AE-FLOW: Autoencoders with Normalizing Flows for Medical Images Anomaly Detection

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**Eleventh International Conference on Learning Representations
May, 2023**

ICLR

Normalizing Flow and Anomaly Detection

NF is to utilize a series of invertible modules to transform the data from an unknown distribution to the standard Gaussian distribution.

■ For a invertiable f and $y = f(x)$,

$$p_x(x) = p_y(f(x)) * |detJf(x)|,$$

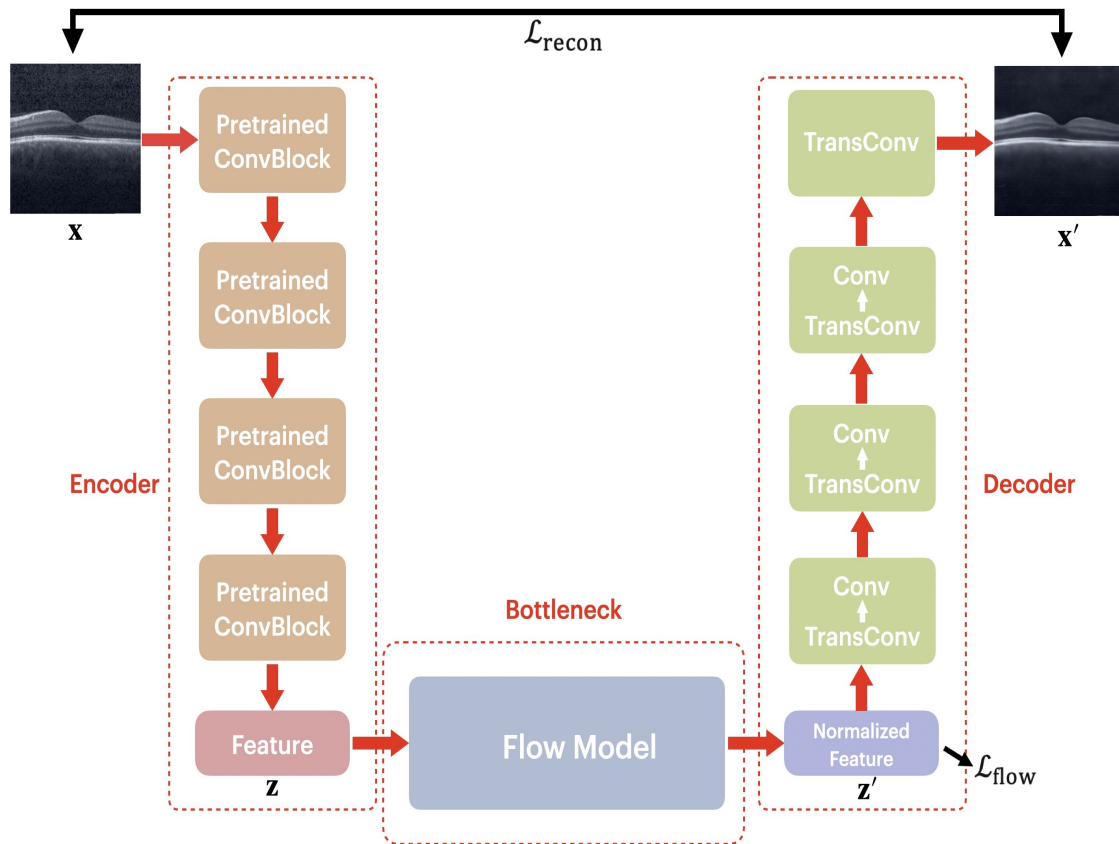$$p_y(y) = p_x(f^{-1}(y)) * |detJf^{-1}(y)|$$

■ Normalizing flow structure
- NICE: Additive coupling layer
- RealNVP: Affine Coupling layers
- GLOW

■ Normal images: adquate
■ Abnormal images: few

We propose to construct a loss function and anomaly score function by an auto-encoder with the normalizing flow bottleneck, namely AE-FLOW.

Proposed Method

Encoder: Pretrained

- $f : \mathbb{X} \to \mathbb{Z}$ i.e. $f : \mathbf{x} \in \mathbb{R}^{3 \times H \times W} \to \mathbf{z} \in \mathbb{R}^{C \times \frac{H}{16} \times \frac{W}{16}}$
- $\mathbf{x}$ is the image and $\mathbf{z}$ is feature
- H and W are the height and width of the original image
- C is the number of channels.

Normalizing flow bottleneck

- $\Phi : \mathbb{Z} \to \mathbb{Z}'$ to transform $\mathbf{z}$ to the feature space $\mathbf{z}' \sim \mathcal{N}(\mathbf{z}' ; 0, I)$

Decoder

- $g : \mathbb{Z}' \to \mathbb{X}'$ i.e. $g : \mathbf{z} \in \mathbb{Z}^{C \times \frac{H}{16} \times \frac{W}{16}} \to \mathbf{x}' \in \mathbb{R}^{3 \times H \times W}$
- $\mathbf{x}'$ is the reconstructed image.

Normalizing flow bottleneck: GLOW

Denote the input as $\mathbf{x}$ and the output as $\mathbf{y}$ at each flow block, flow is formulated as:

$$\mathbf{y} = \boldsymbol{R}\left(\boldsymbol{\Psi}\left(\mathbf{s}_{\text{global}}\right) \odot \text{ Coupling }(\mathbf{x}) + \mathbf{t}_{\text{global}}\right)$$

- $\boldsymbol{R}$ is a 1×1 invertible convolution that reverses the ordering of the channels.
- $\boldsymbol{\Psi}(\cdot)$ is the Softplus activation function $\frac{1}{\beta} * \log(1 + \exp(\beta * \cdot))$ with $\beta = 0.5$.
- $\mathbf{s}_{\text{global}}$ and $\mathbf{t}_{\text{global}}$ are learning parameters.
- $\odot$ is point-wise product.

Split $\mathbf{x}$ into two compositions $(\mathbf{x}_1, \mathbf{x}_2)^\top$, then $\mathbf{u} = (\mathbf{u}_1, \mathbf{u}_2)^\top := \text{ Coupling }(\mathbf{x})$

$$\mathbf{u}_1 = \mathbf{x}_1 \odot \exp\left(2 \tanh\left(\mathbf{s}\left(\mathbf{x}_2\right)\right)\right) + \mathbf{t}\left(\mathbf{x}_2\right)$$

$$\mathbf{u}_2 = \mathbf{x}_2$$

- $\mathbf{s}\left(\mathbf{x}_2\right)$ and $\mathbf{t}\left(\mathbf{x}_2\right)$ represents the scale and bias. $\mathbf{s}(\mathbf{x}_2), \mathbf{t}(\mathbf{x}_2) = \text{NN}(\mathbf{x}_2)$.
- NN is two convolutional layers or ResNets.

Loss Function and Anomaly Score

■ **Loss Function:** $\mathcal{L} = \alpha * \mathcal{L}_{\text{flow}} + (1 - \alpha) * \mathcal{L}_{\text{recon}}$

- ■ α is weight
- ■ Negative logarithm probability likelihood loss: $\mathcal{L}_{\text{flow}} = -\log p_{\mathbb{Z}}(\mathbf{z}) = -\log p_{\mathbb{Z}'}(\mathbf{z}') - \log \left| \det \dfrac{\partial \mathbf{z}'}{\partial \mathbf{z}} \right|$

- ■ Reconstruction loss: $\mathcal{L}_{\text{recon}} = \text{MSE}(\mathbf{x}, \mathbf{x}') = \dfrac{1}{N^2} \sum_{i=1}^{N} \sum_{j=1}^{N} (\mathbf{x}_{i,j} - \mathbf{x}'_{i,j})^2.$

■ **Anomaly Score:** $\mathcal{S} = \beta * \mathcal{S}_{\text{flow}} + (1 - \beta) * \mathcal{S}_{\text{recon}}$

- ■ β is weight
- ■ The negative probability density: $\mathcal{S}_{\text{flow}} = -p_{\mathbb{Z}'}(\mathbf{z}').$
- ■ SSIM Score： $\mathcal{S}_{\text{recon}} = -\text{SSIM}(\mathbf{x}, \mathbf{x}').$

Numerical Results: Medical Image DataSet

- **OCT**
  - Training: 26, 315 normal images
  - Testing : 242 normal images and abnormal image (drusen, CNV and DME) with each category has 242
  Images
- **Chest X-ray**
  - Training: 1, 349 normal images
  - Testing: 234 normal images and 390 abnormal images(pneumonia)
- **ISIC2018**
  - Training: 6705 normal images
  - Testing: 123 normal images and 70 abnormal images
  - Seven categories and NV (nevus) category as normal samples.
- **BraTS2021** (Brain Tumor Segmentation (BraTS) Challenge 2021 dataset)
 - 3D multimodal magnetic resonance imaging (MRI)
  - Training: 11, 739 2D healthy slices
  - Testing: 1, 051 slices with tumors and 459 slices without tumors

Quantitative Comparison

Dataset	OCT (%)					Chest X-ray (%)				
Metric	AUC	F1	ACC	SEN	SPE	AUC	F1	ACC	SEN	SPE
Autoencoder	83.02	88.64	82.13	92.29	51.65	81.02	81.63	73.08	94.87	36.75
f-AnoGAN	85.09	86.70	79.24	89.67	47.93	71.44	79.96	69.39	**96.92**	23.50
GANomaly	90.52	91.09	86.16	93.53	64.05	76.14	81.18	74.36	87.69	52.14
DifferNet	94.27	92.85	89.05	93.80	74.79	86.41	84.62	79.17	90.77	59.83
Fastflow	94.08	92.60	88.43	95.45	67.36	90.25	86.02	80.77	93.59	59.40
Ours	**98.15**	**96.36**	**94.42**	**96.56**	**88.02**	**92.00**	**88.92**	**85.58**	91.28	**76.07**
Dataset	ISIC2018 (%)					BraTS2021 (%)				
Metric	AUC	F1	ACC	SEN	SPE	AUC	F1	ACC	SEN	SPE
Autoencoder	73.97	62.57	64.77	78.57	56.91	70.38	82.47	70.79	**98.38**	07.63
f-AnoGAN	79.80	67.03	68.39	85.71	58.54	78.06	84.89	76.42	94.77	34.42
GANomaly	72.54	60.95	56.99	**90.00**	38.21	74.50	82.33	70.86	97.24	10.46
DifferNet	76.52	64.58	64.25	87.14	51.22	78.94	83.78	74.70	93.53	31.59
Fastflow	80.81	69.95	70.98	**90.00**	60.16	80.94	85.37	78.21	90.96	**49.02**
Ours	**87.79**	**80.56**	**84.97**	81.43	**86.99**	**81.58**	**86.06**	**78.74**	93.91	44.01

Table: Quantitative comparison for different methods.

AUC Curves
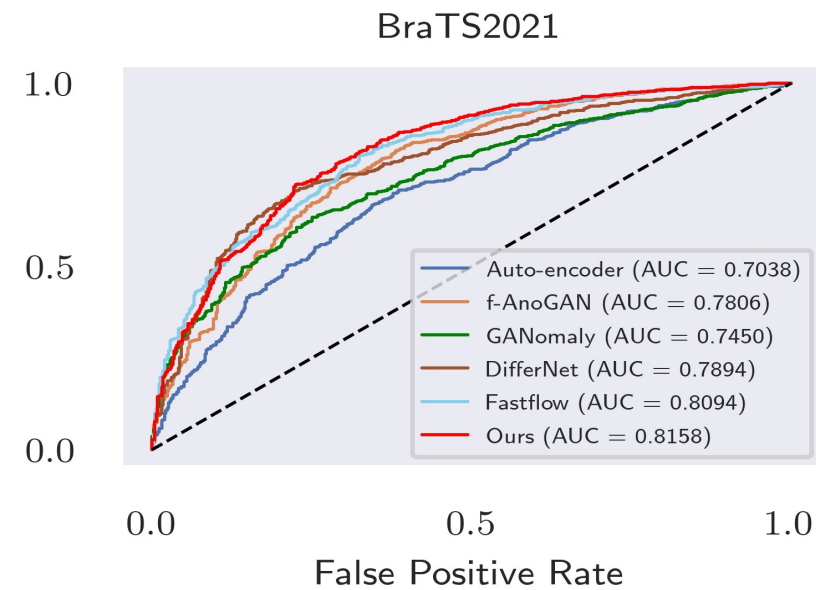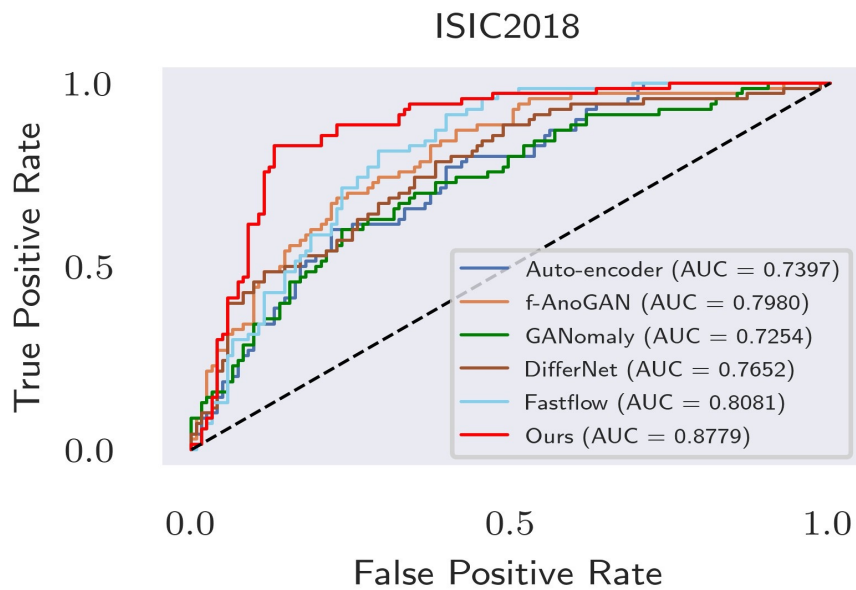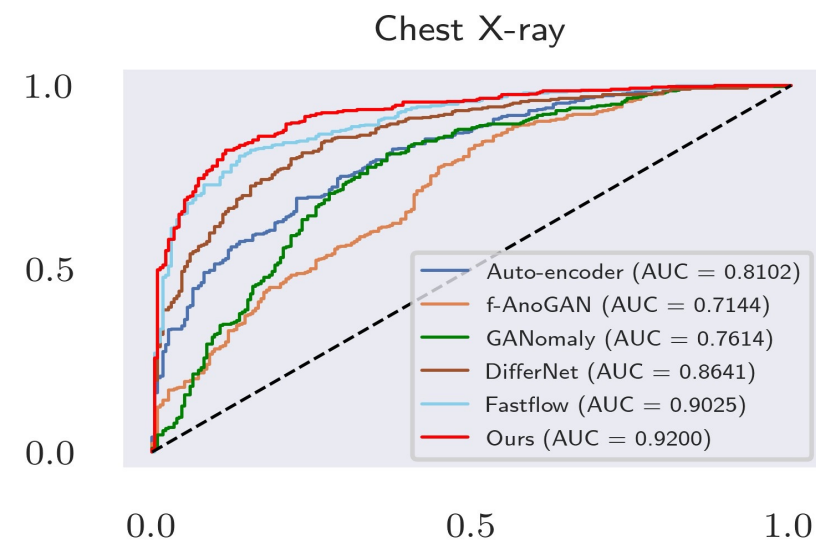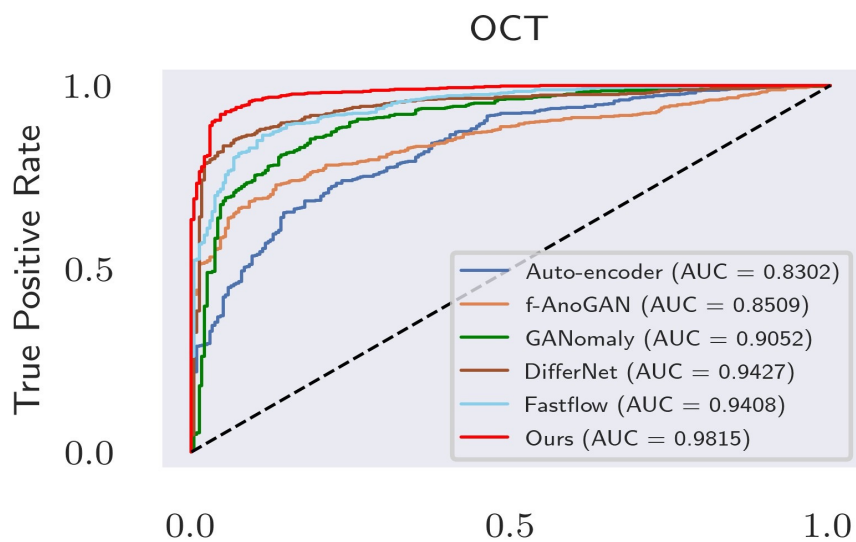
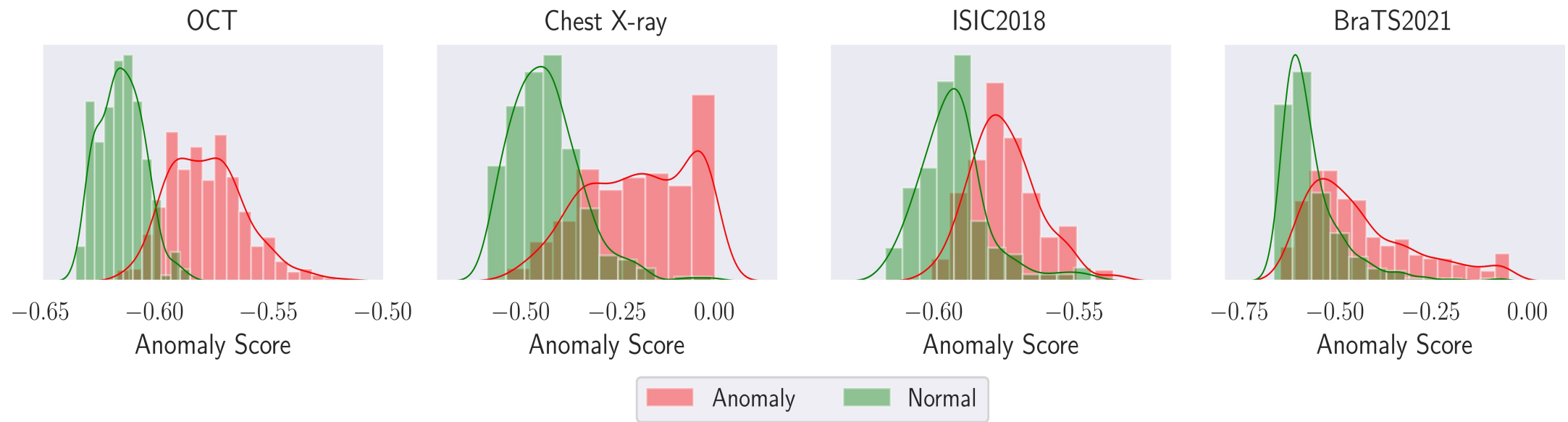# Distribution Curves of the Anomaly Score

Figure: Distribution curves of the anomaly score of the anomaly and normal data.

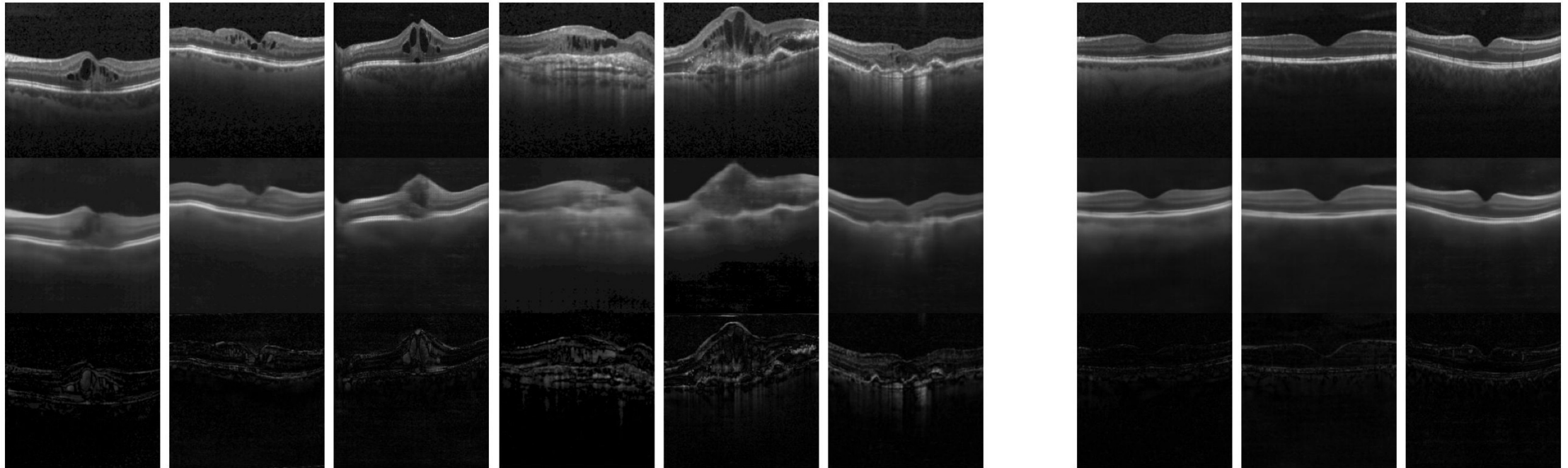# Visual Results: OCT

Abnormal **Normal**

Figure: The comparison of normal and abnormal samples from the OCT dataset. For each sample, we show the original, reconstructed and residual images from top to bottom respectively.

Visual Results: Chest X-ray
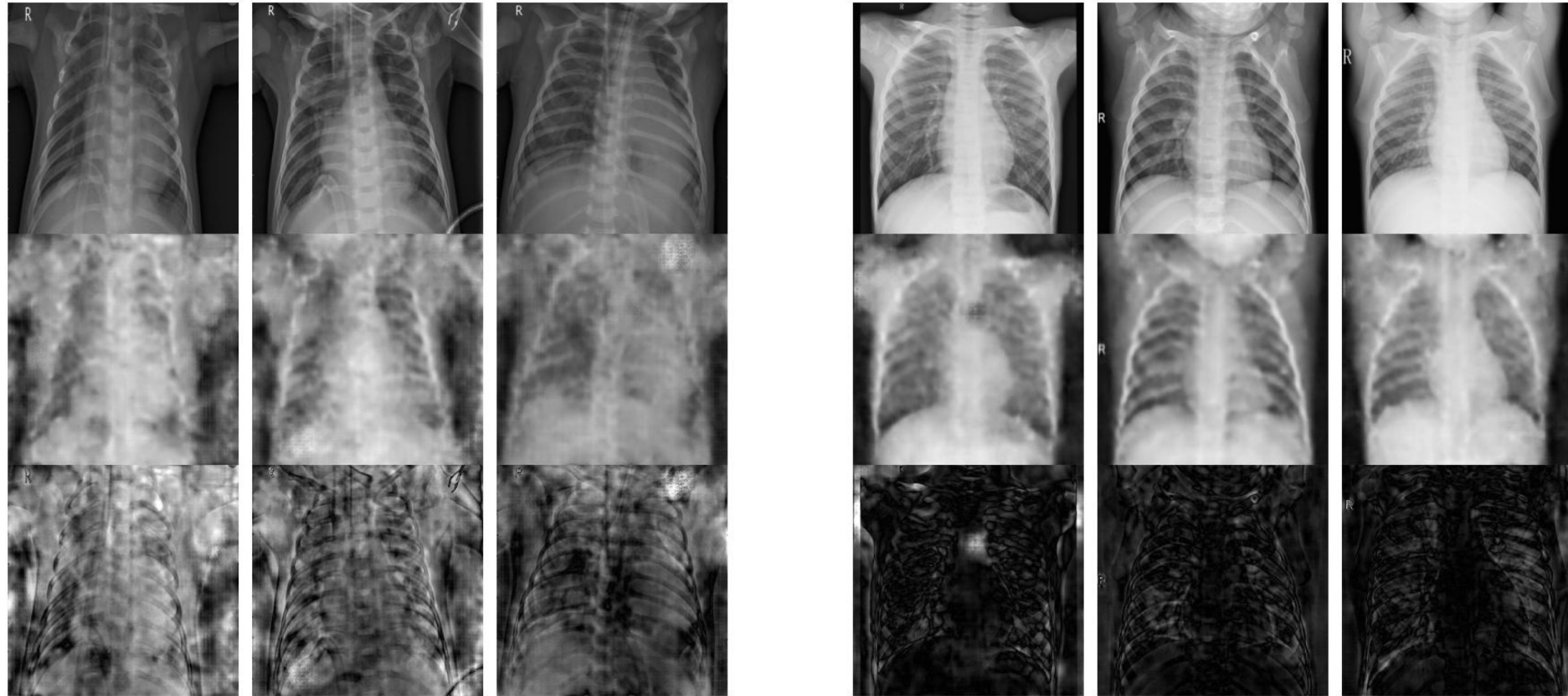
Abnormal   **Normal**

Figure: The comparison of the original, reconstructed and residual images (from top to bottom) of normal and abnormal samples from the Chest X-ray dataset.
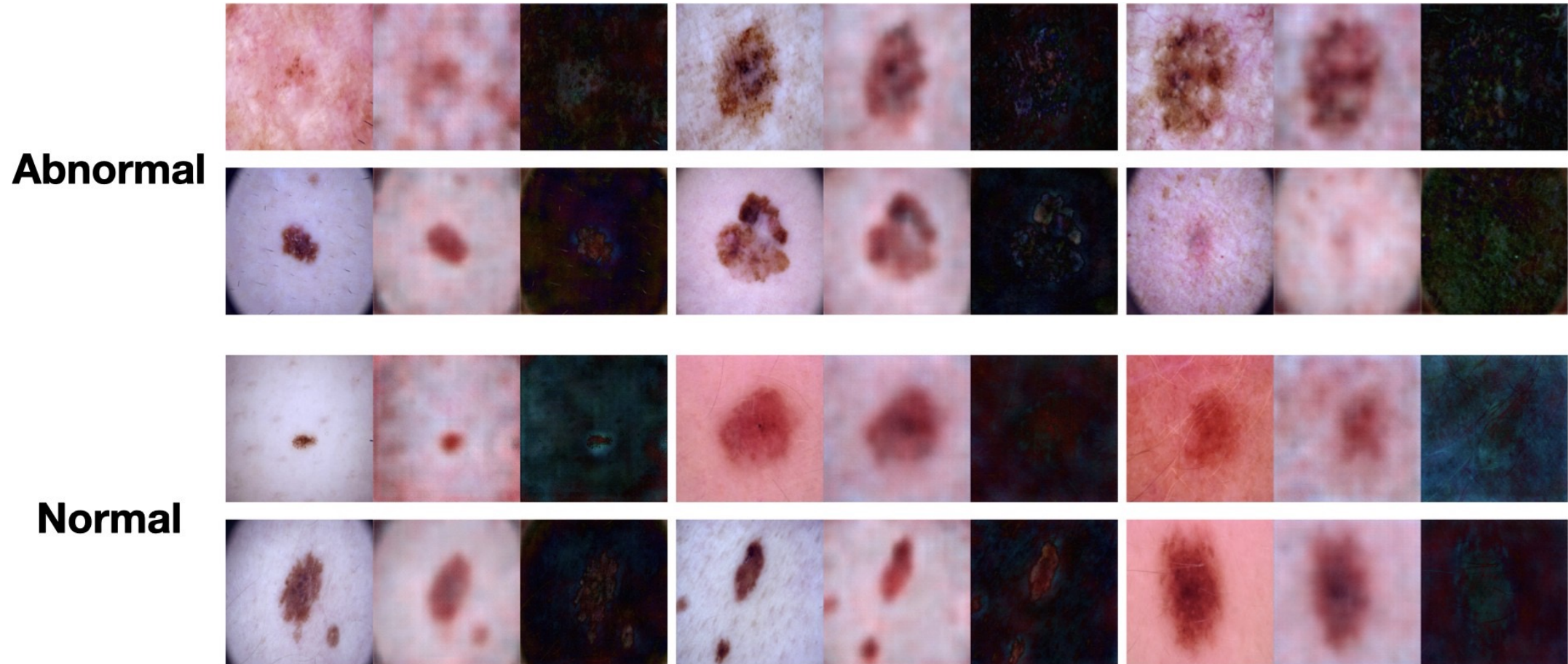
Visual Results: ISIC

Figure: The comparison of normal and abnormal samples from the ISIC2018 dataset.
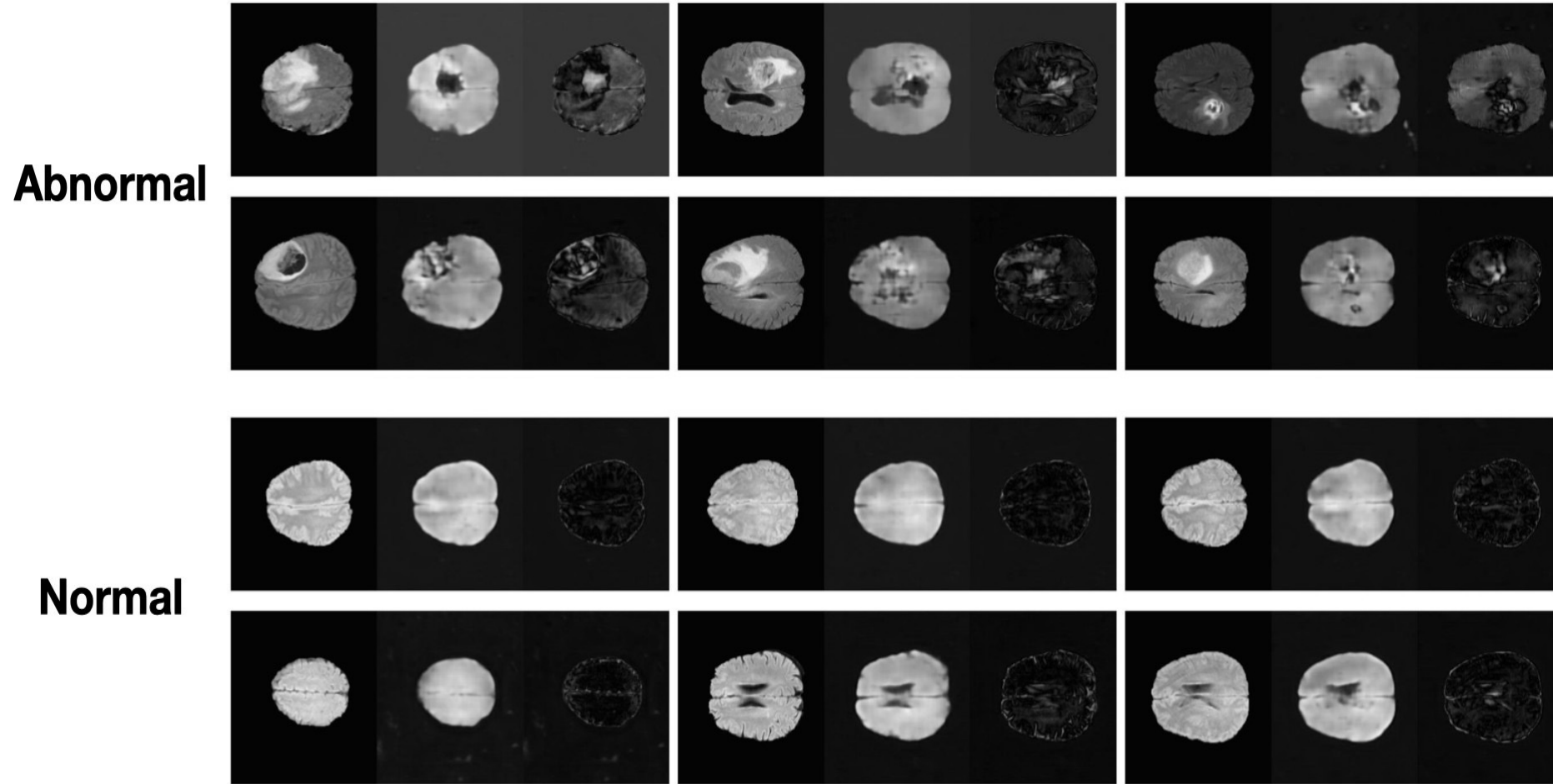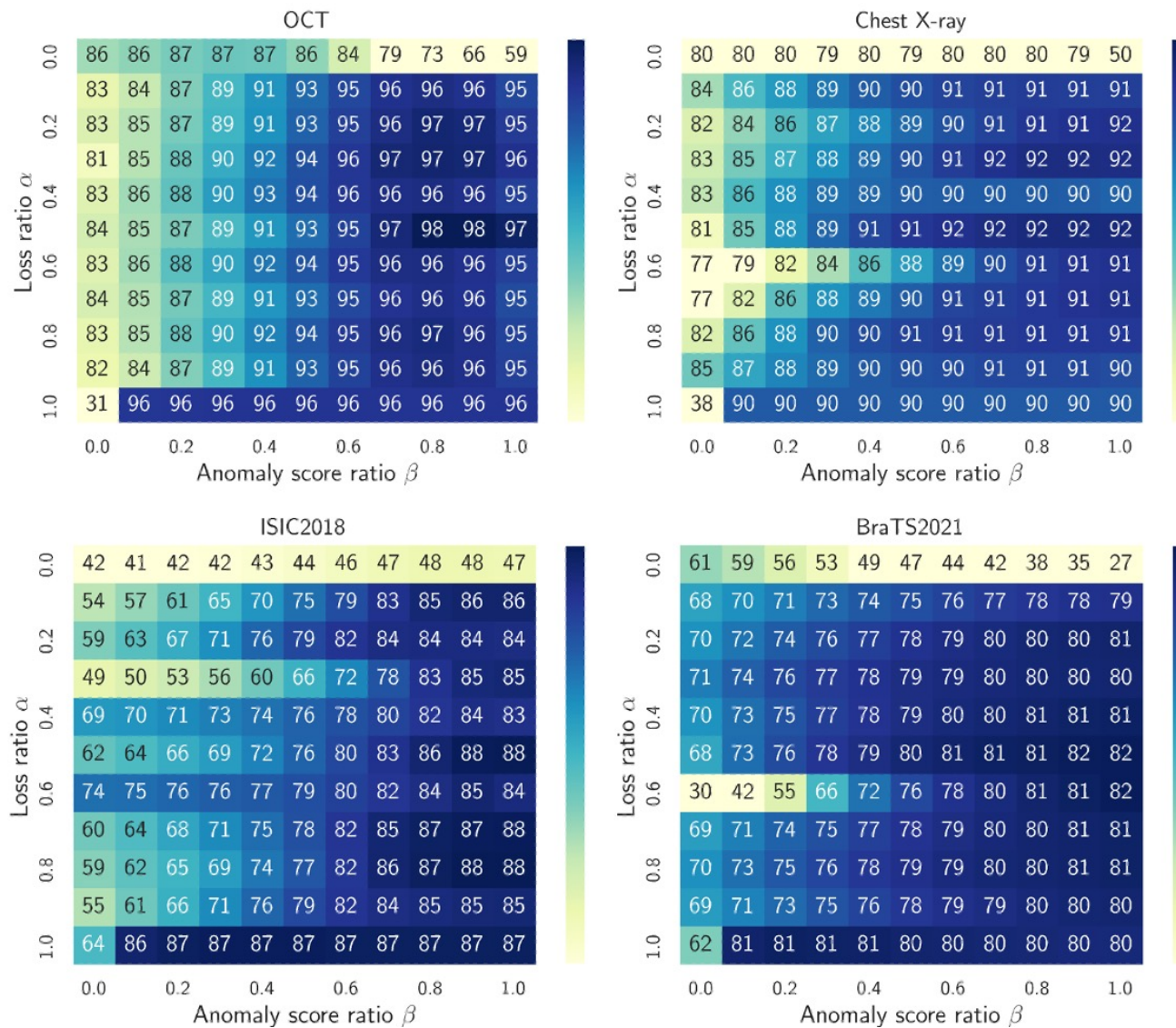
Visual Results: BraTS

Figure: The comparison of normal and abnormal samples from the BraTS2021 dataset.

Parameter selection: α and β

Ablation Study

- Reconstruction Loss: MSE vs. SSIM
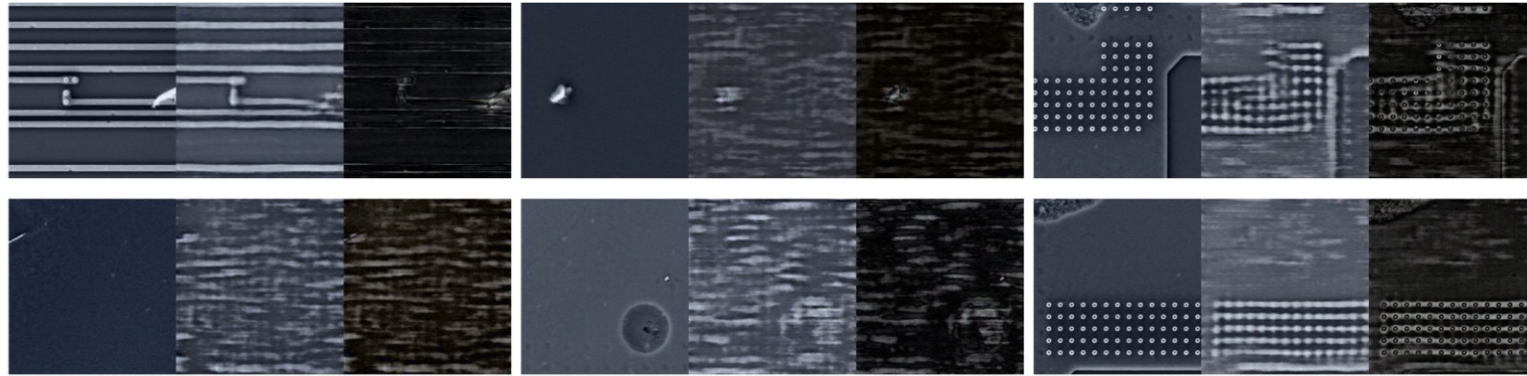- NF subnet architecture: 2-layer CNN vs. ResNets

	OCT (%)		Chest X-ray (%)	
	2-Layer CNN	ResNets	2-Layer CNN	ResNets
MSE	96.43	**98.15**	91.69	89.92
SSIM	94.89	95.31	**92.00**	90.47
	ISIC2018 (%)		BraTS2021 (%)	
	2-Layer CNN	ResNets	2-Layer CNN	ResNets
MSE	81.19	**87.79**	81.55	**81.58**
SSIM	81.22	87.09	78.95	80.33

Table: AUC Comparison under different types of reconstruction loss and NF subnet architecture.

Other Application: MIIC

The MIIC dataset: real microscopic images of integrated circuits (ICs), 23,888 normal images for training, and $1,272$ normal and 116 abnormal images for testing.

Huang et. al Joint Anomaly Detection and Inpainting for Microscopy Images via Deep Self-Supervised Learning, IEEE International Conference on Image processing (ICIP)

Quantitative Comparison of MIIC

Method	AUC	F1	TPR	FPR
f-anoGAN	56.38	31.65	18.96	00.08
GANomaly	93.34	74.64	67.24	01.18
Proposed in Huang IEEE ICIP	97.28	83.48	78.45	00.86
Ours	**98.69**	**89.62**	**81.03**	**00.07**

Summary and Future work

■ Summary:

- We proposed a AE-Flow Model for Different modality medical image anomaly detection.
- Identify the abnormality and provide an interpretability at both image and pixel levels.

■ Future work:

- 3D PET image Anomaly Detection
- Multiple Lesion Segmentation: small lesion, unbalance dataset.

Thanks for your attention!

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