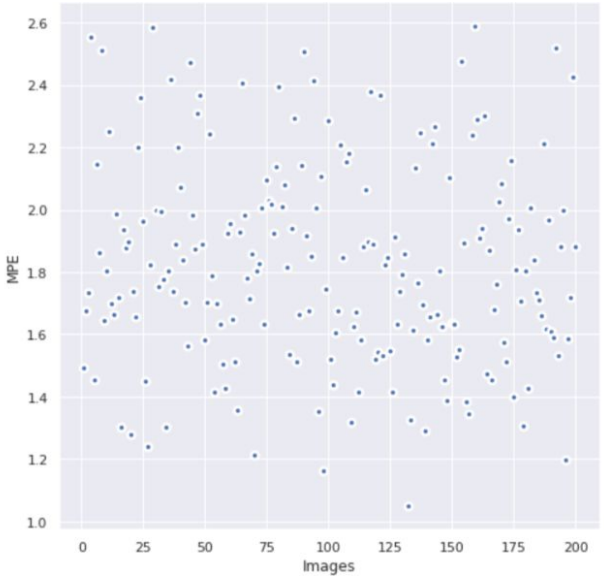


Mean Percentage Error (MPE) Metric Plots (Brain Region)

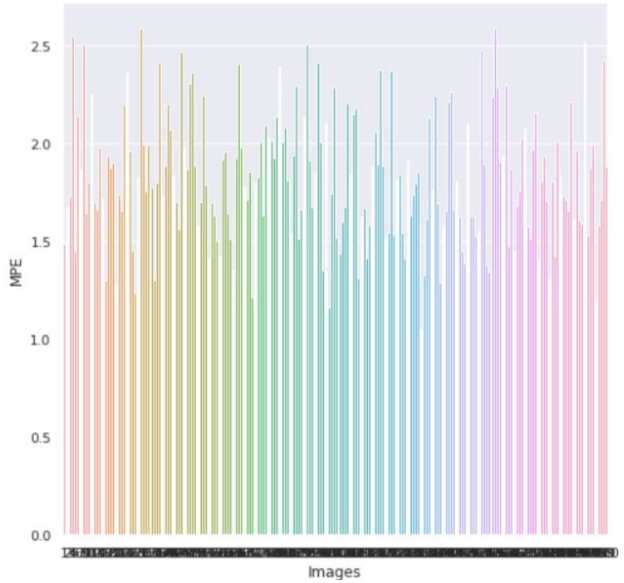
Error Barplot



Scatter Plot



Barplot



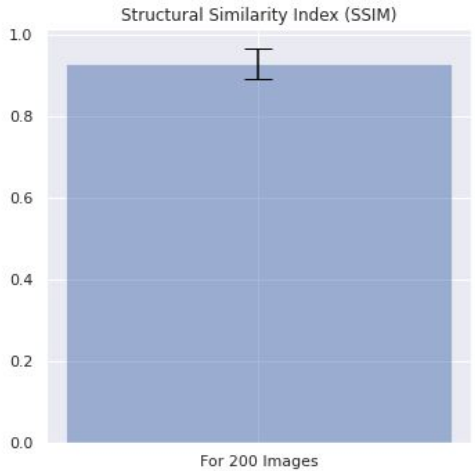
Brain Tissue Metric Table

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

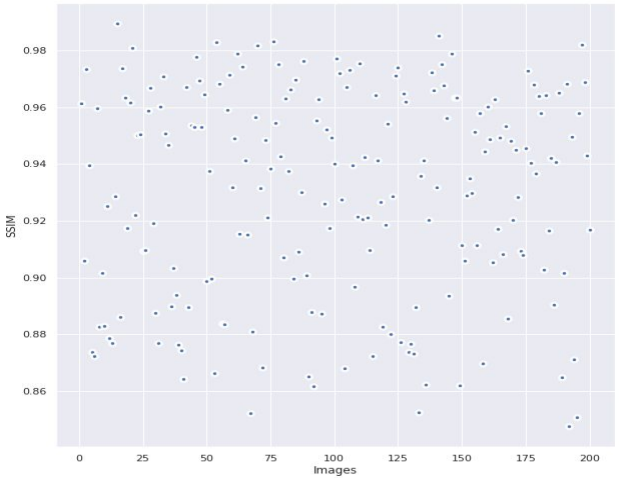
	Mean	Standard Deviation
SSIM	0.9880	0.0037
MAE	0.0182	0.0032
MPE	1.8237	0.3246

SSIM Metric Plots (Tumor Region)

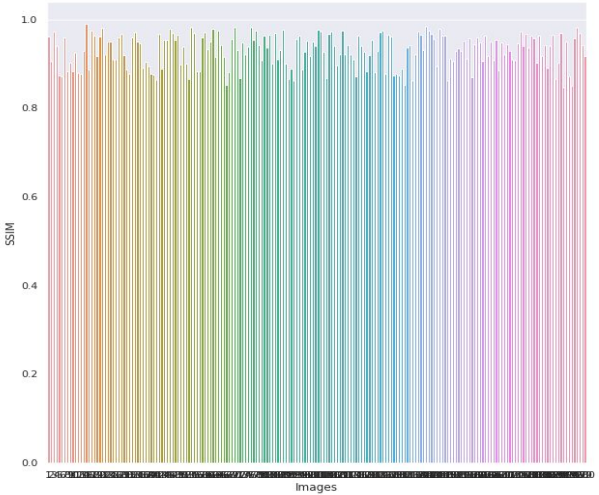
Error Barplot



Scatter Plot

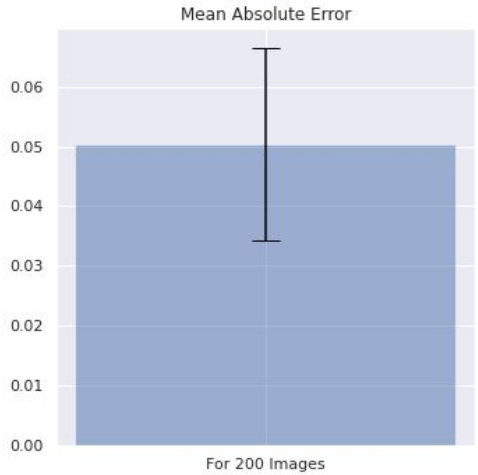


Barplot

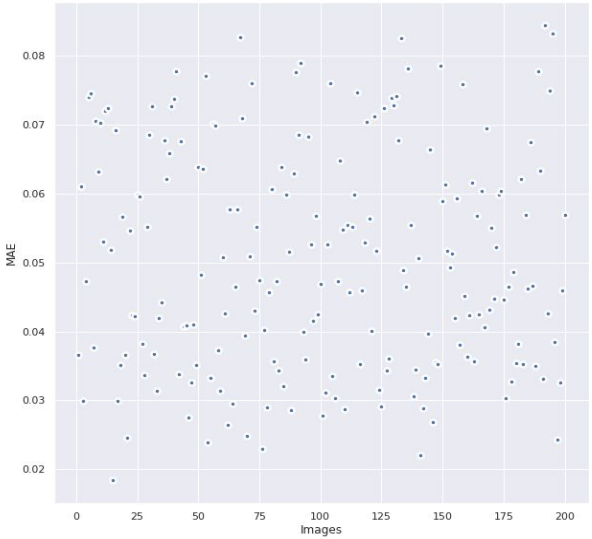


Mean Absolute Error (MAE) Metric Plots (Tumor Region)

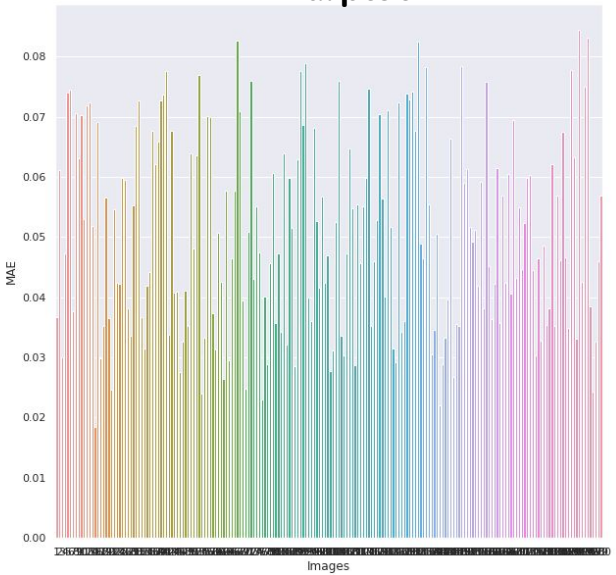
Error Barplot



Scatter Plot

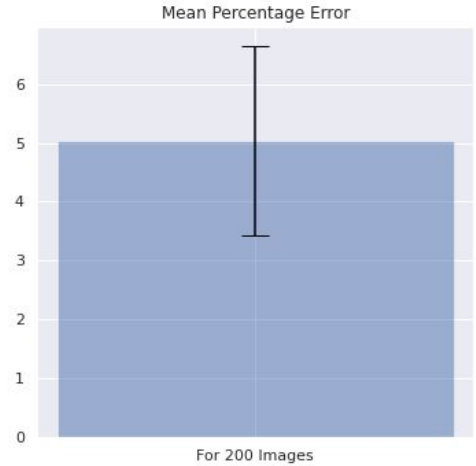


Barplot

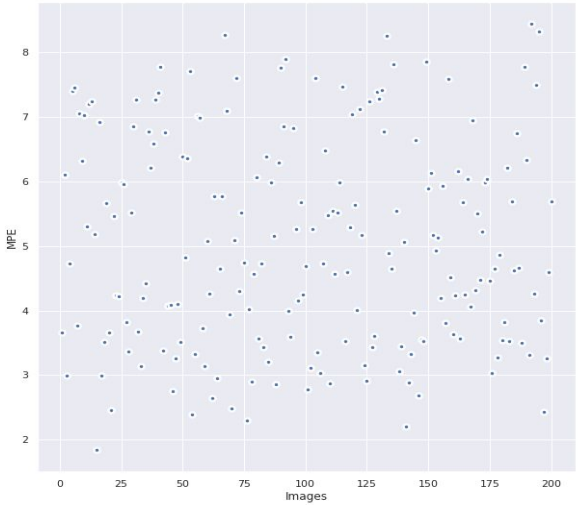


Mean Percentage Error (MPE) Metric Plots (Tumor Region)

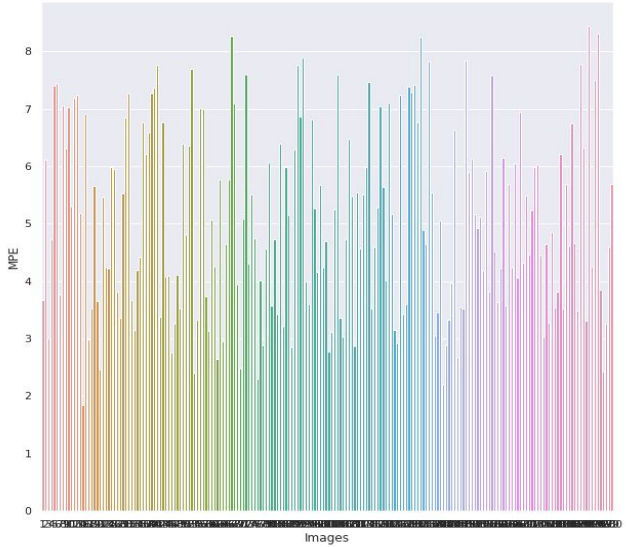
Error Barplot



Scatter Plot



Barplot



Tumor Metric Table

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

	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 [1].
- 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.

References

- [1] 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”.

THANK YOU :)